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November 9, 2005, 11:43:32; Search time 74.6015 Seconds (without alignments) 627.306 Million cell updates/sec
                                                                                                                                                                                                                                                 1 QVQLQESGPGLVKPSETLSL......WLLPDAFDIWGQGTMVTVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                       2105692
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                           2105692 segs, 386760381 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
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649
                                                                                                                                                                                                          Title:
Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2003as:* geneseqp2003bs:*

geneseqp20048:*

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:*

SUMMARIES

		d			SUMMARIES		
Result No.	Score	Query Match	Query Match Length DB	DB	ΩΙ	Description	
-	0 7 7	000	121		**************************************	11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	7 - 1 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2
4 0	7 7	200	777	٠ ،	ADC33772		-1101119
N	649	100.0	121	-	ADC99788	-	Anti-huma
m	649	100.0	121	7	ADD05376	Add05376 Anti	Anti-MUC1
4	649	100.0	121	7	ADD05392	Add05392 Anti	Anti-MUC1
ហ	649	100.0	121	7	ADF09814	Adf09814 Huma	Human ant
9	649	100.0	121	7	ADF09830	Adf09830 Huma	Human ant
7	643	99.1	121	7	ADC99780	Adc99780 Anti	Anti-huma
œ	643	99.1	121	7	ADD05384	Add05384 Anti	Anti-MUC1
6	643	99.1	121	7	ADF09822	Adf09822 Huma	Human ant
10	597	92.0	121	2	ADC99808	Adc99808 Anti	Anti-huma
11	597	92.0	121	7	ADD05412	Add05412 Anti	Anti-MUC1
12	597	92.0	121	7	ADF09850	Adf09850 Huma	Human ant
13	565.5	87.1	243	œ	AD058076	Ado58076 S9 c	S9 cell d
14	547	84.3	121	ហ	ABG92884		Human imm
15	545.5	84.1	121	ហ	ABB07171	Abb07171 ebvH	ebvHigM M
16	545.5	84.1	121	8	ADI26658	Adi26658 Huma	Human ant
17	545.5	84.1	122	7	ADP03887	Adp03887 Muri	Murine-ex
18	545.5	84.1	122	7	ADP03884	_	Murine-ex
6.	544.5	83.9	122	7	ADP03885	_	Murine-ex
	544.5	83.9	122	7	ADP03889	_	Murine-ex
	240	83.2	119	~	AAW27554		Human Ab
	540	83.2	119	9	ABJ18676	-	Antibody
	9	83.1	118	œ	ADP22272	Adp22272 Human	in ant
4	/	83.1	123	9	ADA89258	Ada89258 Human	in ant

120 7 ADP03864 121 7 ADP03864 119 7 ADP03984 119 7 ADP03931 125 7 ADP03931 124 7 ADP03938 124 7 ADP03938 125 7 ADP03986 126 7 ADP03886 127 7 ADP03886 128 8 ADS19313 120 2 AAW90287 126 5 ADP03868 125 7 ADP03868 125 7 ADP03868 125 7 ADP03868 125 7 ADP03876 127 7 ADP03876 128 8 ADP039333	_	Adp03862 Murine-ex	Adp03984 Murine-ex	Adp03973 Murine-ex	Adp03871 Murine-ex	Aay15126 Anti-muri	Adp03933 Murine-ex	Adp03886 Murine-ex	Abp43199 Human ova	Adel9313 Heavy cha	Aaw90287 Human ant	Abg92888 Human imm	Adp03868 Murine-ex	Adp03876 Murine-ex	Abg97827 Human MPL	Abg35304 Thrombopo	Abg97829 Mouse 12E	Abg35331 Thrombopo	Aay06718 Antibody	Ado39737 Human c-m
0010004600000446644	ADP03864	ADP03862	ADP03984	ADP03973	ADP03871	AAY15126	ADP03933	ADP03886	ABP43199	ADS19313	AAW90287	ABG92888	ADP03868	ADP03876	ABG97827	ABG35304	ABG97829	ABG35331	AAY06718	ADO39737
	120 7	0	1 7	7	5 7	9	2 7	4 7	3	8	0	9	5	5 7	4 5	4 5	3	3	4	8
	32.7	32.7	32.7	32.6	32.6	32.5	32.4	32.2	32.2	32.0	31.9	31.9	31.8	31.8	31.6	31.6	31.6	31.6	31.6	31.6
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ALIGNMENTS

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ADC99772 standard; protein; 121

RESULT 1 ADC99772

New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies. anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast; Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 1. 26-DEC-2002; 2002WO-US041581 28-DEC-2001; 2001US-0346299P (first entry) WPI; 2003-587113/55. (ABGE-) ABGENIX INC. lung cancer; human. N-PSDB; ADC99774. WO2003057838-A2 Homo sapiens. 01-JAN-2004 17-JUL-2003. ADC99772; Gudas J;

Claim 1; SEQ ID NO 1; 78pp; English.

a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to WUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of WUC18 on the cell surface such as tumours, specifically melanoma, oesophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithehial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human WUC18 monoclonal antibody The invention relates to a novel isolated monoclonal antibody comprising

Adp03931 Murine-ex

7 ADP03931

122

Length 121;

DB 7;

100.0%; Score 649;

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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds too MVC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MVC18 on the cell surface such as tumours, specifically melanoma, osophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including current sequence is that of the anti-human MVC18 monoclonal antibody heavy chain protein of the invention.
                                                                                                                                 120
                                                                                                                                           anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel isolated monoclonal antibody comprising
                                                                                                 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
                                                                                                                               61 PSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS
                                                                                    QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
                                                                Gaps
                                                                                                                                                                                                                                                                                                                     Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 17
                                                                 ö
                                           Length 121;
                                                                Indels
                                         ; Score 649; DB 7;
; Pred. No. 6.4e-46;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumors, cancers, and other malignancies.
heavy chain protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 17; 78pp; English.
                                                                                                                                                                                                                                                      ADC99788 standard; protein; 121 AA.
                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-DEC-2002; 2002WO-US041581.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-DEC-2001; 2001US-0346299P
                                                                                                                                                                                                                                                                                                 01-JAN-2004 (first entry)
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-587113/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ABGE-) ABGENIX INC
                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                            lung cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ADC99790
                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003057838-A2.
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                    Sequence 121 AA;
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                                                              121;
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                                                                                                                                                                                                                                                                            ADC99788;
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                                                                                                                                                                                                                                                                                                                        61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMYTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour nereststasis, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-MUC18 antibody heavy chain, variable region,
                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
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                                                                                                                                                                                                                                                                                   PSLKSRVT1SVDTSKNQFSLRLSSVTAADTAVYXCARDQQQWLLPDAFD1WQQGTWVTVS
                                                                                                                                             1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGY1YYTWTSNYN
                                                                                                                                                                                         1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 1.
                                                                               Gaps
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                                                                            Indels
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                                    6.4e-46;
                                    100.0%; Pred. No. 6.4 ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADD05376 standard; protein; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-DEC-2002; 2002WO-US041582.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-2004 (first entry)
Query Match
Best Local Similarity 100.
Matches 121; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-577496/54.
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                                                                                                                                                                                                                                                                                                                                                                                                                             121 S 121
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us-10-660-357a-1.rag

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Gaps

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0; Indels

0; Mismatches

Matches 121; Conservative

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                                                                                                                                                           61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYCARDQGQWLLPDAFDIWGQGTWVTVS 120
                                                                                                                                      61 PSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCARDOGOWLLPDAFDIWGOGTMVTVS 120
                                                                    9
                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 17.
                                                                  1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
                                                                                         QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
                                  Gaps
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                                Indels
               Pred. No. 6.4e-46;
                                Mismatches
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                                                                                                                                                                                                                                                                                                                                         ADD05392 standard; protein; 121 AA.
100.08; P.
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                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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         Best Local Similarity 100.
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bar-Eli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-577496/54.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003057006-A2
                                                                                                                                                                                                              121 $ 121
                                                                                                                                                                                                                                                s 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                               ADD05392;
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                                                                                                                                                                                                                                                                                                       RESULT 4
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Score 649; DB 7; Length 121; Pred. No. 6.4e-46;

100.0%;

Query Match Best Local Similarity

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                                                                               61 PSLKSRVTISVDTSKNOPSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid sequence represents a heavy chain from an MUC18 tumour antigen-specific
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.
QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
                                QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGY1YYTWTSNYN
                                                                 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS
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                                                                                                                                                                                                                                                                                                                                                                             cell proliferation inhibition; MUC18 tumour antigen; anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour; carcinoma; cancer; malignancy; heavy chain; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
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                                                                                                                                                                                                                                                                                                                                                   Human anti-MUC18 monoclonal antibody heavy chain #1.
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100.0%; Pred. No. 6.4e-46;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 1; 83pp; English.
                                                                                                                                                                                                                                                  ADF09814 standard; protein; 121 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                S 121
                                                                                                                                                                 S 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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ADF0981
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26-DEC-2002; 2002WO-US041581.
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                                                                                                      (first entry)
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Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-587113/55.
                                                                                                                                                                                                                                                                                                                       (ABGE-) ABGENIX INC
                                                                                                                                                                                    lung cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ADC99782
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   121 S 121
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                                                                                                                                                                                                          Homo sapiens.
                                                                                                      01-JAN-2004
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                                                                                ADC99780;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention comprises a method for inhibiting cell proliferation associated with expression of MUCIB tumour antigen. The method involves administering anti-MUCIB monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUCIB tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid sequence represents a heavy chain from an MUCIB tumour antigen-specific
          61 PSLKSRVIISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTWVTVS 120
PSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCARDOGGWLLPDAFDIWGQGTWVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTWVTVS 120
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anti-
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                                                                                                                                                                                                                 cell proliferation inhibition; MUC18 tumour antigen;
anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
carcinoma; cancer; malignancy; heavy chain; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibiting cell proliferation associated with expression of MUC18 antigen, involves incubating and inhibiting cell by administering
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                                                                                                                                                                                           Human anti-MUC18 monoclonal antibody heavy chain #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 649; DB 7;
100.0%; Pred. No. 6.4e-46;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 17; 83pp; English
                                                                                                                      ADF09830 standard; protein; 121 AA.
                                                                                                                                                                                                                                                                                                                                 26-DEC-2002; 2002WO-US041580
                                                                                                                                                                                                                                                                                                                                                       28-DEC-2001; 2001US-0346414P.
                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antigen, involves incubat:
MUC18 monoclonal antibody
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Best Local Similarity 100.
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-598367/56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  monoclonal antibody
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The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds too MUCIB. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUCIB on the cell surface such as tumours, specifically melanoma, osophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUCIB monoclonal antibody heavy chain protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                    anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g.
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                                                                                                                                                                                                                                                                                  Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 9.
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Pred. No. 2e-45;
2; Mismatches 0; Indels
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ADC99780 standard; protein; 121 AA.
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Human anti-MUC18 monoclonal antibody heavy chain #3
 ADF09822 standard; protein; 121 AA
                                                                         (first entry)
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                                                                         12-FEB-2004
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                                      ADF09822;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds WOC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has cytostatic and can be used in the production of a vaccine. The monoclonal antibodies against the WOC18 antigen are useful for diagnosing and treating tumours, inhibiting cumour growth (e.g. melanoma, lung tumour or tumour metastasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastasic tumour. This sequence represents an anti-WOC18 antibody heavy chain, variable region,
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                                                                                                                                                             monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIROPPGKGLEWIGYIYYTWTSNYN
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                                                                                                                           Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 9.
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Pred. No. 2e-45;
2; Mismatches 0; Indels
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                 ADD05384 standard; protein; 121 AA.
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Best Local Similarity 98.3%;
Matches 119; Conservative 2
                                                                                                                                                                                                                                                                                                                                 26-DEC-2002; 2002WO-US041582
                                                                                                                                                                                                                                                                                                                                                                     28-DEC-2001; 2001US-0346460P
                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Bar-Eli M;
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N-PSDB; ADD05386.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               metastatic tumor.
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                                                                                      01-JAN-2004
                                                                                                                                                                                                                       Homo sapiens
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ADF09822
ADD05384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 OVOLOESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTTNYN
cell proliferation inhibition; MUC18 tumour antigen; anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour; carcinoma; cancer; malignancy; heavy chain; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 2e-45;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 9; 83pp; English.
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                                                                                                                                                                                                                                                                                                                                                        26-DEC-2002; 2002WO-US041580
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Best Local Similarity 98.3%;
Matches 119; Conservative
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Homo sapiens.
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ADF09850
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                                                                                                                                                                                                                                                                                                                                                                   a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to WUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the pancreatic or colorectal tumours, specifically melanoma, oesophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody
                      anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
                                                                                                                                                                                                                                                                                      useful for treating a disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCARDOGGWLLPDAFDIWGQGTMVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                          invention relates to a novel isolated monoclonal antibody comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-WUC18 antibody heavy chain variable region protein, SEQ ID No 37.
                                                                                                                                                                                                                                                                                    New human anti-MUC18 monoclonal antibodies, useful for treating a di
or condition associated with expression of MUC18 in a patient, e.g.
tumors, cancers, and other malignancies.
Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.0%; Score 597; DB 7; Length 121; 90.9%; Pred. No. 1.2e-41; ive 7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 37; 78pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chain protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADD05412 standard; protein; 121 AA.
                                                                                                                                                      26-DEC-2002; 2002WO-US041581.
                                                                                                                                                                            28-DEC-2001; 2001US-0346299P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                 WPI; 2003-587113/55.
                                                                                                                                                                                                   (ABGE-) ABGENIX INC
                                                          lung cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
es 110; Conserv
                                                                                                                                                                                                                                                             N-PSDB; ADC99810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 121 AA;
                                                                                                       WO2003057838-A2
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                                                                                  Homo sapiens
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Matches
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monoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has cytostatic and can be used in the production of a vaccine. The monoclonal antibodies against the MUC18 antigen are useful for diagnosing and treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-MUC18 antibody heavy chain, variable region,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel monoclonal antibody used for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGY1YYTWTSNYN
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anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
carcinoma; cancer; malignancy; heavy chain; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a
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Pred. No. 1.2e-41;
7; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 37; 87pp; English.
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                                                                                                                           26-DEC-2002; 2002WO-US041582
                                                                                                                                                                                             28-DEC-2001; 2001US-0346460P
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Best Local Similarity 90.9
Matches 110; Conservative
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                                                                                                                                                                                                                                                                                                                            Bar-Eli M;
                                                                                                                                                                                                                                                                                                                                                                                              2003-577496/54.
                                                                                                                                                                                                                                                              (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  metastatic tumor.
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WO2003057006-A2
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                                                             17-JUL-2003
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Gaps

Weinberger S, Kischel R;

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Identifying a B cell carrying a surface immunoglobulin molecule having a binding site for an antigen of interest, useful for constructing therapeutic antibodies, comprises contacting a sample with the antigen
                                                                                                                                                                                                                      Claim 22; SEQ ID NO 76; 156pp; English.
                         12-NOV-2003; 2003WO-EP012664.
                                                 13-NOV-2002; 2002EP-00025335
                                                                                                Baeuerle P, Hoffmann P,
                                                                                                                       WPI; 2004-449579/42.
                                                                        (MICR-) MICROMET AG
                                                                                                                                    N-PSDB; ADO58077
                                                                                                                                                                                              and a receptor.
  27-MAY-2004
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ABG92884
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                                                                                                                                                                                                                                                                                         The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid sequence represents a heavy chain from an MUC18 tumour antigen-specific
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                                                                                                                                                                                                                 Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B cell; surface immunoglobulin; Ig; binding site; antigen; human CD28; closed system; detection laser-beam; catcher tube; electrochemical device; fluorescence activated cell sorter; FACS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      92.0%; Score 597; DB 7; 90.9%; Pred. No. 1.2e-41; iive 7; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S9 cell derived human scFvVL-VH protein.
                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 37; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADO58076 standard; protein; 243 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibody variable region; human.
                                                                                  26-DEC-2002; 2002WO-US041580.
                                                                                                         28-DEC-2001; 2001US-0346414P.
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                                                                                                                                 (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                          monoclonal antibody
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Matches 110; Conserv
                                                                                                                                                                                              N-PSDB; ADF09852
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 121 AA;
                                  WO2003057837-A2
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            Homo sapiens.
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124 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYN 183
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                                                                                                                                                                                                                                                                                                        polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                           Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                               Sequence 243 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 S 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S 243
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61 PSLKSRVTMSVDTSKNRFSLKLSSVTAADTAVYYCARDRGSSWYPDAFDIWGGGTMVTVS 120 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS 120

121 S 121 S 121

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Neuromodulatory; central nervous system; CNS; sHIGM22; LYM 22; AKJR4; ebvHigM MsI19D10; ebv HIGM CB2bG8; CB2iE12; CB2iE7; MsI19E5; virucide; antiparkinsonian; neuroprotective; nootropic; vulnerary.

(MAYO-) MAYO FOUND MEDICAL EDUCATION RES.

30-MAY-2000; 2000WO-US014902. 10-MAY-2000; 2000US-00568351.

WO200185797-A1

15-NOV-2001.

Homo sapiens

Pease LR;

Rodriguez M, Miller DJ,

ebvHigM MSI19D10 heavy chain variable region sequence.

(first entry)

13-MAR-2002

ABB07171;

ABB07171 standard; protein; 121 AA.

RESULT 15 ABB07171

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histiocytosis; chemotaxis; infectious disease; autoimmune disease;
Addison's disease; dermatitis; rheumatoid arthritis; allergy;
neurodegenerative disorder; viral infection; poxvirus infection; HIV;
human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;
Pneumocystis carnii infection; cardiovascular disorder; atherosclerosis;
                                Immunoglobulin, variable heavy chain, variable light chain, human, G-protein chemokine receptor, CCR5, HDGNR10; cancer, inflammation, immunologic deficiency syndrome, blood protein disorder, nephritis, ataxia telangiectasia, endotoxin lethality; inflammatory bowel disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                 New human G-protein Chemokine Receptor gene (HDGNR10) useful for treating, preventing, ameliorating or monitoring diseases or disorders associated with aberrant expression of HDGNR10 e.g. cancer.
         Human immunoglobulin variable light domain #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 55; Fig 4; 562pp; English.
                                                                                                                                                                                                                                                                                                                                                                          Ruben SM;
                                                                                                                                                                                                                                                                          2001WO-USO04153.
2001US-0297257P.
2001US-0310458P.
2001US-0328447P.
                                                                                                                                                                                                                                                                                                                           2001US-0341725P
                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                          08-FEB-2002; 2002WO-US003634
                                                                                                                                                                                                                                                                                                                                                                          Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-643455/69.
                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABS68607
                                                                                                                                             lymphocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 121 AA;
                                                                                                                                                                                           MO200264612-A2
                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                 09-FEB-2001;
                                                                                                                                                                                                                                                                           09-FEB-2001;
                                                                                                                                                                                                                                                                                                   08-AUG-2001;
12-OCT-2001;
                                                                                                                                                                                                                                                                                                                          21-DEC-2001;
                                                                                                                                                                                                                   22-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                        Roschke V,
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The invention describes an isolated polynuclectide encoding a first antibody at least 95-100% identical to a second antibody consisting of an antibody at least 95-100% identical to a second antibody consisting of a variable heavy (VH) or variable light (VL) domain of the antibody expressed by a hybridoma cell line consisting of XF3.5F1, XF71.1F8, XF27/28.1885, XF27/28.3F11, XF77/28.1885, XF27/28.3F11, XF77/28.1885, XF27/28.3F11, Or XF27/28.1885, XF27/28.3F11, Or XF27/28.1885, XF27/28.3F11, Or XF27/28.3F12, The antibody is useful treating, preventing, ameliorating, prognosing or monitoring cancers or other diseases or disorders e.g. immunologic deficiency syndromes such as blood protein disorders and ataxia telangiectasia, inflammation associated disorders such as endotoxin lethality, nephritis and inflammatoxy bowel disease, conditions associated with an increase in certain haematoxy bowel disease, conditions associated with an increase in certain haematoxylowells such as histiocytosis defective or aberrant chemotaxis of immune cells or T-cell antigen presenting cell interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ရ ပြ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence of human immunoglobulin sequence associated with the antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dermatitis and rheumatoid arthritis, allergies, a neurodegenerative disorder, a viral infection e.g. HIV infection, cytomegalovirus or poxvirus infection, a Pneumocystis carnii infection, Kaposi's Barcoma, cardiovascular disorders such as atherosclerosis, lymphocytopenias, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression of novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease or disorder associated with aberrant exp
protein chemokine receptor (CCRS) HDGNR10. This
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Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system, useful to treat post-infectious encephalomyelitis.
                                                                                                                                                                                                                                                                                                 Claim 23; Fig 19; 219pp; English
WPI; 2002-066596/09.
                                      N-PSDB; ABA94218
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Matches 104; Conservative

Best Local Similarity

Query Match

84.3%; Score 547; DB 5; Le 86.0%; Pred. No. 1.6e-37; ive 8; Mismatches 9;

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Gaps

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Length 121; Indels

Search completed: November 9, 2005, 12:55:23 Job time: 76.6015 secs

121 g 121 | | 120 g 120

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Appli Appli Appli

142,

Sequence 1 Sequence 1 Sequence 8 Sequence 8

Appl Appli Appl

Sequence Sequence Sequence Sequence Sequence Sequence

Appli Appli Appli Appli Appli Appli

888, App 6, Appli 6, Appli 7, Appli 7, Appli

Sequence 8 Sequence 6 Sequence 6 Sequence

OM protein

Run on:

Sequence:

Searched:

Database

٠ 8

Result

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APPLICANT: Knappik, Achim
APPLICANT: Knappik, Achim
APPLICANT: Back, Peter
APPLICANT: 11ag, Vic.
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Alley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 540; DB 3; Length 119;
Pred. No. 7.3e-45;
5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

SOFTWARE: Petentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REJECOMMUNICATION NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMAT
                     US-08-450-578-5
US-09-017-628-5
US-09-017-888-5
US-09-457-903-5
US-08-652-816A-10
US-08-472-087-86
US-08-793-450-4
US-08-793-450-4
US-08-793-450-8
US-09-771-276-888
US-09-343-698-6
US-09-343-698-6
US-08-35-955-6
US-08-35-955-6
US-08-373-453-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 39, Application US/09025769B; Patent No. 6300064; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 86.8%;
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
  TOPOLOGY: linear
MOLECULE TYPE: protein
ZIP: 10021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-025-769B-39
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                                                                                                                                                                                                                                                         477
476
472.5
471
471
470.5
469.5
(without alignments)
480.403 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 39, Sequence 65, Sequence 65, Sequence 65, Sequence 39, Sequence 65, Sequence 25, Sequence 25, Sequence 25, Sequence 25, Sequence 27, Sequence 27, Sequence 27, Sequence 27, Sequence 27, Sequence 47, Asequence 47, Aseq
                                                                                                                                                                           November 9, 2005, 11:29:55 ; Search time 18.802 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
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Sequence 2
Sequence 1
Sequence 1
Sequence 1
Sequence 1
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Sequence 1
Sequence 1
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649
1 QVQLQESGPGLVKPSETLSL.......WLLPDAFDIWGQGTMVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-025-769B-65
US-09-490-070A-39
US-09-490-153-39
US-09-490-153-65
US-09-490-153-65
US-09-490-153-65
US-09-490-324-65
US-09-490-324-25
US-09-490-324-27
US-09-490-324-27
US-09-490-324-27
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US-09-490-324-27
US-09-490-324-27
US-09-490-324-27
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US-09-800-729-145
US-08-545-809A-140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-014-880-11
US-08-450-363-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                          513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                        - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Issued Patents AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
                                                                                                                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
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498.5
494.5
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Gaps

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Query Match
Best Local Similarity
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                                                                                            61 PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARWGGDGFY--AMDYWGQGTLVTVS 118
                                                                          61 PSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTWVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYXWSWIRQPPGKGLEWIGYIYYTWTSNYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: AND PROPERMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 540; DB 3; Length 11
Pred. No. 7.3e-45;
5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          c/o Fish & Neave
                                                                                                                                                                                                                                                                                                                                APPLICANT: Knappi, Achim
APPLICANT: Rnappi, Achim
APPLICANT: Back, Peter
APPLICANT: Ge, Lining
APPLICANT: Ge, Lining
APPLICANT: Ge, Lining
APPLICANT: Pluecktun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CUTY: New York
STATE: New York
STATE: New York
                                                                                                                                                                                                                                                                                  Sequence 65, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: 11ag, Vic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: FIOPDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 83.2%;
Best Local Similarity 86.8%;
Matches 105; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (212) 596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear;
MOLECULE TYPE: protein
US-09-025-769B-65
                                                                                                                                                                                        S 119
                                                                                                                                                    121 S 121
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61 PSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYN 60
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                                                                                                                                                                                                                                                                                      ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 119;
                                                                                            Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckhuu, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 540; DB 4;
Pred. No. 7.3e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-070A-39
; Sequence 39, Application US/09490070A; Patent No. 6696248; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
US-09-490-070A-65
; Sequence 65, Application US/09490070A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 119 amino acids
                                                                     APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202) 912-:
INFORMATION FOR SEQ ID NO: 39
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20006
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                            CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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TITLE OF INVENTION: Protein/(Poly)peptide libraries
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APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                      ADDRESSEE: James F. Haley, Jr., Esq. STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/S
TELECEMENTALION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                                                                                                       COUNTRY: USA ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 65, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 119 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212)596-9090
                             NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 39
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 86.8 Matches 105; Conservative
                                                                                                               CITY: New York
STATE: New York
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US-09-490-153-65
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STREET: 1666 K Street, N.W., Suite 300
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                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: EADAGE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 83.2%; Score 540; DB 4; Length 11 Best Local Similarity 86.8%; Pred. No. 7.3e-45; Matches 105; Conservative 5; Mismatches 9; Indels
                                                                                        Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 39, Application US/09490153
Patent No. 6706494
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202) 912-2020 INFORMATION FOR SEQ ID NO: 65: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 119 amino acids TYPE: amino acid
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                   Pack, Peter
                                                                                                                                                                                                                                                                                                             CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
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US-09-490-153-39
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61 PSLKSRVTISVDISKNOFSLRLSSVIRADIAVYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
c/o Fish & Neave
                                                                                                                                                                                                  COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.2%; Score 540; DB 4; Length 119;
86.8%; Pred. No. 7.3e-45;
tive 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Knappik, Achim
APPLICANT: Knappik, Achim
Pack, Peter
11ag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Nk
STREET: 1251 Avenue of the Americas
CITY: New York
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SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                     APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
FILING DATE: 18-FEB-1998
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 540; DB 4;
Pred. No. 7.3e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Mismatches
               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-324-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 65, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 86.8%;
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10021
COMPUTER READABLE FORM:
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
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US-09-490-324-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLQESGFGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYN 60
                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-dan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 83.2%; Score 540; DB 4; Best Local Similarity 86.8%; Pred. No. 7.3e-45; Matches 105; Conservative 5; Mismatches 9
                                                                                                                                                                                                                                                                                                                     NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794 REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (1215)596-9000
TELEFAX: (212)596-9000
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 119 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                               ZIP: 10021
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 8 119
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US-09-490-324-39
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61 PSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
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                                                                                                                                                    1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYN 60
                                                                                                          1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Date of the compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
Length 119;
                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckhun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
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TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLGGY: linear
MOLECULE TYPE: protein
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                                                                   : 118 amino acids
amino acid
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STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                Query Match
Best Local Similarity 85.1
Matches 103; Conservative
                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino ació
                                                                                                                                                 ; MOLECULE TYPE: protein US-09-025-769B-25
                                                                                                                                  linear
                                                                                                        STRANDEDNESS:
TOPOLOGY: 11
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US-09-490-070A-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence 25 Application US/09025769B
; Patent No. 630064
; GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ge, Liming
APPLICANT: Ge, Liming
APPLICANT: Pluckhuu, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jamee F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
FILING DATE: 18-MUSER: EP 95 11 3021.0
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
                                                      ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-324-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: James F. Haley, Jr., Esq. STREET: 1251 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REPERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
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ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
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                                                                                                          1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN 60
                                                                                                                                                        1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGEIYHSGSTNYN 60
                                                         Gaps
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Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
Plueckthun, Andreas
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/09/490, 070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
81.9%; Score 531.5; DB 3; Length
85.1%; Pred. No. 4.8e-44;
ive 7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: EP 95 11 3021.0 FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION: NAME: Colin G. Sandercock, Esq. REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6656248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
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TELEFAX: (202) 912-2020
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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61 PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGRGG---GGVFDYWGQGTLVTVS 117
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                                                                            1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGEIYHSGSTNYN
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COMPUTER: INP PC COMPATIBLE
COMPUTER: PRE-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30 (EPO)
CURBIN APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AGJ-1995
ATTORNEY/AGENT INPORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: James F. Haley, Jr., Esq. STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; ; MOLECULE TYPE: protein; ; SEQUENCE DESCRIPTION: SEQ ID NO: 25: US-09-490-324-25
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 25
SEQUENCE CHARACTERISTICS
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Best Local Similarity 85.11
Matches 103; Conservative
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STATE: New York
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US-09-490-324-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                    81.9%; Score 531.5; DB 4; Length 118; 85.1%; Pred. No. 4.8e-44; 1.1ve 7; Mismatches 8; Indels 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ge, Liming
Moroney, Simon
Plueckthur, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-070A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 25: US-09-490-153-25
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TELEPHONE: (212)596-9000
TELEFAK: (212)596-9000
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 118 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
                                                                               Query Match
Best Local Similarity 85.1
Matches 103; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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Best Local Similarity 85.1
Matches 103; Conservative
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
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116 $ 116
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US-09-138-091A-77
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PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQ-WLLDDAFDIWGQGTWVTV 119
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                                                                                                                                                   Sequence 20, Application US/09424840B
; Sequence 20, Application US/09424840B
; Batent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtcld, Peter
; APPLICANT: Berchtcld, Peter
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR PAPLICATION NUMBER: DE 19755227.7
; PRIOR PILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR PILING DATE: 1997-06-06
; NUMBER: OF SEC ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEC ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 120;
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APPLICANT: W.
APPLICANT: Gurney, Mustin M.
APPLICANT: Fendly, Brian M.
THILE OF INVENTION: Agonist Antibodies
FILE REPERENCE: P0979
CURRENT FILING DATE: 1997-08-25
CURRENT FILING DATE: 1997-08-25
SEQ ID NO 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 79, Application US/08918148A Patent No. 6342220 GENERAL INFORMATION:
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; ORGANISM: artificial
US-08-918-148-79
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Best Local Similarity
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     2; Indels
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Sequence 77, Application US/09138091A

Patent No. 6737249

GENEAL INFORMATION

APPLICANT: Carrer, Paul J.

APPLICANT: Carrer, Paul J.

APPLICANT: Gurney, Austin L.

TITLE OF INVENTION: Agonist Antibodies

FILE REFERENCE: 949-0413-27

CURRENT APPLICATION NUMBER: US/09/138,091A

CURRENT FILING DATE: 1998-08-21

PRIOR APPLICATION NUMBER: US 60/056,736

PRIOR APPLICATION NUMBER: US 60/056,736

NUMBER OF SEQ ID NOS: 77

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 77

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102; Conservative 10; Mismatches
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Job time: 19.802 secs
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ORGANISM: Artificial Sequence
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Title: Perfect score:

Sequence:

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Scoring table:

Searched:

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; Bublication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFREENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; RICHAR APPLICATION NUMBER: 60/346299
; NUMBER OF SEQ ID NOS: 400
; SOFTWARE: FREELESC for Windows Version 4.0
; SEQ ID NO 1
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          US-10-292-088-109
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US-10-309-762-163
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US-10-844-424-20
US-10-805-177-56
US-10-067-800-68
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TYPE: PRT
ORGANISM: Homo Sapiens
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LENGTH: 121
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Sequence 1, A
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Compugen Ltd.
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US-10-660-357-17
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            GenCore version (c) 1993 - 2005
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Maximum Match 100%
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                                                                                                                                                                                                           APPLICATE: Gudas, Jean
TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
FILE REFERENCE: ABGENIX.031A
CURRENT APPLICATION NUMBER: US/10/330,530
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: US 60/346414
PRIOR APPLICATION NUMBER: US 60/346414
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FASTESEQ for Windows Version 4.0
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Publication No. US20040115205A1

GENERAL INFORMATION:
APPLICANT: BA-Eli, Menashe
APPLICANT: Green, Larry L.
TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
TITLE OF INVENTION: ANTIGEN
FILE REFERENCE: ABGENIX.030C1
CURRENT APPLICATION NUMBER: US/10/660,357
CURRENT PILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 10/330,580
PRIOR FILING DATE: 2002-12-26
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FRASESEQ for Windows Version 4.0
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100.0%; Pred. No. 1.8e-50;
iive 0; Mismatches 0;
                                                                                                                                            Sequence 17, Application US/10330530; Publication No. US20030152514A1; GENERAL INFORMATION:
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ORGANISM: Homo Sapiens
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ORGANISM: Homo Sapiens
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Best Local Similarity
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; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: WETHODS FOR USING ANTI-MUC18 ANTIBODIES; FILE REFERENCE: ABGENIX.031A; CURRENT APPLICATION UNMERR: US/10/330,530; CURRENT FILING DATE: 2002-12-26; PRIOR APPLICATION NUMBER: US 60/346414; PRIOR FILING DATE: 2001-12-18; NUMBER OF SEQ ID NOS: 40; SEQ ID NO 1: LENGTH: 121
                                                                                                       Sequence 17, Application US/10330613

Publication No. US20030147809A1

GENERAL INFORMATION:

APPLICANT GUGAS, Jean

TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN

FILE REFRENCE: ABGENIX.022A

CURRENT APPLICATION NUMBER: US/10/330,613

CURRENT FILING DATE: 2002-12-26

PRIOR APPLICATION NUMBER: G0/346299

PRIOR FILING DATE: 2001-12-18

NUMBER OF SEQ ID NOS: 40

SEQ ID NOS: 40

SEQ ID NOS: 7
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100.0%; Pred. No. 1.8e-50;
iive 0; Mismatches 0;
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ORGANISM: Homo Sapiens
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                                                                                                                                                                                                                                                                                                                          APPLICANT: Gudas, Jean
TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
FILE REFERENCE: ABGENIX.031A
CURRENT APPLICATION UNMBER: US/10/330,530
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: US 60/346414
PRIOR PILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20040115205A1

GENERAL INFORMATION:

APPLICANT: BAr-Ell, Menashe

TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18

TITLE OF INVENTION: ANTIGEN

TITLE OF INVENTION: ANTIGEN

CURRENT APPLICATION NUMBER: US/10/660,357

CURRENT FILING DATE: 2003-09-10

CURRENT FILING DATE: 2003-09-10

PRIOR FILING DATE: 2002-12-26
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99.1%; Score 643; DB 16;
Best Local Similarity 98.3%; Pred. No. 6.1e-50;
Matches 119; Conservative 2; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 121
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-660-357-9
                                                                                                                                                                                                                                                          ; Sequence 9, Application US/10330530; Publication No. US20030152514A1; GENERAL INFORMATION:
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TYPE: PRT
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US-10-330-530-9
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61 PSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
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Publication No. US200301478091
GENERAL INFORMATION:
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
FILE REFERENCE: ABGENIX.02A
CURRENT APPLICATION NUMBER: US/10/330,613
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: 60/346299
PRIOR PILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                      Sequence 17, Application US/10660357

Publication No US20040115205A1

GENERAL INPORMATION:

APPLICANT: Bar-Eli, Menashe

APPLICANT: Green, Larry L.

TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18

TITLE OF INVENTION: ANTIGEN

FILE REFERENCE: ABGENIX.030C1

CURRENT APPLICATION NUMBER: US/10/660,357

CURRENT APPLICATION NUMBER: 10/330,580

PRIOR APPLICATION NUMBER: 10/330,580

PRIOR FILING DATE: 2002-12-26

NUMBER OF SEQ ID NOS: 40

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 17

LENGTH: 121
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Pred. No. 6.1e-50;
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98.3%;
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Best Local Similarity 100.0
Matches 121; Conservative
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Best Local Similarity 98.3
Matches 119; Conservative
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US-10-660-357-17
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Best Local Similarity 90.9%; Pred. No. 8e-46;
Matches 110; Conservative 7; Mismatches 4; Indels
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Publication No. US20030211100A1
GENERAL INFORMATION:
APPLICANT: BEDIAM, VAHE
APPLICANT: CGRVALAN, JOSE
APPLICANT: CGRVALAN, JOSE
APPLICANT: JIA, XIAO-CHI
APPLICANT: JIA, XIAO-CHI
APPLICANT: ANTENDEDIES TO CD40
TITLE OF INVENTYON: ANTENDER: US/10/292,088
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 60/348,980
PRIOR PLILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 142
LENGTH: 118
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ORGANISM: Homo Sapiens
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US-10-660-357-37
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                                                                                                  61 PSLKSRVIISVDTSKNQFSLRLSSVTAADTALYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
                                                                           61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
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QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
                      QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTUYN
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| Publication No. US20030152514A1
| GENERAL INFORMATION:
| APPLICANT: Gudas, Jean
| TITLE OF INVENTION: WETHODS FOR USING ANTI-MUC18 ANTIBODIES
| FILE REFERENCE: ABGENIX.031A
| CURRENT PELLICATION NUMBER: US/10/330,530
| CURRENT FILING DATE: 2002-12-26
| PRIOR APPLICATION NUMBER: US 60/346414
| PRIOR APPLICATION NUMBER: US 60/346414
| NUMBER OF SEQ ID NOS: 40
| SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 92.0%; Score 597; DB 14; Length 121; Best Local Similarity 90.9%; Pred. No. 8e-46; Matches 110; Conservative 7; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 14; Length 121;
                                                                                                                                                                                                                                                                                          Sequence 37, Application US/10330613
Publication No. US20030147809A1
GENERAL INFORMATION
FILE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
FILE REFERENCE: ABGENIX.0226
CURRENT APPLICATION NUMBER: US/10/330,613
CURRENT FILING DATE: 2002-12-26
PRIOR PILICATION NUMBER: 60/346299
PRIOR PILICATION NUMBER: 60/346299
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 37
LENGTH: 121
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90.9%; Pred. No. 8e-46;
live 7; Mismatches
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Best Local Similarity 90.9
Matches 110; Conservative
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US-10-330-530-37
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US-10-330-530-37
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LENGTH: 121
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61 PSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCARDOGGWLLPDAFDIWGOGTMVTVS 120
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1 QVQLQESGPGLVKPSETLSLTCTVSGGSISTYYWSWIRQPPGKGLEWIGYIYYTGNTYYN
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US-10-067-800-60
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Fublication No. US20030100058A1
GENERAL INFORMATION:
APPLICANT: Roschke, Viktor
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
FILE REFERENCE: 1488.1150001
CURRENT APPLICATION NUMBER: US/10/067,800
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84.7%; Score 549.5; DB 15; Length 118;
Best Local Similarity 87.6%; Pred. No. 1.4e-41;
Matches 106; Conservative 5; Mismatches 7; Indels 3;
                                                                                        DB 15; Length 118;
                                                                                                                                  5; Indels
                                                                                 Query Match 85.3%; Score 553.5; DB 1. Best Local Similarity 87.6%; Pred. No. 6.2e-42; Matches 106; Conservative 7; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 109, Application US/10292088
Publication No. US20030211100A1
GENERAL INFORMATION:
APPLICANT: BEDIAM, VAHE
APPLICANT: GLADUE, RONALD P.
APPLICANT: GLADUE, RONALD P.
APPLICANT: JAA, XIAO-CHI
APPLICANT: JAA, XIAO-CHI
APPLICANT: FENG, XIAO-CHI
APPLICANT: FENG, XIAO-CHI
APPLICANT: FENG, XIAO-CHI
CURRENT FILIK DATE: 2013-14
CURRENT FILIKU DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 60/348,980
PRIOR APPLICATION NUMBER: 60/348,980
PRIOR PILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 147
SEQ ID NO 109
LENGTH: 118
                  ; ORGANISM: Homo sapiens
US-10-292-088-142
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US-10-292-088-109
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US-10-067-800-60
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TYPE: PRT
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61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
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PRIOR APPLICATION NUMBER: PCT/USO1/04153
PRIOR FILING DATE: 2001-02-09
PRIOR PELICATION NUMBER: 09/779, 080
PRIOR PELICATION NUMBER: 09/779, 080
PRIOR APPLICATION NUMBER: 60/297, 257
PRIOR FILING DATE: 2001-06-12
PRIOR PELICATION NUMBER: 60/310, 458
PRIOR PELICATION NUMBER: 60/310, 458
PRIOR APPLICATION NUMBER: 60/310, 458
PRIOR PELING DATE: 2001-10-12
PRIOR PLING DATE: 2001-10-21
NUMBER OF SEC ID NOS: 70
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            completed: November 9, 2005, 12:42:57 e : 68.2222 secs
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ORGANISM: Homo sapiens
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GenCore version 5.1.6
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	Seconds
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1 QVQLQESGPGLVKPSETLSL.......wLLPDAFDIWGQGTMVTVSS 121 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	variable re	g heavy cha	heavy	וטו	g heavy	Ig heavy chain V r	g heavy	g heavy	5	g heavy	g heavy chain	g lambda chain	g heavy	heavy	g heavy	g heavy chain	g heavy	g heavy	g heavy	heavy	g heavy	g heavy chain	g heavy	heavy chain	g heavy cha	מ	heavy o	g gamma-1 h	chai
SUMMARIES	QI	3778	3151	31	3151	æ	S30534	S31676	S20780	813519	S78052	878051	S44125	826906	S09711	B26340	S12416	S44113	A49045	830530	S31696	A26340	S44114	_	S78055	4	S	S26803	A49444	PH0876
	Length DB	140													146 2												•			
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S12412 .	B49028	S26804	S18557	D41287	S26801	S54906	809710	S44110	G1HUH2	S12418	S69912 :	A24770	PH1673	531604	S57464
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66	143	97	116	122	66	134	146	110	146	66	122	140	109	135	115
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71.6	71.2	70.9	70.9	70.8	70.6	70.6	70.6	70.2	70.0	70.0	6.69	9.69	69.5	69	69.5
465 71.6	462 71.2	460 70.9	_	459.5 70.8			458 70.6			454 70.0		452 69.6		_	449 69.2

ALIGNMENTS

RESULT 1

Query Match 83.7%; Score 543; DB 2; Length 140; Best Local Similarity 86.0%; Pred. No. 3.5e-41; Matches 104; Conservative 5; Mismatches 12; Indels

ô 1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN 60 20 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYN 79 Gaps ò ð

61 PSLKSRVTISVDTSKNQPSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS 120 q g ò

140 S 140 121 S 121 ð a

Journal of Amery Chain - human (Species: Homo sapiens (man) (Space) (Space

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C;Species: Homo sapiens (man).
C;Species: Homo sapiens (man).
C;Species: Homo sapiens (man).
C;Date: 2-2-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31586
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: 831585
                                                                                                                                                                                                                                                                                                                                 61 PSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCARDOG--QWLLPDAFDIWGQGTMVT 118
                                                                                                                                                                                                                                                                                                                                                                      93 PPLKSRVTISVDTSKNQFSLKVSSVTAADTAVYYCARGGGISSWYDYYGMDVWGQGTTVT 152
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
C;Accession: S30534
R;Mariette, X.
                                                                                                                                                                                                                                           33 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTGSATYN
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Pred. No. 1e-39;
6; Mismatches 10; Indels
                                                                                                               13; Indels
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                                         Query Match 82.1%; Score 533; DB 2, Best Local Similarity 83.7%; Pred. No. 3e-40; Matches 103; Conservative 5; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, October 1992 A;Reference number: $30520 A;Accession: $30534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 518.5;
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Best Local Similarity 86.0°
Matches 104; Conservative
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A;Molecule type: mRNA
A;Residues: 1-130 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-139 <CUI>
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Cibbers Homo sapiens (man)
Cibbers Homo sapiens (man)
Cibbers 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
Cibbers 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
Cibbers 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
Cibbers 13-Jan-1995 #sequence_revision C: Theze, J: Zouali, M.
Richastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
Richastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
A; Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autch A; Reference number: S11509
A; Rocession: S1151
A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-155 cCHA>
A; Coss-references: EMBL: X69866; NID:g33094; PIDN:CAA49500.1; PID:g33095
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; McWaords: heterotetramer; immunoglobulin
F; 47-129/Domain: immunoglobulin homology < IMM>
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C; Species: Homo sagiens (man)
C; Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C; Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C; Accession: 81690
R; Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
R; Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A; Reserve commer: 831585
A; Recession: 831690
A; Accession: 831690
A; Accession: S1690
A; Accession: S1690
A; Accession: S1690
A; Accession: Freferences: EMBL, A.
A; Cross-references: EMBL, 214199; NID:g30984; PIDN:CAA78568.1; PID:g30985
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin homology < Keywords: het
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                                                                      Length 155;
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                                                                                                                                             Indels
                                                                                                                                          12;
                                                                   82.6%; Score 536; DB 2;
82.9%; Pred. No. 1.6e-40;
iive 7; Mismatches 12;
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84.0%; Pred. No. 2.5e-40;
ive 5; Mismatches 11;
F;47-129/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 84.0%;
Matches 105; Conservative
                                                                                                    Best Local Similarity 82.9
Matches 102; Conservative
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C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: 813519
R;Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.
Nucleic Acids Res. 19, 673, 1991
A;Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked A;Accession: 813519; MUD:91187691; PMID:2011536
A;Status: preliminary
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A;Reference number: 878051
A;Accession: 878052
A;Accession: 878052
A;Molecule type: mRNA
A;Residues: 1-140 <hR>
A;Cross: references: EMBL:X54441; NID:g37815; PIDN:CAA38308.1; PID:g930118
B;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkin Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and
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C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78052; S23717
C;Harindranath, N.
                                                                                                     61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS
                                                                                                                                                                                          61 PSLKSRVTMSVDTSKNQFSLKMTSVTAADTAVYSCARDRGR---DGGFDIWGQGTMVTVS
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                                                                       1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
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                           Gaps
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C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heterotetramer; immunoglobulin
F;41-125/Domain: immunoglobulin homology <IMM>
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                           9; Indels
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77.8%; Score 505; DB 2;
Best Local Similarity 82.1%; Pred. No. 8.6e-38;
Matches 101; Conservative 7; Mismatches 11.
                        11; Mismatches
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A;Residues: 15-111 <HAW>
A;Cross-references: EMBL:X54441
                           98; Conservative
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A;Residues: 1-147 <MOR>
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: 831676
C;Accession: 831676
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C) Accession: $20780
R) Morteari, F.; Wang, J.; Schroeder, H.W.
R) Morteari, F.; Wang, J.; Schroeder, H.W.
R) Description: Analysis of human cord blood Ig heavy chain IgA and IgG repertoire.
A;Reference number: $20764
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
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C.Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
                                                                                                                                      1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGSYYWSWIRQPAGKGLEWIGRIYTSGSTN
                                                                                         QVQLQESGPGLVKPSETLSLTCTVSGGSIS--SYYWSWIRQPPGKGLEWIGYIYYTWTSN
                                               Gaps
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A;Cross-references: EMBL:Z11958; NID:g33893; PIDN:CAA78015.1; PID:g33894
A;Cross-references: EMBL:Z11958; NID:g33893; PIDN:CAA78015.1; PID:g33894
C;Superfeamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
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                                               Indels
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. 4.8e-39;
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Pred. No. 1.7e-38;
6; Mismatches 11;
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                      Pred. No. 4.8e
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  heavy chain V region - human (fragment)
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9
                 81.5%;
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81.0%;
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Best Local Similarity 83.5%;
Matches 101; Conservative
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                                          Matches 106; Conservative
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                                                                                                                                                                                                                                                                                   112 GOGTMVTVSS 121
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                   Best Local Similarity
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A;Molecule type: mRNA
A;Residues: 1-137 <CUI>
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Best Local Similarity
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Figure 1. Strokes In the EMBL Data Library, March 1994
Submitted to the EMBL Data Library, March 1994
Submitted to the EMBL Data Library, March 1994
Albestription: Idiotypic vaccination against human B-cell lymphoma: rescue of variable A; Reference number: $44105
A; Reference number: $44105
A; Accession: $44125
A; Accession: S44125
A; Accession: Acc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tig heavy chain V region (DP-71 / VH 4.11 / 4.15) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: S26906; S09421; S12415
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-799, 11992
A;Title: The repercoire of human germline V(H) sequences reveals about fifty groups A;Reference number: S26885; MUID:93021117; PMID:1404388
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A;Status: preliminary
A;Molecule type: DNA
A;Reafdues: 1-97 <TOA>
A;Cross-references: EMBL:Z12371; NID:g32962; PIDN:CAA78241.1; PID:g32963
A;Cross-references: EMBL:Z12371; NID:g32962; PIDN:CAA78241.1; PID:g32963
A;Note: designated DP-7; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D. EMBO J. 8; 3741-3748; 1989
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Pred. No. 1.3e-36;
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A;Cross-references: EMBL:X56359
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroteramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology < IMM>
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Pred. No. 1.4e-36;
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l Similarity 94.8%;
92; Conservative 4
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A, Cross-references: EMBL:X56355
A, Note: designated 4.11
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Best Local Similarity
Matches 92; Conserv
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Best Local Similarity
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          C; Accession: S44125
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S26906
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A, Molecule type: mRNA
A, Rocession: S78051
A, Molecule type: mRNA
A, Recession: S78051
A, Molecule type: mRNA
A, Recession: S18051
A, Molecule type: mRNA
A, Cross-references: EMBL:X54437; NID:g37814; PIDN:CAA38306.1; PID:g930117
B; Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkine
Int. Immunol. 3, 865-875, 1991
A, Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
A, Reference number: S23716; MUD:92031262; PMID:1718404
A, Accession: S23716
A, Molecule type: mRNA
A, Released type: mRNA
A, Released to B, Manunoglobulin V region; immunoglobulin homology
C, Superfamily: immunoglobulin V region; immunoglobulin F;1-13/Domain: signal sequence (fragment) #status predicted <8IG>F;14-135/Product: Ig heavy chain (fragment) #status predicted <8NAT>F;27-111/Domain: immunoglobulin homology 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 FNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARLGPDDYTLDGMDVWGQGTTVT 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain precursor V-D-J region (clone mAB 61VH) - human (fragment) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Decies: Howo-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999 C;Accession: S78051; S23716 R;Harindranath, N.
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
                                                                                                                                                                                                                                                                                                                                                1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
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                                                         F:114/Domain: signal sequence (fragment) #status predicted <SIG>F:15-140/Product: Ig heavy chain (fragment) #status predicted <MAT>F:29-111/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                               Length 140;
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Superfamily: immunoglobulin V region; immunoglobulin homology Keywords: immunoglobulin
                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                               15;
                                                                                                                                                                                                    76.8%; Score 498.5; DB 2
77.0%; Pred. No. 3.1e-37;
tive 9; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, August 1990
A;Reference number: S78051
                                                                                                                                                                                                 Query Match 76.88 Best Local Similarity 77.09 Matches 97; Conservative
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C'Species: Doble 1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
C'Accession: B26340
R'Kodaira, M.; Kinashi, T.; Umemura, I.; Matsuda, F.; Noma, T.; Ono, Y.; Honjo, T.
J. Mol. Biol. 190, 529-541, 1986
A;Title: Organization and evolution of variable region genes of the human immunoglobulin A;Reference number: A26340; MUID:87061007; PMID:3097326
                                                                                                                                                                                            C;Accession: S09711
R;Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990
A;Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains A;Reference number: S09710; MUID:90262535; PMID:2111699
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Species: Homo sapiens (man)
Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-116/Product: Ig heavy chain V region 71-4 #status predicted <MAT>
F;34-116/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-146 <HUGA
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-118/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-116 < KOD>
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Hypothetical protein.
                                                     (Human)
                                                                                                    SEQUENCE FROM N.A
                                                                                  NCBI_TaxID=9606;
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                                                                     1 QVQLQESGPGLVKPSETLSLTCTVSGGSISS -- YYWSWIRQPPGKGLEWIGYIYYTWTSN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN 60
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                                                     Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDINE-98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; MuX.r. Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 79.4%; Score 515; DB 2; Length 119; Best Local Similarity 82.6%; Pred. No. 1e-43; Matches 100; Conservative 8; Mismatches 11; Indels
                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;
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119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;
                            Query Match 79.5%; Score 516; DB 2; L. Best Local Similarity 79.7%; Pred. No. 3.6e-43; Matches 102; Conservative 10; Mismatches 8;
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EMBL, AR035041, AADS6277.1; -.
FIR; PHO876; PHO876.
PIR; SI2416; SI2416.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig.v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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                                                                                                                                                                                                                                                                     SUBGENCE FROM N.A.

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

REDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Rausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.P., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.P., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahesley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

M. Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,

Jand B. M. M. Schein J. B. More C. Man Schein J.E.,

R. Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.4e-41;
6; Mismatches 13; Indels 3
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Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011857; A4H11857.2; -.
PIR; S15590; S15590.
R HSPS; P01820; 1G7J.
R HSPS; P01820; 1G7J.
R InterPro; IPR001359; Ig.
R InterPro; IPR00110; Ig-like.
R InterPro; IPR001359; Ig.
R InterPro; IPR001359; Ig.
R InterPro; IPR001359; Ig.
R InterPro; IPR001359; Ig.
R SMART; SM00409; IGC; 2.
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PROSITE; PS00290; IG MHC; UNKNOWN 3.
SEQUENCE 620 AA; 68125 MW; 990A1A4A6E8FF27B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                            (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
  620 AA
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82.0%;
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Matches 100; Conservative
PRELIMINARY;
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Homo sapiens (Human).
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TISSUB-Primary B-Cells;

XEQUENCE FROM N.A.

TISSUB-primary B-Cells;

XEAUSDE-Primary B-C. Farmer L., Shenmen C.M., Schuler G.D.,

XEAUSDE-PRIMARY B-C., Wagner L., Schaefer C.F., Bhat N. K.,

XEAUSDE-PRIMARY B-C., More M., Moore T., Max S. I., Wang J., Haish F.,

XEAD Brownstein M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

XEAUSDE-PRIMARY B-C., Abramson R.D., Mullahy S.J.,

XEAUSDE-PRIMARY B-C., Allaes S., Garciach P. P., Wallahy S.J.,

XEAUSDE-PRIMARY B-C., Allaes S., Garciach C., Mullahy S.J.,

XEAUSDE-PRIMARY B-C., Allaes S., Garciach C.J., Lu X., Gibbs R.A.,

XEAUSDE-PRIMARY B-C., Shevchenko Y., Boulfard G.G.,

XEAUSDE-PRIMARY B-C., Shevchenko Y., Boulfard G.G.,

XEAUSDE-PRIMARY B-C., Schmutz J., Myers R.M., Butterfield Y.S.,

XEAUSDE-PRIMARY M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

XEAUSDE-PRIMARY B-C., Galmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

XEAUSDE-PRIMARY B-C., Galmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

XEAUSDE-PRIMARY B-C., Galmwood J., Schmutz J., Myers R.M., Schein J.E.,

XEAUSDE-PRIMARY B-C., Galmwood J., Schmutz J., Myers R.M., Schein J.E.,

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XEAUSDE-PRIMARY B-C., Galmwood J., Schmutz J., Myers R.M., Schein J.E.,

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XEAUSDE-PRIMARY B-C., Galmwood J., Schmutz J., Myers R.M., Schein J.E.,

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XEAUSDE-PRIMARY B-C., Galmwood J., Schmutz J., Myers R.M., Schein J.E.,

XEAUSDE-PRIMARY B-C., Galmwood J., Schmutz J., Myers R.M., Schein J.E.,

XEAUSDE-PRIMARY B-C., Galmwood J., Schmutz J., Myers R.M., Schein J.E.,

XEAUSDE-PRIMARY B-C.M., Schmutz J., Myers R.M., Schein J.E.,

XEAUSDE-PRIMARY 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 PSLKSRVTLSLDTSKNQFSLRLNSVTAADTAVYYCAHG-SSW--DFAFDYWGQGTLVTVS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 76.8%; Score 498.5; DB 2; Length 477; Best Local Similarity 81.0%; Pred. No. 2e-41; Matches 98; Conservative 8; Mismatches 12; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.; Strausberg R.; Strausberg R.; Submitted (Jun-2004) to the EMBL/GenBank/DDBJ databases. BMBL; BC073765; AAH73765.1; -
InterPro; IPR003599; Ig. InterPro; IPR003597; Ig. C1.
InterPro; IPR003597; Ig. C1.
InterPro; IPR003596; Ig. MHC.
InterPro; IPR003596; Ig. WHC.
Pfam; PF00647; C1-8et; Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 477 AA, 51631 MW; 9FES9C09C50CFF85 CRC64;
                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
477 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00409; IG; 4.
SMART; SM00407; IG; 3.
SMART; SM00406; IGV; 1.
PROSITE; PS00290; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
PRT;
                                                                                05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences."
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
                                                                                                                                                                                                                Hypothetical protein
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 S 121
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59 YNPSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCARDOGOWLLPDAFDIWGOGTWVT 118
                                                                                                                                                                                                                                                                                     79 YNPSLESRLSISIDTSKNOPSLRINSLTAADTAVYFCARGVG---LGTAFDIWGGGTVVT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 YNPSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 YNPSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCAR-----LGMGAFDFWGHGTMVT 134
                                                                                                                                                                                                       19 QVQLQESGPGLVKPSQTLSLTCTVSGGSIGSGDYFWSWIRQAPGRGLEWMGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 QLQLQESGPGLVKPSETLSLSCTVSGGSISSTNYYWGWIRQPPEKGLEWIGSLHNSGSDY
                                                                                                                                                                                  1 QVQLQESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYTWTSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLQESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYTWTSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                      DB 2; Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.3%; Score 482.5; DB 2; Length 150; 79.7%; Pred. No. 2.3e-40; ive 6; Mismatches 12; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VH4 heavy chain variable region.
                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
Submitted (CCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF103795; AAC79084.1; -.
PIR; S131673; S14673.
PIR; S78056; S78056.
HSSP, P01820; 1G7J.
InterPro; IPR007110; Ig-like.
InterPro; IPR003196; Ig-v.
SMART; SM00406; IGV;
                                                          478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 AA; 16315 MW; 85664E04938AA7C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
VH4 heavy chain variable region precursor (Fragment)
                                                                                                  76.0%; Score 493.5; DB 2; 77.2%; Pred. No. 6.5e-41; ive 15; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                576 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Potential.
PROSITE; PS00290; IG_MHC; UNKNOWN_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                   Best Local Similarity 77.28 Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19
                Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   136 VSS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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SEQUENCE
                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=IGM;
                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Q6P4I8
ID Q6P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
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NA FT S
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TISSUE-Human rectum tumor;

TISSUE-Human rectum tumor;

Polocker H., Boecher M., Weil B., Amid C., Osanger A.,

Polocker H., Wiemann S.;

L. Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BX538066; CAD97996.1; -.

REMBL; BX538066; CAD97996.1; -.

REMBL; BX538066; CAD97996.1; -.

REPTO; IPRO0110; Ig-11ke.

RICHEPTO; IPRO01306; Ig-C1.

RICHEPTO; IPRO03596; Ig-C1.

RICHEPTO; IPRO03596; Ig-V.

Peam; PF07654; C1-set; Z.

SMART; SMO0406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGY1YYTWTSNYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYN
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                       01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Full-length cDNA clone CSODL004YM19 of B cells (Ramos cell line)
Homo sapiens (Human) (Fragment).
                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Genoscope,
Submitted (FBB-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (FBB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BX248300; CA662627.1; -.
HSSP; P01820; 1G7J.
InterPro; IPR007110; Ig-like.
InterPro; IRR00356; Ig-v.
SMART; SM004106; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUEs cells;
Li W.B., Gruber C., Jessee J., Polayes D.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER 1 -1
SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2003 (TrEWBLrel. 25, Created)
01-0CT-2003 (TrEWBLrel. 25, Last sequence update)
01-MAR-2004 (TrEWBLrel. 26, Last annotation update)
Hypothetical protein DKFZp686K04218 (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98
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                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. TISSUE=B cells;
                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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Q72379;
                                                        86SX2;
                                   Q86SX2
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Matches
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                Q86SX2
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PRELIMINARY;
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Q96KX8
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                                                                                                                                                                                                                                                                                                          CISSUE-Erimary B-Cells,

RECURNE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RETAUSDERGR R.D., Feingold E.A., Grouse L.H., Derge J.G.,

RETAUSDERGR R.D., Feingold E.A., Grouse L.H., Derge J.G.,

RETAUSDERGR R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RAD Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

Rronstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergern B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Radriguez A.C., Grimwood J., Smailus D.E., Schnerch A., Schein J.E.,

Rodriguez A.C., Grimwood J., Smailus D.E., Schnerch A., Schein J.E.,

Rodriguez A.C., Marra M.A.;

Rad mouse cDNN sequences.",

R. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQESGPGLVKPSETLSLTCTVSGGSI-SSYYWSWIRQPPGKGLEWIGYIYYTWTSNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                              Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC063384; AAH63384.1; -.
HSSP; P01820; 1A7N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; Pr00047; ig; 1.
SMART; SM00409; IG; 1.
SMART; SM00409; IG; 1.
SMART; SM00407; IGC1; 3.
SMART; SM00407; IGC1; 3.
PROSITE; PS00290; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
SEQUENCE 576 AA; 63363 MW; FBB97C949D720F1E CRC64;
                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig c1.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig v.
Pfam; PF07654; C1-set; Z.
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Best Local Similarity 76.2'
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
                                                                                                                                                          Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                     GHD protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116
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DDT TAREA TO THE TOTAL TO THE T
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RESULT 10

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59 YNPSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARD-QGQ--WLLPDAFDIWGQGT 115
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ILSUBE-Human rectum tumor;

A FODO G., Han M., Mewes H.W., Weil B., Amid C., Osanger A.,

B loecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,

R FODO G., Han M., Wiemann S.,

IL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

R SS18077, CAD98001.1;

R HSSP, PO1820; 1G7J.

R INCEPTO; IPR003159; 1G —1.

R INCEPTO; IPR004059; 1G —1.

R ROSITE; PSS0815; 1G LIKE; 4.

PROSITE; PSS0815; 1G LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLQESGPGLVKPSETLSLTCTVSGGSIS--SYYWSWIRQPPGKGLEWIGYIYYTWTSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Lung;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;
                                Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.7%; Score 472; DB 2;
75.4%; Pred. No. 9.5e-39;
ive 9; Mismatches 12;
01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence upda')
01-MAR-2004 (TrEMBLrel. 26, Last annotation up
Hypothetical protein DKFzp686C02218 (Fragment)
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
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Homo sapiens (Human).
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147 LVTVSS 152
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Best Local Similarity
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QBWUX4;
01-MAR-2002 (
01-MAR-2004 (
                                                                                                                                        DOMAIN
DISULFID
NON TER
SEQUENCE
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Best Local 8
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DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLQESGPGLVKPSETLSLTCTVSGGSI -- SSYYWSWIRQPPGKGLEWIGYIYYTWTSN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 ÓLÓLÓESGPGLVKSSETLSLTCTVSGGSISSSSÝÝWGWIRÒPPGKGLEWIANTÝÝSGITY 79
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N 122

N 
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Kozywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 496;
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUB-Lung;
Strausberg R.;
Strausberg R.;
Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC016369; AAH16369.1; -.
HSSP; PO1876; 10W0.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003596; Ig_wHC.
InterPro; IPR003596; Ig_w.
PE07654; CI-set; Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WN 1.
D346929849040D69 CRC64;
                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 460.5; DB 2;
Pred. No. 1.4e-37;
8; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
IIG heavy chain V-II region ARH-77 precursor.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00406; IGV; 1.
PROSITE; PSS0835; IG LIKE; 4.
PROSITE; PS00290; IG MC; UNKNOWN
SEQUENCE 496 AA; 53391 MW; D34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.0%;
74.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 74.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TMVTVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLVTVSS 143
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HV2I HUMAN
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TISSUE=Lymph;

KX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

KR Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Frange C.,

RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Nillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Adriguez A.C., Grimwood J., Schmutch A., Schein J.E.,

RA Jones S.J., Marra M.A.,

RA Jones S.J., Marra M.A.,

RA Jones S.J., Marra M.A.,

RA "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 TSLKSRVTISLDTSKNLFSLKLSSVTAADTAVYYCARGLLRGGWNDVDYYYGMDVWGQGT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARD--QGQWLLPDAF---DIWGQGT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 QVQLQQWGAGLVKPSETLSLTCAVFGGSFSGYYWSWIRQPPGRGLEWIGEINHSGSTNYK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                        Ig heavy chain V-II region ARH-77. V segment. U Segment. U Segment. U segment. By similarity.
                                                                                                                                                                                                                                                                                                                                                                                  2.
                                                                                                                                                                                                                                                                                                                               DB 1; Length 146;
                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO19235; AAH19235.2; -.
PIR; G34964; G34964.
HSSP; P01861; 1ADQ.
                                                                                                                                                                                                                                                                         16228 MW; 8D7FD52BB218171F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                         Score 454.5; DB 1
Pred. No. 1.4e-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   595 AA.
                                                                                                                                                                                                                                                                                                                                                                                  11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
SMART; SM00406; IGv; 1.
RMSOITE; PSS0835; IG LIKE; 1.
Immunoglobulin V region; Signal.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-WAR-2002 (TrEMBLrel. 20, Ca
01-WAR-2004 (TrEMBLrel. 26, La
01-WAR-2004 (TrEMBLrel. 26, La
Hypothetical protein.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                            70.0%;
                                                                                                                                                                                                                                                                                                                                                                               91; Conservative
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117
127
146
115
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                                                                                                                                                                                                                                                                      146 AA;
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142
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X STAGENEE R.D., Felngold E.A., Grouse L.H., Derge J.G.,

A Klausher R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

W. Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human

"The Stalks B. "Touchman M." "Touc
                                                                                                                                                                                                                                                                                                                                                                                          61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCAR-----DQGQWLLPDAFDIWG 112
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                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                        Ouery Match 69.5%; Score 451; DB 2; Length 595; Best Local Similarity 69.8%; Pred. No. 1.5e-36; Matches 90; Conservative 10; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.; Strausberg R.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. InterPro; IPR03599; IG. InterPro; IPR003599; IG. InterPro; IPR003597; IG. InterPro; IPR003506; Ig. InterPro; IPR003596; Ig. InterPro; IPR003596; Ig. HC.
                     SMART; SM00409; IG; 2.
SWART; SM00407; IGc1; 4.
SWART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS50290; IG_MHC; UNKNOWN_3.
Hypothetical protein.
SEQUENCE 595 AA; 65290 MW; 0D4B50776545714E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human)
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Pfam; PF07654; C1-set; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 QGTMVTVSS 121
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MALGARIA S.D., Collins F.S., Magner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Bronstein M.J., Usdin T.B., Toshiyuki S., Carnino: P., Marabe F., Bronstein M.J., Usdin T.B., Toshiyuki S., Carnino: P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Myers R.W., Jucken M.J., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Junara M.A.; Maria M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCAR-----DQGQWLLPDAFDIWG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 QVQLQQWGAGLLKPSETLSLTCGVXGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYN 79
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                               Length 597;
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002963; AAH02963.1; -.
HSSP; P01861; 1ADQ.
                                                                                                                                                                                                        Hypothetical protein. SeQUENCE 597 AA; 65304 MW; 2A1E75F6AED85230 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                      ch 69.5%; Score 451; DB 2; Similarity 69.8%; Pred. No. 1.5e-36; 90; Conservative 10; Mismatches 17;
Pfam, PF07654; Cl-set; 4.
Pfam, PF00767; ig; 4.
SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 4.
SMART; SM00406; IGV; 1.
PROSITE; PS500155; IG LIKE; 5.
PROSITE; PS001290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QGTMVTVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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November 9, 2005, 11:43:32 ; Search time 72.1353 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                      - protein search, using sw model
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(without alignments) 627.306 Million cell updates/sec		L QVQLQESGPGLVKPSQTLSLARGGDGYKYWGQGTLVTVSS 117	
	US-10-660-357A-5	1 QVQLQESGPGLVKPSQTLSL	
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Sequence:	1 QVQLQESGPGLVKPSQTLSLARGGDGYKYWGQGTLVTVSS
Scoring table: BLOSUM62 Gapop 10	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	2105692 seqs, 386760381 residues
Total number of	Total number of hits satisfying chosen parameters: 2105692

seq length: 0 seq length: 200000000 88 Minimum I Maximum I Ď

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	. A Geneseq 16Dec04:* 1: geneseqp1980s:* 3: geneseqp2190s:* 4: geneseqp2001s:* 5: geneseqp2001s:* 6: geneseqp2003s:* 7: geneseqp2003s:*
Post-processing:	Database : 11 2 2 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	776 Anti-huma	- 1				846 Human ant	784 Anti-huma	388 Anti-MUC1	826 Human ant	_	_	974 Murine-ex	373 Murine-ex	775 Human HIV	377 Antibody	_	765 Human HIV	745 Human HIV	935 Murine-ex	_	977 Murine-ex	981 Murine-ex	133 Antibody	976 Heavy cha	114 anti-Ob-R
	Descri	Adc99776	Add05380	Ad£09818	Adc99804	Add05408	Adf09846	Adc99784	Add05388	Adf09826	Adp03968	Adp03870	Adp03974	Adp03873	Aab62775	Adj80377	Adp03970	Aab62765	Aab62745	Adp03935	Adp03934	Adp03977	Adp03981	Aaw78433	Abb97976	Adg88414
	ID	ADC99776	ADD05380	ADF09818	ADC99804	ADD05408	ADF09846	ADC99784	ADD05388	ADF09826	ADP03968	ADP03870	ADP03974	ADP03873	AAB62775	ADJ80377	ADP03970	AAB62765	AAB62745	ADP03935	ADP03934	ADP03977	ADP03981	AAW78433	ABB97976	ADG88414
	DB	7	7	7	7	7	7	7	7	7	7	7	7	7	4	7	7	4	4	7	7	7	,	N	ß	7
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de	Query Match	100.0	100.0	100.0	9.96	96.6	96.6	93.9	93.9	93.8	91.4	91.4	8.06	90.8	89.8	89.5	89.4	89.1	89.0	89.0	88.9	88.9	88.8	88.8	88.8	88.8
	Score	625	625	625	604	604	604	587	587	587	571.5	571	567.5	567.5	561	559.5	559	557	556.5	556.5	555.5	555.5	555	555	555	555
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_	Adp03868 Murine-ex	Adp03876 Murine-ex	Adp03875 Murine-ex	Adp03871 Murine-ex	Aau81276 Human trk	Adp03872 Murine-ex	Adp22366 Human ant		Abp45608 Human BLy	Adg96435 Single ch				_		Aau81273 Human trk	Aay15126 Anti-muri	Adp22124 Human ant	Adp22104 Human ant
ADP03869	ADP03868	ADP03876	ADP03875	ADP03871	AAU81276	ADP03872	ADP22366	ADP03982	ABP45608	ADG96435	ABP45983	ADG96810	ADP03961	ADP03969	ADQ91396	AAU81273	AAY15126	ADP22124	ADP22104
123 7		125 7								253 7									
		88.5	88.4	88.3	88.3		88.1	88.0	88.0	98.0	87.9	87.9	87.8	87.8	87.7	87.6	87.6	87.4	87.4
555	553	553	552.5	552	552	551	550.5	550	550	550	549.5	549.5	549	548.5	548	547.5	547.5	546.5	546.5
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast; Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 5. ADC99776 standard; protein; 117 AA. 26-DEC-2002; 2002WO-US041581. 28-DEC-2001; 2001US-0346299P. (first entry) WPI; 2003-587113/55. (ABGE-) ABGENIX INC lung cancer; human. WO2003057838-A2. Homo sapiens. 01-JAN-2004 17-JUL-2003. ADC99776; Gudas J; RESULT 1 ADC99776

ADC997776

ADC997776

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ADC997776

ADC99777

New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.

N-PSDB; ADC99778

Claim 1; SEQ ID NO 5; 78pp; English.

The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the cell surface such as tumours, specifically melanoma, oesophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody

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Gaps ö

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Best Loca Matches

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RESULT 2 ADD05380

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The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other mallghancies. The present amino acid sequence represents a heavy chain from an MUC18 tumour antigen-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.
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                                                                                                                                                                                                     61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGDGYKYWGQGTLVTVSS 117
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                                                                                                      1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell proliferation inhibition; MUC18 tumour antigen; anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour; carcinoma; cancer; malignancy; heavy chain; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human anti-MUC18 monoclonal antibody heavy chain #2.
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Pred. No. 1.7e-45; Mismatches 0;
                                   Mismatches
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       100.08;
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                                   117; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                               ADF09818;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gudas J;
                                Matches
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ADF09818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
                                                                                                                                                                                                                                                                                                                         YNPSLKSRVTISVDISKNQFSLKLSSVTAADTAVYYCARGGDGYKYWGQGTLVIVSS 117
                                                                                                                                                                                                                                                                                                YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGDGYKYWGQGTLVTVSS 117
                                                                                                                                                                                                   1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGY1YYSGSTY
                                                                                                                                                                                                                                 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY
                                                                                                                                                      Gaps
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                                                                                                 Length 117;
                                                                                                    100.0%; Score 625; DB 7; 100.0%; Pred. No. 1.7e-45;
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                                                                                                                                                   0; Mismatches
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     heavy chain protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 5; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADD05380 standard; protein; 117 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bar-Eli M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-577496/54.
                                                                                                                          Local Similarity
les 117; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB, ADD05382.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         metastatic tumor.
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                                                       Sequence 117 AA;
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                                                                                                      Query Match
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Length 117; Indels us-10-660-357a-5.rag

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monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
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                                        Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 33; 87pp; English.
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                                                                                                                                                                                                                                                                                                        28-DEC-2001; 2001US-0346460P
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                          Gudas J, Bar-Eli M;
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                                                                                                                                                                                                                                                                                                                                                 (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        metastatic tumor.
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01-JAN-2004
                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                    anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the cell surface such as tumours, specifically melanoma, oesophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.
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                                                                                                                                                                                                  Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 33
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Pred. No. 1.1e-43;
7; Mismatches 0; Indels
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                                                                          ADC99804 standard; protein; 117 AA.
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Best Local Similarity 94.0%;
Matches 110; Conservative
                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-587113/55.
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                                                                                                                                                                                                                                                                                                      lung cancer; human.
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                                                                                                                   ADC99804;
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                                                       ADC99804
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The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the antibody comprists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds MUCIS, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has cytostatic and can be used in the production of a vaccine. The monoclonal antibodies against the MUCIS antigen are useful for diagnosing and
                                                                                                                                                                                                                                                                                                  treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or tumour metastasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-ufC18 antibody heavy chain, variable region,
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Pred. No. 1.1e-43;
7; Mismatches 0; Indels
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Best Local Similarity 94.0%;
Matches 110; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                              protein of the invention.
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ADD05408 standard; protein; 117

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a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the cell surface such as tumours, specifically melanoma, oesophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithehial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody heavy chain protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                              New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel isolated monoclonal antibody comprising
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Pred. No. 2.9e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 13; 78pp; English.
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   26-DEC-2002; 2002WO-US041581
                                                                      28-DEC-2001; 2001US-0346299P
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Matches 110; Conservative
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N-PSDB; ADD05390.
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N-PSDB; ADC99786.
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                                                                                                                                         (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 117 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid sequence represents a heavy chain from an MUC18 tumour antigen-specific
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-
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anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour; carcinoma; cancer; malignancy; heavy chain; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 33; 83pp; English.
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ses 110; Conservative
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                                                                                                         Homo sapiens
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Length 117; Indels vaccine; chain.

Homo

RESULT 7 ADC99784

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Use of monoclonal antibodies against MUC18 antigen, for diagnosing an treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having Claim 1; SEQ ID NO 13; 87pp; English. metastatic tumor.

The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the monoclonal antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has cytostatic and can be used in the production of a vaccine. The monoclonal antibodies against the MUC18 antigen are useful for diagnosing and treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or tumour metastasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumour. This sequence tepresents an anti-MUC18 antibody heavy chain, variable region, protein of the invention.

Sequence 117 AA;

ö QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY 60 9 YNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCARGGDGYKYWGQGTLVTVSS 117 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYCAREGDGFDYWGQGTLVTVSS 117 1 QVQLQESGRGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY Gaps .; 0 Score 587; DB 7; Length 117; Pred. No. 2.9e-42; 4; Mismatches 3; Indels 93.9%; Query Match Best Local Similarity 94.0 Matches 110, Conservative ч 61 g g 8 ઠે

RESULT 10

ADP03968

ADF09826 standard; protein; 117 12-FEB-2004 ADF09826; RESULT 9 ADF09826

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Human anti-MUC18 monoclonal antibody heavy chain #4 (first entry)

anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour; carcinoma; cancer; malignancy; heavy chain; human.

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WO2003057837-A2

17-JUL-2003

26-DEC-2002; 2002WO-US041580

28-DEC-2001; 2001US-0346414P.

(ABGE-) ABGENIX INC

Gudas J;

WPI; 2003-598367/56. N-PSDB; ADF09828. Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.

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                                                         The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid sequence represents a heavy chain from an MUC18 tumour antigen-specific
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94.0%; Pred. No. 2.9e-42;
ive 4; Mismatches 3; Indels
                  Claim 1; SEQ ID NO 13; 83pp; English.
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                                                                                                                                                                                                                                                                   monoclonal antibody.
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110; Conserv
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monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen; cytostatic; colorectal neoplasm; renal call carcinoma; cervical intraepithelial squamous neoplasia; cervical intraepithelial glandilar neoplasia; oesophageal; breast cancer; gene therapy; murine; mouse; human; heavy chain variable domain. Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 138 ADP03968 standard; protein; 118 AA (first entry) 29-JUL-2004 ADP03968;

Unidentified

WO2003048328-A2

12-JUN-2003.

02-DEC-2002; 2002WO-US038550.

03-DEC-2001; 2001US-0337275P

(ABGE-) ABGENIX INC

Gallo Σ Handa Gudas J, Foltz I,

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WPI; 2003-523295/49.

New anti-CA IX monoclonal antibody, useful for treating a tumor e.g., colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical intraepithelial aquamous and glandular neoplasia or esophageal tumors.

Example 2; SEQ ID NO 138; 89pp; English.

The invention relates to a novel isolated monoclonal antibody (mAb) comprising a heavy chain polypeptide and light chain polypeptide having a sequence chosen from one of 53 fully defined amino acid sequences given in the specification, where the antibody specifically binds carbonic anhydrase IX (CA IX) tumour antigen. The antibody of the invention demonstrates cytostatic activity and may be useful for treating a tumour,

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transgenic mouse strain.

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Sequence 123

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The invention relates to a novel isolated monoclonal antibody (mAb) comprising a heavy chain polypeptide and light chain polypeptide having a sequence chosen from one of 53 fully defined amino acid sequences given in the specification, where the antibody specifically binds carbonic anhydrase IX (CA IX) tumour antigen. The antibody of the invention demonstrates cytostatic activity and may be useful for treating a tumour, such as colorectal neoplasm, renal cell carcinoma, cervical intraeptibelial squamous and glandular neoplasia, oseophageal tumour or breast cancer, possibly via gene therapy. The current sequence is that of a murine-expressed anti-human CA IX monoclonal antibody VH (heavy chain variable domain) protein of the invention. The protein was generated via the introduction of the human CA IX protein into
                cervical intraepithelial squamous and glandular neoplasia, oesophageal tumour or breast cancer, possibly via gene therapy. The current sequence is that of a murine-expressed anti-human CA IX monoclonal antibody VH (heavy chain variable domain) protein of the invention. The protein was generated via the introduction of the human CA IX protein into a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer;
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  colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                    monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen; cytostatic; colorectal neoplasm; renal cell carcinoma; cervical intraepithelial squamous neoplasia; cervical intraepithelial glandular neoplasia; oesophageal; breast gene therapy; murine; mouse; human; heavy chain variable domain.
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                                                                                                                                                                                                 Score 571.5; DB 7; Length 118; Pred. No. 6.1e-41; 1; Mismatches 5; Indels 1
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Matches 111; Conservative
                                                                                                                    transgenic mouse strain.
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                                                                                                                                                              Sequence 118 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel isolated monoclonal antibody (mAb) comprising a heavy chain polypeptide and light chain polypeptide having a sequence chosen from one of 53 fully defined anino acid sequences given in the specification, where the antibody specifically binds carbonic anhydrase IX (CA IX) tumour antigen. The antibody of the invention demonstrates cycostatic activity and may be useful for treating a tumour, such as colorectal neoplasm, renal cell carcinoma, cervical intraepithelial squamous and glandular neoplasia, oseophagaal tumour or breast cancer, possibly via gene therapy. The current sequence is that of a murine-expressed anti-human CA IX monoclonal antibody VH (heavy chain variable domain) protein of the invention. The protein was generated via the introduction of the human CA IX protein into
                                                                                                                                                YNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCARGGDGY-----KYWGQGTLVT 114
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                                      Gaps
91.4%; Score 571; DB 7; Length 123; 90.2%; Pred. No. 7e-41;
                                      1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                  ADP03974 standard; protein; 120 AA.
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                                       Conservative
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                    Local Similarity
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   Query Match
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Best Local Similarity 91.0%;
Matches 111; Conservative
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                                                                                                                                   monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen; cytostatic; colorectal neoplasm; renal cell carcinoma; cervical intraepithelial squamous neoplasia; cervical intraepithelial glandilar neoplasia; oesophageal; breast cancer; gene therapy; murine; mouse; human; heavy chain variable domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel isolated monoclonal antibody (mAb) comprising a heavy chain polypeptide and light chain polypeptide having a sequence chosen from one of 53 fully defined anno acid sequences given in the specification, where the antibody specifically binds carbonic anhydrase IX (CA IX) tumour antigen. The antibody of the invention anhydrase IX (CA IX) tumour antigen. The antibody of the invention such as colorectal neoplasm, renal cell carcinoma, cervical intraepithelial squamous and glandular neoplasia, oseophagaal tumour or breast cancer, possibly via gene therapy. The current sequence is that of a murine-expressed anti-human CA IX monoclonal antibody VH (heavy chain variable domain) protein of the invention. The protein was generated via the introduction of the human CA IX protein into
                                                                                               9
                                                                         9
                                                                                                                                                                                                                                                                                                                                     Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 13
                                                                                     QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTY
                                                                                                                        YNPSLKSRVTISVDISKNOFSLKLSSVTAADIAVYYCARGGDGYKY-----WGQGTLVTV
                                                                       QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
intraepithelial squamous and glandular neoplasia or esophageal tumors.
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.
                                               7;
                         Length 120;
                                                 Indels
                       Score 567.5; DB 7
Pred. No. 1.4e-40;
; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallo M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 13; 89pp; English.
                                                                                                                                                                                                                                                            ADP03873 standard; protein; 120 AA
                                              2;
                     Query Match 90.8%;
Best Local Similarity 91.0%;
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-DEC-2002; 2002WO-US038550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-DEC-2001; 2001US-0337275P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Handa M,
                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transgenic mouse strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-523295/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Foltz I,
Sequence 120 AA;
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                                                                                                                                                                                               SS 120
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                                                                                                                                                                         SS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human monoclonal antibody immunoreactive with human immunodeficiency virus-1 glycoprotein gpl20, useful for detecting HIV-1 in biological sample and providing passive immunotherapy to HIV-1 infected mammal.
                                                                                                                                                                                                                                        61 YNPSLKSRVIISVDISKNOPSLKALSSVTAADTAVYYCAR--DGYNYWYFDLWGRGTLVTV
                                                                                                     1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY
                                                                                                                                  1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTY
                                                                                                                                                                                                           61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGDGYKY-----WGQGTLVTV
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                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus-1; HIV-1; human monoclonal antibody; envelope glycoprotein; gp120; diagnosis.
                                                        7;
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Pred. No. 4.8e-40;
3; Mismatches 5; Indels
                                                     Indels
Score 567:5; DB 7;
Pred. No. 1.4e-40;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human HIV-1 monoclonal antibody SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB62775 standard; protein; 120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 69; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUN-2000; 2000WO-US017327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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Best Local Similarity 91.6
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reitz MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-112438/12.
N-PSDB; AAF29076.
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                                                                                                                                                                                                                                                                                                              SS 117
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The invention relates to a method of producing a hybrid antibody or hybrid antibody fragment by: (1) providing an initial antibody having specificative for a target; (ii) determining the sequence of a variable region of the initial antibody; (iii) selecting a first component of the variable region consisting of FR1, FR2, FR3 and FR4; (iv) comparing the sequence of the first component to sequences contained in a reference database of antibody sequences or antibody fragment sequences from a target species; (v) selecting a sequence from an antibody in the database which demonstrates a high degree of homology to the first component; (vi) selecting a second component selected from the group consisting of FR1, FR2, FR3 and FR4; (vi) comparing the sequence of the second component to sequences contained in a reference database of antibody sequences or antibody fragment sequence attabase of antibody sequences or antibody fragment sequence attabase of antibody sequences from the database which demonstrates a high degree of homology to the second component and which is from a different antibody than the selected antibody; and (ix) operatively linking the selected framework sequences to one or more complementarity determining antibody tragment claimed). The antibody and fragment. The method is useful for producing a hybrid antibody or hybrid antibody tragment (claimed). The antibody and fragment claimed). The antibody wariable heavy or variable light chain to receive the CDRs. This produces antibodies that are highly homologous and exhibit reduced immunogenicity while maintend antibody variable heavy chain which has good homology to an initial antibody variable heavy chain which has good homology to an initial maintend antibody variable heavy chain which has good homology to an initial maintend antibody variable heavy chain which has good homology to an initial maintend antibody was used to generate a hybrid antibody of the invention.
                                                                                                                                                                                       Antibody variable heavy chain with homology to mouse anti-human antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Producing a hybrid antibody or hybrid antibody fragment by operatively linking the selected framework sequences to one or more complementarity determining regions of the initial antibody.
                                                                                                                                                                                                                                      hybrid antibody; antibody; framework region; homology; immunogenicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; SEQ ID NO 137; 77pp; English
                                              ADJ80377 standard; protein; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                              03-DEC-2002; 2002WO-US038450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-DEC-2001; 2001US-0336591P.
                                                                                                                                           06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ALEX-) ALEXION PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-513753/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wu D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                 402003048321-A2
                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                               12-JUN-2003
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                                                                                             ADJ80377;
RESULT 15
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2 VQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGXIXYSGSTYY 5 89.5%; Score 559.5; DB 7; Length 121; 89.3%; Pred. No. 6.5e-40; ive 3; Mismatches 5; Indels 5 Best Local Similarity 89.3 Matches 108; Conservative

Query Match

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62 NPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCARG-----GDGYKYWGQGTLVTVS 116 9, 2005, 12:55:24 Search completed: November Job time: 73.1353 secs 117 S 117 121 S 121 d ò à

1 VQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWNWIRQHPGKGLEWIGYIYYSGSTYY 60

2, Appli 142, App 3, Appli

Sequence Seq

OM protein

Run on:

Sequence:

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STREET: 1021
COMPILEY: JAMES S.
STREET: 1021
COUNTRY: USA
COMPRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
FILING DATE: 18-FEB-1998
FILING DATE: 18-FEB-1998
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-FEB-1995
ATTORNEY/AGENT: 18-AUG-1995
ATTORNEY/AGENT: 18-AUG-1995
ATTORNEY/AGENT: 18-AUG-1995
TELECOMMUNICATION NUMBER: A77,794
REFERENCE/DOCKET NUMBER: A0RPHO/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFO
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Pred. No. 7e-47;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AFPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: 11ag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Halev
             US-09-472-087-7.
US-09-472-087-86
US-09-472-087-86
US-09-138-018-148-79
US-09-138-0918-148-79
US-08-480-774A-2
US-08-45-809A-142
US-09-471-276-837
US-08-476-39-75
US-08-476-39-75
US-08-476-39-75
US-08-476-39-75
US-08-476-10
                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 39, Application US/09025769B; Patent No. 630066; GENERAL INFORMATION; APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 90.1%;
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
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MOLECULE TYPE: protein
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800.4
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39, Appl
39, Appl
39, Appl
65, Appl
55, Appl
5, Appl
5, Appl
5, Appl
11, Appl
11, Appl
11, Appl
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Sequence 4, Appli
                                                                                                                      9, 2005, 11:29:55; Search time 18.1805 Seconds (without alignments) 480.403 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 39, 1
Sequence 65, 2
Sequence 39, 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, A Sequence 11, Sequence 11, Sequence 11, Sequence 11,
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625
1 QVQLQESGPGLVKPSQTLSL......ARGGDGYKYWGQGTLVTVSS 117
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Sequence 65,
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Sequence 39,
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Sequence
Sequence
Sequence
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Compugen Ltd.
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US-09-490-070A-55
US-09-490-153-65
US-09-490-153-65
US-09-490-124-39
US-09-09-324-65
US-08-360-125-5
US-08-360-125-5
US-08-1017-628-5
US-08-1017-628-11
US-08-467-90-5
US-08-467-90-5
US-08-467-90-11
US-08-461-11
                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-490-153-25
US-09-490-324-25
US-09-720-493-2
                                                                                                                                                                                                                                                                                                                                513545 segs, 74649064 residues
             GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                     - protein search, using sw model
                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                          length: 0
length: 200000000
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Match Length
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Perfect score:
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Minimum DB Maximum DB

Database

Result No.

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Gaps

us-10-660-357a-5.rai

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US-09-490-070A-39
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      용
                                                                                                                      59 YNPSLKSRVIISVDISKNQFSLKLSSVIAADTAVYYCARWGGDGFYAMDYWGQGTLVTVS 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARWGCDGFYAMDYWGQGTLVTVS 118
                                                                                               YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-GGDGY---KYWGQGTLVTVS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQESGPGLVXPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY 60
                                    1 QVQLQESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYSGSTN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.9%; Score 543; DB 3; Length 119; 90.1%; Pred. No. 7e-47; ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER: ELAPBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: EP 95
FILING DATE: 18 -FEB-1998
FILING DATE: 18 -FEB-1998
FILING DATE: 18 -REB-1998
FILING DATE: 18 -RUG-1995
FILING DATE: 18 -RUG-1995
FILING DATE: TRUENDRAFILON:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     c/o Fish & Neave
                                                                                                                                                                                                                                                                                                                         Sequence 65, Application US/09025769B

Patent No. 6300064

GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 119 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 90.1
Matches 109; Conservative
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                                                                                               61
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59 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARWGGDGFYAMDYWGQGTLVTVS 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORPUTER: Floppy disk

COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: COlin G. Sandercock, ESG.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 31,298
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

86.9%; Score 543; DB 4; Length 119;
Best Local Similarity 90.1%; Pred. No. 7e-47;
Matches 109; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                     TITLE OF INDEXTION: Protein/ (Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1666 K Street, N.W., Suite 300 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 119 amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-070A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
US-09-490-070A-65
; Sequence 65, Application US/09490070A
Sequence 39, Application US/09490070A Patent No. 6696248 GENERAL INFORMATION:
                                                                                             APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 39
SEQUENCE CHARACTERISTICS
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ZIP: 20006
COMPUTER READABLE FORM:
                                                                                                                        Pack, Peter
Ilag, Vic
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61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-GGDGY---KYWGQGTLVTVS 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Knappik, Achim
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                       c/o Fish & Neave
                                                                                                                                                                                            COMPUTE: 19021

COMPUTE: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,153

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
    IITLE OF INVENTION: Protein/(Poly)peptide libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4;
                                                                     Haley, Jr., Esq. of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 86.9%; Score 543; DB 4; Best Local Similarity 90.1%; Pred. No. 7e-47; Matches 109; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18 FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18 AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/S
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 65, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                  ADDRESSEE: James F. STREET: 1251 Avenue
                       NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                              CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 S 117
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US-09-490-153-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Gaps
                                                                                                                                                                                                                                        ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe STREET: 1666 K Street, N.W., Suite 300 STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                     Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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Pred. No. 7e-47;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INPORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 39, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
                                       APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.9%;
                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20006
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 109; Conserva
                       GENERAL INFORMATION:
Patent No. 6696248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 $ 117
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Gaps

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59 YNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCARWGGDGFYAMDYWGQGTLVTVS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLQESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYSGSTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-GGDGY---KYWGQGTLVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 65, Application US/09490324

Patent No. 6828422

GENERAL INFORMATION:

APPLICANT: Raappik, Achim

Pack, Peter

Ilag, Vic

Ge, Liming

Moroney, Simon

Pluckthun, Andreas

TITLE OF INVENTION: Protein/(Poly) peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-3an-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 543; DB 4;
Pred. No. 7e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
PLING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 596-9000
TELEFAX: (212) 596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: 11near

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-324-39
                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 90.1
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10021
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US-09-490-324-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-GGDGY---KYWGQGTLVTVS
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Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
                                          ZIP: 10021

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IENC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 86.9%; Score 543; DB 4; Length 119; Best Local Similarity 90.1%; Pred. No. 7e-47; Matches 109; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FREJ-1998
APPLICATION NUMBER: EP 95
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                      NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 39, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 119 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELEFAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 65: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pack, Peter
Ilag, Vic
Ge, Liming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 $ 117
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TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL TYPE: antibody GAH
CELL LINE:
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US-08-450-578-5
; Sequence 5, Application US/08450578
; Patent No. 5837845
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: TOSHIARI TAGAWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOCUMENT NUMBER:

FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-5
                        REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
    REGISTRATION NUMBER: 33,367
                                                                                          TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
AUTHORS:
                                                                                                                                                                                                    single
                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                     STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                               FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                              HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANELLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL:
VOLUME:
ISSUE:
PAGES:
                                                                                                                                                                                                                                                                              ANTI-SENSE:
                                                                                TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYSGSTN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5767246ihiko ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Geolifically Binding to Surface Antigen of Cancer
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                  6; Gaps
                                                                                                                                                                                                                                                                                                                                                                     Query Match 86.9%; Score 543; DB 4; Length 119; Best Local Similarity 90.1%; Pred. No. 7e-47; Matches 109; Conservative 3; Mismatches 3; Indels
                                                                      NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REGISTRENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,125
                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; SEQUENCE DESCRIPTION: SEQ ID NO: 65: US-09-490-324-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,5
FILING DATE: June 29, 1992
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WATTEN M. Cheek, Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 8 117
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US-08-360-125-5
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1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY 60
                                                                                                                                                                                            1 QVQLQESGFGLVKPSQTLSLTCTVSGGSISSCGFYWNWIRQHPGKGLEWIGYIYYSGSTY 60
                                                                                                                                                                                                                                                                                              61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGG--DGYKYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                    61 YNPSLKSRVTISLDTSKSQFSLKLSSLTAADTAVYYCARSTRLRGADYWGQGTWVTVSS 119
                                                                           Gaps
Query Match
Best Local Similarity 86.6%; Pred. No. 4.4e-46;
Matches 103; Conservative 7; Mismatches 7; Indels
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1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY 60
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Patent No. 5990287

GENERAL INFORMATION

APPLICANT: HOSCKAWA, Saiko

APPLICANT: HOSCKAWA, Solko

APPLICANT: HOSCKAWA, Yoshiaki

APPLICANT: HOSCKAWA, Yoshiaki

APPLICANT: TO, No. 59902871hiko

APPLICANT: ITO, No. 59902871hiko

TITLE OF INVENTION: HUMBAR MONOCLONAL ANTIBEDDY SPECIFICALLY BINDING TO

TITLE OF INVENTION: HUMBARE, SAINGEN

FILE REFERENCE: 177/527361KH

CURRENT PALLICANT: 1998-02-02

EARLIER PAPLICATION NUMBER: 08/360,125

EARLIER APPLICATION NUMBER: 08/360,125

EARLIER PAPLICATION VORTE: 1994-12-20

NUMBER OF SEO ID NOS: 42

SOFTWARE: PATENTIN VORTE: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-014-880-5
US-09-014-880-5
Sequence 5, Application US/09014880
Sequence 5, Application US/09014880
Sequence 5, Application US/09014880
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA et al.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
TITLE OF INVENTION: HUMBRANE
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSCGFYWNWIRQHPGKGLEWIGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                             1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY
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                                                                                                                                                                                                                                                          Query Match 85.6%; Score 535; DB 2; Length 119; Best Local Similarity 86.6%; Pred. No. 4.4e-46; Matches 103; Conservative 7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; OTHER INFORMATION: Hybridoma producing human antibody GAH
US-09-017-628-5
                                                                                           DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Unknown
JOURNAL:
VOLUME:
ISSUE:
PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 5
LENGTH: 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-017-628-5
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                   APPLICANT: No. 58378451hiko ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESSE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COMPREY: U.S.A.
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL LINE:
ORGANELE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: DISKCTE, 5.25 INCN, 50 COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: MORDFREECT 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,578 FILING DATE: MS/25, 1995 CLASSIFICATION DATA:
APPLICATION NUMBER: 08/360,125 FILING DATE: December 20, 1994 FILING DATE: December 20, 1994 PRIOR APPLICATION NUMBER: 07/905,534 FILING DATE: June 29, 1992 ATTORNEY AGENT INFORMATION: NAME: WARTEN MC. CHECK, JT. REGISTRATION NUMBER: 33,367 REGISTRATION NUMBER: 33,367 REGISTRATION NUMBER: 33,367 REGISTRATION NUMBER: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
LOCATION:
DENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
    Yoko HIRAKAWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY:
    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
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ZIF: Z0005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordDerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,363
FILING DATE: May 25, 1995
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 03/360,125
FILING DATE: December 20, 1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: WALTEN M. Cheek, Jr.
RESTRENCEY/DOCKET NUMBER: 33,367
REERRENCEY/DOCKET NUMBER: 33,367
TELEEPAM: ZOZ-371-8850
TELEFAM:
TELEFAX:
                       STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL TYPE: antibody GAH
CELL LINE:
ORGANELLE:
INMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION:
MAP POSITION:
UNITS:
FRATURE:
NAMP FOSITION:
UNITS:
FRATURE:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
PUBLICATION INFORMATION:
PUBLICATION INFORMATION:
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
ANTI-SENSE:
FRAGNET TYPE:
ORIGINAL SOURCE:
  ADDRESSEE: Wenderoth,
                                                                      : D.C.
RY: U.S.A.
20005
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FILING DATE:
PUBLICATION DATE:
                                                                                           COUNTRY:
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                                                   CITY: STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGG--DGYKYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-08-450-363-5
; Sequence 5, Application US/08450363
; Patent No. 6436434
; GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
; APPLICANT: Tochiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 6436434ihiko ITO
APPLICANT: Wazuliro NAGAIKE
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY
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Best Local Similarity 86.6%; Pred. No. 4.4e-46;
Matches 103; Conservative 7; Mismatches 7; Indels
                                                                        CUTY: washing.cui
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 2006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compacible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,880
FILING DATE: January 28, 1998
CLASSIFICATION S36
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/450,578
FILING DATE: MAY 25, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/450,578
FILING DATE: June 29, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INPORMATION:
NAWE: Watten M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                  E: Wenderoth, Lind & Ponack, L.L.P.
2033 K Street, N.W., #800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 annino acids
TYPE: annino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
CELL TYPE: Hybridoma producing human
CELL TYPE: antibody GAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
CORRESPONDENCE ADDRESS:
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CORRESPONDENCE ADDRESS:
                                                                 Washington
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61 YNPSLKSRVTISVDTSKNOPSLKLSSVTAADTAVYYCARGG--DGYKYWGQGTLVTVSS 117
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APPLICANT: Saiko HOSOKAWA
APPLICANT: TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5767246ihiko ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
TITLE OF INVENTION: Cell Membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSCGFYWNWIRQHPGKGLEWIGYIYYSGSTY
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                                                                                                                                                                                     HAPLOTYPE: «Unknown»
TISSUE TYPE: «Unknown»
CELL TYPE: Hybridoma producing human
antibody GAH
CELL LINE: «Unknown»
ORGANELLE: «Unknown»
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805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                               DEVELOPMENTAL STAGE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                            CHROMOSOME/SEGMENT: <Unknown>
                                                                                                              STRAIN: <Unknown>
INDIVIDUAL ISOLATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 11, Application US/08360125; Patent No. 5767246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
                                                                                             ORGANISM: <Unknown>
                      HYPOTHETICAL: <Unknown>
ANTI-SENSE: <Unknown>
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                     LIBRARY: «Unknown»
CLONE: «Unknown»
POSITION IN GENOME:
MOLECULE TYPE: protein
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PUBLICATION DATE:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth
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Best Local Similarity
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VOLUME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE
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US-08-360-125-11
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                                                                                                                                                                                                                                                          61 YNPSLKSRVTISVDISKNOFSLKLSSVTAADIAVYYCARGG--DGYKYWGQGTLVTVSS 117
                                                                                                                                                        1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY
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                                                                                                                   Gaps
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                                                                    Length 119
                                                                                                                 7; Indels
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COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/467,903
FILING DATE: 21-Dec-1999
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION NUMBER: 08/450,363
FILING DATE: May 25, 1995
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
FILING DATE: June 29, 1992
APPLICATION NUMBER: 07/905,534
FILING DATE: June 28, 1991
APPLICATION NUMBER: JP188860/1991
FILING DATE: June 28, 1991
APPLICATION NUMBER: JP188860/1991
FILING DATE: June 28, 1991
APPLICATION NUMBER: JP188860/1991
FILING DATE: June 28, 1991
APPLICATION NUMBER: JP188861/1991
APPLICATION NUMBER: JP188861/1991
                                                                  85.6%; Score 535; DB 4;
86.6%; Pred. No. 4.4e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSER: Wenderoth, Lind & Ponack
STREET: 2033 K Street, N.W., #800
CITY: Washington
                                                                                                                 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Warren M.Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: June 28, 1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09467903
Patent No. 6787153
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 202-721-8200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Saiko HOSOKAWA
Toshiaki TAGAWA
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yoko HIRAKAWA
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MEDIUM TYPE: Diske
                                                                                        Best Local Similarity 86.6
Matches 103; Conservative
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US-08-450-363-5
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                                                                  Query Match
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COUNTRY:

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61 YNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCARGG-DGYKY----WGGGTLVTV 115
                                                                                     1 QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGSIYYSGSTY 60
                                            1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY
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INDIVIDUAL ISOLATE;
INDIVIDUAL ISOLATE;
INDIVIDUAL ISOLATE;
BUSULOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL TYPE:
CELL LINE:
CREALLINE:
CREALLINE:
CREANILLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
CHROMOSOME/SEGMENT:
MAP POSITION:
MAP POSITION:
MAP POSITION:
MAP POSITION:
MANE/KEY:
LOCATINES:
MANE/KEY:
LOCATINES:
MANE/KEY:
MANE/KEY:
MOTHER INFORMATION:
MUTHS:
MUTHORS:
MANE/KEY:
              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,125
FILING DATE: June 29, 1992
APPLICATION NUMBER: O7/905,534
FILING DATE: June 29, 1992
APPLICATION NUMBER:
FILING DATE: MARCH INFORMATION:
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER: TELEDEMONE: 202-371-8850
TELEDEMONE: 202-371-8850
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JOURNAL:
JOURNAL:
JUSTUE:
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SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
U.S.A.
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THE PAGE BLAWK (USPTO)

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Sequence 5, 1
Sequence 5, 1
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Sequence
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               GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-10-310-530-5
US-10-660-357-5
US-10-330-613-33
US-10-310-530-33
US-10-660-357-33
US-10-330-613-13
US-10-60-357-13
US-10-60-357-13
US-10-60-357-13
US-10-309-762-138
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Maximum Match 100%
Listing first 45 summaries
                                                                                                sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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100.0%; Pred. No. 1.7e-47;
iive 0; Mismatches 0;
             US-10-309-762-144

US-10-309-762-144

US-10-910-9010-20

US-10-908-17-137

US-10-908-17-137

US-10-908-17-137

US-10-908-162-140

US-10-908-360-40

US-10-908-360-40

US-10-309-762-147

US-10-309-762-147

US-10-309-762-151

US-10-309-762-16

US-10-309-762-16

US-10-309-762-16

US-10-309-762-16

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US-10-309-762-18

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US-09-880-748-1994
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Fublication No. US20030147809A1
GENERAL INFORMATION:
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC
FILE REFERENCE: ABGENIX.02A
CURRENT APPLICATION NUMBER: US/10/330,613
CURRENT FILING DATE: 2002-12-26
FRIOR PELING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 40
SEQ ID NO 5
SEQ ID NO 5
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   Query Match
Best Local Similarity 100.
Matches 117; Conservative
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ORGANISM: Homo Sapiens
 US-10-330-613-5
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RESULT

FITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN

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Sequence 5. Application US/10330530
Publication No. US20030152514A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
FILE REFERENCE: ABGENIX.031A
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: US 60/346414
PRIOR APPLICATION NUMBER: US 60/346414
PRIOR PILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 5, Application US/10660357

Publication No. US20040115205A1

GENERAL INFORMATION:
APPLICANT: Bar-Eli, Menashe
APPLICANT: Green, Larry L.
TILLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
TILLE REFERENCE: ABGENIX 030C1
CURRENT APPLICATION NUMBER: US/10/660,357
CURRENT APPLICATION NUMBER: 10/330,580
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
NUMBER OF SEQ ID NOS: 40

SOOTWARE: FastSEQ for Windows Version 4.0
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; Pred. No. 1.7e-47;
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100.0%; Pred. No. 1.7e-47;
tive 0; Mismatches 0;
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; Sequence 33, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
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Best Local Similarity 100.0%;
Matches 117; Conservative 0
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Best Local Similarity 100.
Matches 117; Conservative
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; ORGANISM: Homo Sapiens
US-10-660-357-5
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LENGTH: 117
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Sequence 33, Application US/10330530

Sequence 33, Application US/10330530

Publication No. US20030152514A1

GENERAL INFORMATION:

APPLICANT: Gudas, Jean

TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES

FILE REPERENCE: ABGENIX.031A

CURRENT APPLICATION NUMBER: US/10/330,530

CURRENT FILING DATE: 2002-12-26

PRIOR APPLICATION UNWBER: US 60/346414

PRIOR PILING DATE: 2001-12-18

NUMBER OF SEQ ID NOS: 40

SOFTWARE: PASESEQ FOR Windows Version 4.0

SEQ ID NO 33
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Pred. No. 1.2e-45;
7; Mismatches 0; Indels
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96.6%; Score 604; DB 14; Length 1

Best Local Similarity 94.0%; Pred. No. 1.2e-45;

Matches 110; Conservative 7; Mismatches 0; Indels
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Publication No. US20040115205A1

GENERAL INFORMATION:
APPLICANT: Bar-El1, Menashe
TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
TITLE OF INVENTION: USE OF ANTIGEN
FILE REFERENCE: ABGENIX.030C1
CURRENT APPLICATION NUMBER: US/10/660,357
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 10/330,580
FILE REFERENCE: ABGENIX.022A
CURRENT APPLICATION NUMBER: US/10/330,613
CURRENT FILING DATE: 2002-12-26
FRIOR APPLICATION NUMBER: 60/346299
FRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
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Best Local Similarity 94.0%;
Matches 110; Conservative
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; ORGANISM: Homo Sapiens
US-10-330-530-33
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                                                                                                    Gaps
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                                                       Length 117;
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                                                                                                                                                                                                                                                                                                                                                           RESULT 9
US-10-660-357-13

US-10-660-357-13

Sequence 13, Application US/10660357

Publication No. US20040115205A1

GENERAL INFORMATION:
APPLICANT: Bar-Eli, Menashe
APPLICANT: Green, Larry L.
TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
TITLE OF INVENTION: ANTIGEN
TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
CURRENT PEPLICATION NUMBER: US/10/660,357

CURRENT FILING DATE: 2003-09-10

PRIOR FILING DATE: 2002-12-26

NUMBER OF SEQ ID NOS: 40

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                               Score 587; DB 14;
Pred. No. 3.8e-44;
4; Mismatches 3;
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Pred. No. 3.8e-44;
4; Mismatches 3;
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Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOX
FILE REFERENCE: AGGENIX.027A
CURRENT APPLICATION NUMBER: 60/337275
FRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 94.0%;
Matches 110; Conservative
                                                    Query Match
Best Local Similarity 94.0%;
Matches 110; Conservative
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US-10-660-357-13
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CAGANISM: Homo sapiens
US-10-309-762-138
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     US-10-330-530-13
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                                                                                                                                                                                                                                                                                                                                                                                                           61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGDGYKYWGQGTLVTVSS 117
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| Publication No. US20030152514A1
| Publication No. US20030152514A1
| Publication No. US20030152514A1
| APPLICANT: Gudas, Jean
| TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
| FILE REPERBURC: ABGENIX. 0.31A
| CURRENT FILING DATE: 2002-12-26
| PRIOR APPLICATION NUMBER: US 60/346414
| PRIOR APPLICATION NUMBER: US 60/346414
| PRIOR PILING DATE: 2001-12-18
| NUMBER OF SEQ ID NOS: 40
| SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                   Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.9%; Score 587; DB 14; Length 117; 94.0%; Pred. No. 3.8e-44; tive 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/10330613

Publication No. US20030147809A1

GENERAL INPORMATION:
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN

FILE REFERENCE: ABGENIX.022A

CURRENT APPLICATION NUMBER: US/10/330,613

CURRENT FILING DATE: 2002-12-26

PRIOR FILING DATE: 2001-12-18

NUMBER OF SEQ ID NOS: 40

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                 Query Match 96.6%; Score 604; DB 16; Best Local Similarity 94.0%; Pred. No. 1.2e-45; Matches 110; Conservative 7; Mismatches 0;
PRIOR FILING DATE: 2002-12-26
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 94.0
Matches 110; Conservative
                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-33
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TYPE: PRT
ORGANISM: Homo Sapiens
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ORGANISM: Homo Sapiens
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LENGTH: 117
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61 YNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCARGGDGYKY-----WGQGTLVTV 115
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                                                                                                                                                                                                                                                                                                                                                 1 QVQLQBSGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTY
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                                                                                                                                      Length 120;
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APPLICANT: Handa, Masahisa
APPLICANT: Handa, Masahisa
FAPLICANT: Gallo, Michael
FILE APPLICANT: Gallo, Michael
FILE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REPRENCE: ABGENIX: 027A
CURRENT APPLICATION NUMBER: US/10/309,762
FROM FILING DATE: 2002-12-02
PRIOR FILING DATE: 2001-12-03
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSEQ for Windows Version 4.0
FUND 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 120;
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                                                                                                                                                                               2; Indels
                                                                                                                                 Query Match 90.8%; Score 567.5; DB 15; Best Local Similarity 91.0%; Pred. No. 2e-42; Matches 111; Conservative 2; Mismatches 2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 567.5; DB Pred. No. 2e-42; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 144, Application US/10309762; Publication No. US20040018198A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 53, Application US/10805177; Publication No. US20050084449A1; GENERAL INFORMATION:
APPLICANT: Landes, Gregory M.
APPLICANT: Chen, Francine
APPLICANT: Bezabeh, Binyam
APPLICANT: Foltz, Ian
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US-10-309-762-144
                   LENGTH: 120
TYPE: PRT
CRGANISM: Homo sapiens
US-10-309-762-13
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Best Local Similarity
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SEQ ID NO 13
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                                                                                                                                                            1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTY 60
                                                                                                                                                                                                                                61 YNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCARYYGSGSDYWGOGTLVTVSS 118
                                                                                                                                                                                                          61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-GGDGYKYWGQGTLVTVSS 117
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                                                                    Gaps
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Sequence 10, Application US/10309762

Publication No. US2004018198A1

GENERAL INPORMATION:

APPLICANT: Gudas, Jean

APPLICANT: Foliz, Ian

APPLICANT: Gallo, Michael

TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX

TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN

FILE REFERENCE: ABGENIX.027A

CURRENT APPLICATION NUMBER: US/10/309,762

CURRENT APPLICATION NUMBER: 05/02-12-03

PRIOR FILING DATE: 2001-12-03

NUMBER OF SECIED NOS: 246

SOFTWARE: FastSEQ ID NOS: 246

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/10309762

Publication No. US20040018198A1

GENERAL INFORMATION:

APPLICANT: Gudas, Jean

APPLICANT: Handa, Masahisa

APPLICANT: Gallo, Michael

TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN

FILE REPERENCE: ABGENIX.027A

CURRENT APPLICATION NUMBER: US/10/309,762

CURRENT FILING DATE: 2002-12-02

PRIOR APPLICATION NUMBER: 60/337275

PRIOR APPLICATION NUMBER: 60/337275

PRIOR APPLICATION NUMBER: 60/337275

PRIOR APPLICATION NUMBER: 60/337275

NUMBER OF SEQ ID NOS: 246

SOFTWARE: FastSEQ for Windows Version 4.0
                     DB 15; Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.4%; Score 571; DB 15; Length 123; 90.2%; Pred. No. 1e-42;
                   Score 571.5; DB 15; Length
Pred. No. 8.8e-43;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                   Query Match
Best Local Similarity 94.1%;
Matches 111, Conservative
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Best Local Similarity 90.24
Matches 111; Conservative
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ORGANISM: Homo sapiens
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Sequence 20, Application US/10984960A

Publication No. US20050142137A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Chui, Daniel

APPLICANT: Ara, Gulahan

APPLICANT: LaRochelle, William J.

TITLE OF INVENTION: ANTIBODIES AGAINST SECRETORYLEUKOCYTE PROTEASE INHIBITOR

TITLE OF INVENTION: ANTIBODIES AGAINST SECRETORYLEUKOCYTE PROTEASE INHIBITOR

CURRENT APPLICATION NUMBER: US/10/984,960A

CURRENT APPLICATION NUMBER: 60/518,275

PRIOR FILING DATE: 2004-11-09

PRIOR FILING DATE: 2003-11-07

NUMBER OF SEQ ID NOS: 112

SEQ ID NO 20

LEMENT: LAROCHELLA VERSION 0.1

SEQ ID NO 20

LEMENT: LAROCHELLA VERSION 0.1

SEQ ID NO 20
                                                           APPLICANT: Starling, Gary
APPLICANT: Starling, Gary
APPLICANT: Starling, Gary
APPLICANT: Mezes, Peter
TITLE OF INVENTION: ANTIBODIES AGAINST T CELL IMMUNOGLOBULIN
TITLE OF INVENTION: DOMAIN AND MUCIN DOMAIN 1 (TIM-1) ANTIGEN AND USES THEREOF
TITLE OF INVENTION: DOMAIN AND MUCIN DOMAIN 1 (TIM-1) ANTIGEN AND USES THEREOF
TITLE OF INVENTION: DOMAIN AND MUCIN DOMAIN 1 (TIM-1) ANTIGEN AND USES THEREOF
CURRENT PILLING DATE: 2004-03-19
RIOR PELLING DATE: 2003-03-19
NUMBER OF SEQ ID NOS: 141
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 53
LENGTH: 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGG-----DGYKYWGQGTLV 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYMSWIRQHPGKGLEWIGYIYYSGSTY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 90.5%; Score 565.5; DB 17; Length 125; Best Local Similarity 87.9%; Pred. No. 3.2e-42; Matches 109; Conservative 3; Mismatches 5; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 90.3%; Score 564.5; DB 18; Length 1 Best Local Similarity 89.3%; Pred. No. 3.8e-42; Matches 109; Conservative 4; Mismatches 4; Indels
                         Jeffers, Michael
                                             Mesri, Mehdi
Starling, Gary
Mezes, Peter
Tse, Kam Fai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CORGANISM: Homo sapiens
US-10-984-960A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-805-177-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 TVSS 117
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Search completed: November 9, 2005, 12:42:58 Job time : 66 secs

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5.1.6
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2005
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sw model OM protein - protein search, using

9, 2005, 12:25:58 ; Search time 12.609 Seconds (without alignments) 892.802 Million cell updates/sec November Run on:

US-10-660-357A-5 625 Title: Perfect score:

1 QVQLQESGPGLVKPSQTLSL......ARGGDGYKYWGQGTLVTVSS 117 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum I Maximum I

DB seq length: 0 DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sv

•• Database

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		de ,				٠
Result No.		Query Match	Lengt]	DB	Ω	Description
1	536	85.8	147	5	S13519	Iq heavy chain V r
~	527	84.3	1	~	137782	g variab
٣	523		13	7	831690	י ס
4	522	83.5	11	~	₹*	a mu cha
S	519	83.0	Н	~	S78051	ain
9	516	82.6	12	~	S44113	q heavy
7	511.5	81.8	13	~	S30534	g heavy
œ	511	81.8	σ	~	S26801	q heavy
0	511	81.8	15	~	S31511	g heavy chain -
10	509	81.4	15	7	S31512	g heavy
11	503.5		13	~	S31586	g heavy chain V
12	503		12	~	S31514	g heavy
13	502	80.3	66	~	S26803	q heavy
14	497	•	σı	7	S26802	g heavy
15	96		12	N	S44114	g heavy
16	-	•	12	~	S69912	D-D-7
17	491		11	~	A26340	g heavy chain pa
18	489		12	7	830530	q heavy chain
19	489	78.2	14	~	809711	g heavy
20	487.5	•	13	~	S31676	g heavy
21	487	77.9	14	~	809710	0
22	482	77.1	13	7	831696	q heavy
23	480.5		14	7	S78055	g heavy chain pr
24	480	76.8	10	~	S44125	q lambda chain
22	479		9	~	S12418	ס
56	479		14	N	A49045	g heavy chain V
27	٠		13	~	S31585	g heavy chain V
28	476	76.2	66	N	S26807	g heavy chain V
59	476	76.2		7	S31604	וטו

Iq heavy chain V r	Ig heavy chain pre	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain pre	heavy	Ig heavy chain V r	heavy	heavy	Ig heavy chain V r	Ig mu chain precur	Ig heavy chain V r	Ig heavy chain V r	hypotherical hybri	Ig heavy chain V r	
319668	S78052	826906	S12412	B26340	\$20780	S12416	S44110	E34964	826899	PT0370	S26800	S31684	A24770	S24443	PL0118
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α	N	~	N			••	•	.,	N	7	N	"	N	~	.,
127 2	140 2	97 2	99 2	116	118	97	110	117 2	99 2	120 2	99 2	124 2	140 2	118 2	97
	75.9 140 2														
76.0		75.8	75.7	75.7	75.6	75.5	75.4	75.4	75.4	75.4	75.2	75.2	74.9	74.5	74.4

ALIGNMENTS

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patient with X-linked
S13119
S13119
G13bavy chain V region precursor - human
C15pecies: Homo sapiens (man)
C15pecies: Homo sapiens (man)
C15pecies: Homo sapiens (man)
C15pecies: Homo S1319
R15pecies: Homo S13519
R25pecies: S13519
R3519
R3711e: Immunoglobulin variable heavy chain cDNA sequence from a patient with X Apreference number: S13519; MUID:91187691; PMID:2011536
A; Reference number: S13519; MUID:91187691; PMID:2011536
A; Rocession: S13519
A; Rocession: B13519
A; Rocession: S13519
A; Rocession: MURA
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Gaps 4 DB 2; Length 147; Query Match 85.8%; Score 536; DB 2; Length 14 Best Local Similarity 86.0%; Pred. No. 7e-40; Matches 104; Conservative 6; Mismatches 7; Indels

ij

61 YNPSLKSRVTISVDTSKNOPSLKLSSVTAADTAVYYCARG----GDGYKYWGQGTLVTVS 116 1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY 60 86 d ઠ ઠે

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S 147 147

S 117

117

ò g RESULT 2

ig variable region (VDJ) (clone T23-9) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
C;Accession: 137782, S25476
C;Accession: 137782, S25476
C;Accession: 137782, S25476
C;Accession: 137782, S25476
A;Thereison, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A;Thle: Somatic diversification in the heavy chain variable region genes expressed by A;Reference number: A36876; MUID: 94119917; PMID: 8290556
A;Accession: 137782
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-140 cRES.
A;Residues: 1-140 cRES.
A;Cross-references: EMBL:X67906; NID: 913582; PIDN: CAA48104.1; PID: 933583
C;Superfamily: immunoglobulin V region; immunoglobulin homology

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C, Accession: S78051; S23716
R, Harindranath, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: S78051
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A; Molecule type: mRNA
A; Residues: 1-135 <HAR>
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R. Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
Submitted to the EMBL Data Library, June 1992
A. Description: Mechanisms that generate human immunoglobulin diversity operate from the A; Reference number: 331885
A. Accession: 531690
A. Status: preliminary
A; Molecule type: m2NA
A; Residues: 1-130 < CUI>
A; Residues: 1-130 < CUI>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 20-102/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C'Species: Homo sapiens (man)
C'Species: Homo sapiens (man)
C'Date: Oc-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C'Accession: 837456
R'McIntosh, R.S.; Tandon, N.; Weetman, A.P.
Submitted to the EMBL Data Library, September 1993
A', Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from A', Reference number: 837453
                                                                                 7
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                                                                                                                                                                                                                       61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGD------GYKYWGQG 110
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C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-116 <MCI>
A;Residues: 1-116 <MCI>
A;Cross-references: EMED:X75024; NID:g404313; PIDN:CAA52932.1; PID:g758095
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: immunoglobulin
F;6-90/Domain: immunoglobulin homology <IMM>
                                                                                                                     QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY
                                                                                 Gaps
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                                                                                 8;
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                                       Length 140;
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                                                                             6; Indels
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Pred. No. 8.4e-39;
                                     Score 527; DB 2;
Pred. No. 4.1e-39;
3; Mismatches 6
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F;46-128/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.7%;
                                     Query Match
Best Local Similarity 86.2%;
Matches 106, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 82.73
Matches 105; Conservative
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A;Status: preliminary
A;Molecule type: mRNA
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A;Cross-references: EMBL:X54437; NID:g37814; PIDN:CAA38306.1; PID:g930117
N: Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkin Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain V region - human (grant to sapiens (man) (c) Species: Homo sapiens (man) (man) (c) Species: Homo sapiens (man) (c) Species: Homo sapiens (man) (c) Species: Homo sapiens (man) (c) Species: Homo 1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001 (c) Saccession: S44113 (c) Species: March 1994 (c) Hamblin, T.J.; Stevenson, F.K. Submitted to the EMBL Data Library, March 1994 (c) Appsied to the EMBL Data Library, March 1994 (c) Appsied to the EMBL Data Library, March 1994 (c) Appsied to the EMBL Data Library, March 1994 (c) Appleated to the EMBL Data Library, March 1994 (c) Appleated to the EMBL Data Library, March 1994 (c) Hamble (c) Appleated to the EMBL Data Library, DNA Appleated to the EMBL Data Library (c) Appleated to the EMBL DATA Appleated to the EMBL Data Library (c) Appleated to the EMBL DATA Appleated to the EMBL DA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain precursor V-D-J region (clone mAB 61VH) - human (fragment) C;Species: Homo sapiens (man) C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TISVDTSKNOFSLKLSSVTAADTAVYYCARGGYSYGYYYYYYMDVWGKGTTVTVSS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 QLQLQESGPGLVKPSETLSLTCTVSGGSISRGSHYWGWIRQPPGKGLEWIGSIYYSGNTY
                                                                                                                                                                                                                                                          GLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTYYNPSLKSRV
                                                                                                                                                                                                                                                                                                                                                                             1 GLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSLKSRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 TISVDISKNOFSLKLSSVTAADTAVYYCARGGDGYKY------WGQGTLVTVSS 117
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      Length 116;
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A;Molecule type: mRNA
A,Residues: 13-11 (HMA)
A;Cross-references: BMBL:X54437
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
Query Match 83.5%; Score 522; DB 2; Length 11
Best Local Similarity 87.1%; Pred. No. 9.1e-39;
Matches 101; Conservative 2; Mismatches 5; Indels
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A;Reference number: S23716; MUID:92031262; PMID:1718404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDKGGFWSGYYTRNSRAAFDIW 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cispecies: Homo sapiens (man)
Cipate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
CiAccession: S30534
R;Mariette, X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Graduary chain V region (DP-65) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Sacession: S26601; S26900
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Bur. J. Immunol. 22, 1075-1082, 1992
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A;Reference number: S26800; MUID:92201299; PMID:1348029
A;Cross-references: EMBL:Z31389; NID:g472967; PIDN:CAA83264.1; PID:g940524 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;15-99/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                          YNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCARGGDGY----KYWGQGTLVTVS
                                                                                                                                                                                                                 1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY
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A;Molecule type: DNA
A;Residus: 1-99 < WEN>
A;Residus: 1-99 < WEN>
A;Cross-references: EMBL:Z14237; NID:g37706; PIDN:CAA78606.1; PID:g1335372
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
                                                                                                                                                                       Gaps
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                                                                                                                      Score 516; DB 2; Length 121;
Pred. No. 3.2e-38;
5; Mismatches 12; Indels
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>
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Pred. No. 8.4e-38;
4; Mismatches 10;
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79.2%;
                                                                                                                      Query Match
Best Local Similarity 82.6%;
Matches 100; Conservative
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Best Local Similarity 79.2
Matches 103; Conservative
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A;Residues: 1-130 <MAR>
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Ig heavy chain - human (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: 831512
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
Submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA aut A;Reference number: 831509
A;Accession: 831512
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J. Mol. Biol. 227, 776-798, 1992
A.Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A.Reference number: S26885; MUID:93021117; PMID:1404388
A.Accession: S26900
A.Status: preliminary
A.Moceoule type: DMA
A.Residues: 1-99 cTOM>
A.Cross-references: EMBL:Z12365; NID:g32948; PIDN:CAA78235.1; PID:g32949
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
F:15-99/Domain: immunoglobulin homology < IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain - human Cispecies: Homo sapiens (man) Cispecies: Homo sapiens (man) Cispecies: Homo sapiens (man) Cispecies: Ja-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999 Ciscession: Sals1 Richastagner, P.; Demaison, C.; Theze, J.; Zouali, M. submitted to the EmBib Data Library, December 1992 A;Description: Dominance of clonotypic patterns and variable gene usage of A;Reference number: S31509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTY
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A;Residues: 1-155 <CHA>
A;Residues: 1-155 <CHA>
A;Cross-references: EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PID:g33095
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;47-129/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                     Length 99;
                                                                                                                                                                                                                                                                                                                                                  Score 511; DB 2; Length 99
Pred. No. 7e-38;
1; Mismatches 1; Indels
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Best Local Similarity 98.0%;
Matches 97; Conservative
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A; Status: preliminary
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Best Local S:
Matches 102
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61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGDGYKY----WGQGTLVTVS 116
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C'Bate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C'Bate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C'Accession: S56802
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Bur. J Immunol. 22, 1075-1082, 1992
A;Fitle: Polymorphism of human mmunoglobulin V(H)4 germ-line genes.
A;Reference number: S26800; MUID:92201299; PMID:1348029
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
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                                                                                                                                                                                                                                                                                          QVQLQESGPGLVRPSQTLSLTCTVSGGSISSGGFYWSWIRQHPGMALEWIAHIYFSGSTY
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                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                     A;Cross-references: EMBL:X69862; NID:g33086; PIDN:CAA49496.1; PID:g33087
(Subperfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;22-106/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Accession: S26803
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Bur. J. Immunol. 22, 1075-1082, 1992
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line
A;Reference number: S26800; MUID:92201299; PMID:1348029
A;Accession: S26803
                                                                                                                                                                                                           11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 4.2e-37;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR
                                                                                                                                                      Score 503; DB 2;
Pred. No. 4.6e-37;
9; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F,15-99/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 502;
                                                                                                                                                                                  80.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.3%;
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                                                                                                                                                                                                             97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 97.0
Matches 96; Conservative
                                                                                                                                                      Query Match
Best Local Similarity
Matches 97; Conserv
1-128 <CHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99 <WEN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128
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C'Date: 13-Jan.1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C'Accession: 831514
R'Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
R'Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
A'Description: Data Library, December 1992
A'Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autch?Reference number: 831509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: 831586
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
A;Description: Mechaniems that generate human immunoglobulin diversity operate from the A;Reference number: 831586
A;Accession: 831586
A;Accession: 831586
A;Accession: 831586
A;Accession: Brillshary
A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                          61 YNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCARGGD-----GYKYWGQGTL 112
                                                                                                                                                                                                                                                                                                                                                                                                                        61 YNPSLKSRVTISVDISKNOFSLKLSSVTAADTAVYYCARGGDG----YKYWGQGTLVTV 115
                                                                                                                                                                                                                                                                                                                      QVQLQESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYTGSAT 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                       1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 QVQLQESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPAGKGLEWIGRIYTSGSTN 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 OVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY
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                                                                                                                                                                                                                                      Gaps
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                A, Residues: 1-155 < CHA>, A, Residues: 1-155 < CHA>, A, Cross-references: EMBLX69860, NID:g33082, PIDN:CAA49494.1; PID:g33083 C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                               Length 155;
                                                                                                                                                                                                                                   Indels
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Pred. No. 4.5e-37;
5; Mismatches 8;
                                                                                                                                                                               Score 509; DB 2; L
Pred. No. 1.7e-37;
5; Mismatches 9;
                                                                                             C; Keywords: heterotetramer; immunoglobulin homology <IMM>
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Best Local Similarity 83.6%;
Matches 102; Conservative
                                                                                                                                                                               81.4%;
                                                                                                                                                                          Query Match
Best Local Similarity 80.8
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 VTVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S31514
Ig heavy chain - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SS 139
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A; Status: prelimina
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                                                     1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY
                           Gaps
                            ;
0
Score 497; DB 2; Length 99;
Pred. No. 1.2e-36;
1; Mismatches 3; Indels
                                                                                                         Query Match
Best Local Similarity 96.0%;
Matches 95; Conservative 1
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C;Accession: S44114
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable A;Reference number: S44105
A;Accession: S44114
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-129 <HAM>
A;Residues: 1-129 <HAM>
A;Cross-references: EMBH:Z31579; NID:g472968; PIDN:CAA83451.1; PID:g940525
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology <IMM>

1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY 60 Gaps 9; DB 2; Length 129; Indels Query Match 79.4%; Score 496.5; DB 2; Best Local Similarity 80.0%; Pred. No. 1.7e-36; Matches 100; Conservative 6; Mismatches 10; ઠે

3;

1 QVQLQESGPGLVKPSGTLSLTCAVSGSISSSNW-WSWVRQPPGKGLEWIGEIYHSGSTN 59

g ઠે g 113 VTVSS 117 ઠે

120 VTVSS 124

Search completed: November 9, 2005, 13:08:01 Job time: 12.609 secs

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                 Copyright
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- protein search, using sw model OM protein

9, 2005, 11:46:52; Search time 60.406 Seconds (without alignments) 991.843 Million cell updates/sec November Run on:

US-10-660-357A-5 625 Title: Perfect score:

1 QVQLQESGPGLVKPSQTLSL.....ARGGDGYKYWGQGTLVTVSS 117 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB e Maximum DB e Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q6gmx1 homo sapien	homo	homo	homod	Q6gmx7 homo sapien	рошо	homo	Q6p4i8 homo sapien	homo	рошо	homo	homo	P01824 homo sapien	homo	Q8wux4 homo sapien	Q6gmx5 homo sapien	homo	homo	O61bq5 mus musculu	-	Q9bqb8 homo sapien	Q8tc63 homo sapien	mus m	Q9ul75 homo sapien	พนธ แ	Q65zil mus musculu	Q7z3y6 homo sapien	mus m	homo	7 homo	P18533 mus musculu
SUMMARIES	B ID	2 Q6GMX1	2 Q7Z379	2 QGGMX6	2 Q9UL73	2 Q6GMX7	2 095973	2 Q96KX8	2 Q6P4I8	2 Q96EY0	2 Q81ZD7	2 Q7Z374	2 Q86SX2	1 HV2F HUMAN	2 QGNYH3	2 Q8WUX4	2 QGMX5	2 Q9BU10	2 Q96AA6	2 Q6LBQ5	1 HV2I HUMAN	2 Q9BQB8	2 Q8TC63	2 Q99M22	2 Q9UL75	1 HV46_MOUSE	2 Q65ZĪ1	2 Q7Z3Y6	1 HV47 MOUSE	1 HV2G_HUMAN	2 Q6MZX7	1 HV62_MOUSE
	Length DB	;	478	465	119	477	150	496	576	620	130	492	139	129	478	595	597	597	625	136	146	597	473	479	122	137	262	116	113	117	476	117
٠	Query Match Length		83.1	80.1	80.0	79.6	78.3	78.2	78.2	77.8	9.9/	76.3	75.8	72.5	71.2	69.4	69.4	69.4	69.4	68.7	68.7	68.5	68.1	68.0	66.2	66.1		•	64.5	64.5	64.2	61.9
	Score	551	519.5	500.5	200	497.5	489.5	488.5	488.5	486.5	478.5	477	474	453	445	434	434	434	434	429.5	429.5	428	425.5	425	413.5	413	410	404	403	403	401	387
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HV61 MOUSE	HV60 MOUSE	Q9UL.96	Q811U5	Q91X92	HV43 MOUSE	HV02_XENLA	Q99NG4	Q9UL74	HV2C HUMAN	Q61N78	Q6GMY2	Q9UL93	Q9Y509
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					350	345.5	343.5	330	330	330	326.5	325	324.5

ALIGNMENTS

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MEDINE-5pleen,

RX MEDINE-218825; PubMed=12477932; DOI=10.1073/pnas.242603899;

RY Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rab S.A., Doguellano M.F., Casavant T.L., Scheetz T.E.,

Rab S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Wonley K.C., Hale S., Garcia A.M., Gab R.A., Gabs N.A.,

Richards S., Wonley K.C., Hale S., Garcia A.M., Gabs R.A.,

Richards S., Wonley K.C., Hale S., Garcia A.M., Gabs R.A.,

Richards S., Wonley K.C., Revchenko Y., Bouffard G.G.,

Rabey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

Jones S.J., Marra M.A.;

and mouse C.DNA sequences.";

And mouse C.DNA sequences.";
                                                                                                                                 Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R., Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. EMBL, BC073773; AAH73773.1; -.
                                                                            Created)
Last sequence update)
Last annotation update)
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                                        476 AA
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InterPro; IPR003599; IG.
InterPro; IPR007110; IG-like.
InterPro; IPR003597; IG.1.
InterPro; IPR003506; IG WHC.
InterPro; IPR003506; IG WHC.
InterPro; IPR003506; IG WHC.
InterPro; IPR00405; IG Y.
Pfam; PF00407; IG; 2.
SMART; SM00407; IGC1; 3.
SMART; SM00406; IGV: 1.
PR0SITE; PS00250; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                        PRT;
                                                                            05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                        PRELIMINARY;
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rissum-Spleen;
                                                                          05-JUL-2004
05-JUL-2004
RESULT 1
Q6GMX1
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Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9UL73
Q9UL73;
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                                                                                                                           61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGG------DGYKYWGQG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 YNPSLKSRVTISVDISKNQFSLKLSSVTAADTAVYYCARG---GDGYKYWGQGTLVTVSS 117
                                                                          9
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                                                                                     20 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGDYYWSWIRQPPGKGLEWIGYIYYSGSTY
                                                                       1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 QVQLQESGPGLVKPSQTLSLTCTVSGGSIGSGDYFWSWIRQAPGRGLEWMGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Human rectum tumor;
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
Submitted (JUN 2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX538066; CAD97996.1;
HSSP; P01820; 107J.
                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. NCBI_TaxID=9606,
                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.1%; Score 519.5; DB 2; Length 478; 80.8%; Pred. No. 5e-43; ive 12; Mismatches 8; Indels 3
                              88.2%; Score 551; DB 2; Length 476; 82.7%; Pred. No. 3.8e-46;
                                                    5; Indels
 Hypothetical protein.
SEQUENCE 476 AA; 52286 MW; 622AABASC62DDE9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;
                                                                                                                                                                                                                                                   01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp686K04218 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
                                         Pred. No. 3.8e-46; 7; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      465 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR007110; Ig-like.
Interpro; IPR003597; Ig cl.
Interpro; IPR00306; Ig_MHC.
Interpro; IPR003596; Ig_V.
Pfam; PP07654; Cl-set; Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97; Conservative
                                        Best Local Similarity 82.7
Matches 105; Conservative
                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
                                                                                                                                                         111 TLVTVSS 117
                                                                                                                                                                             140 TMVTVSS 146
                                                                                                                                                                                                                                                                                             Name=DKFZp686K04218;
                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (05-JUL-2004 (05-JUL-2004 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                               Query Match
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Matches
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TISSUB-Primary B-Cells;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Ratusherg R.L., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A platchenko.L., Marusina K., Farmer A.A., Wahin G.M., Hong L.,

B tapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S.S., Grimwood J., Schwultz J., Myers R.M., Butterfield Y.S.,

Rhing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Ratcywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLQESGPGLVXPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 QVQLQESGPGLVKPSETLSLTCTVSGGSISG--YYWSWIRQPAGKGLEWIGRIYTSGSTN 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 YNPSLKSRVTISVDŢSKNQFSLKLSSVTAADIAVYYCARGGDGY-KYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Hōmo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Strausberg R.;
Submitted (JUN 2004) to the EMBL/GenBank/DDBJ databases.
EMBL, BC073766, AA473766.1;
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003596; Ig.
R InterPro; IPR003596; Ig.
R Pfam; PPC0047; ig; 4
SMART; SM00409; IG; 2.
SMART; SM00409; IG; 2.
SMART; SM00406; IGV; 1.
R PROSITE; PS50835; IG_LIKE; 4.
R PROSITE; PS50835; IG_LIKE; 4.
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
(Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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TISSUE=Primary B-Cells;
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61 YNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCARGGD---GYKYWGQGTLVTVSS 117
     "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potential.
VH4 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Indels
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                                                                                                    Straubberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
BMBL; BC073765; ARH73765.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig. c1.
InterPro; IPR003597; Ig. c1.
InterPro; IPR003596; Ig. mHC.
InterPro; IPR003596; Ig. w.
Pfam; PF0054; C1-set; Z.
Pfam; PF00647; Ig. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
Subnitted (CCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF103795; AAC79084.1; -.
PIR; S31673; S31673.
PIR; S78056; S78056.
                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS02200; IG MHC; UNKNOWN_2.
Hypothetical protein:
SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CFF85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 AA; 16315 MW; 85664E04938AA7C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
VH4 heavy chain variable region precursor (Fragment)
                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 497.5; DB 2
Pred. No. 7.6e-41;
8; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.3%; Score 489.5; DB 2, ilarity 80.5%; Pred. No. 1.4e-40; Conservative 10; Mismatches 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1999 (TrEMBLrel. 10, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro, IPR007110; Ig-like.
InterPro, IPR003596; Ig.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                      79.6%;
81.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 81...
Best Conservative
                       and mouse cDNA sequences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                       TISSUE=Primary B-Cells;
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>150
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SMART; SM00407; IGc1; SMART; SM00406; IGv; 1.
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95; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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SEQUENCE
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Best Local {
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NEDINE-2138257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
A Sconstein M.J., Ugdin T.B., Toshiyuki S., Carninoi P., Parange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Miting M., Madan A., Young A.C., Shevchenko Y., Butterfield Y.S.,
Maraye Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Maraye M. M.L., M., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Maraye J., M.I., M., Salska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 YTPSLKSRVTISVDRSKNOFSLKLTSLTAADTAVYFCARLSNWGPYYPDYWGOGTLYTVS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 YNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCAR----GGDGYKYWGQGTLVTVS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLQESGPGLVKPSETLSLTCTVSGGSICS--YYWSWIRQPPGKGLEWIGYIYYSGSTN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.

Homo sapiens (Human).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                        "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                  SEQUENCE FROM N.A.
MEDLINE=98277139; Pubmed=9614934; DOI=10.1006/clin.1998.4531;
WW X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                      Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Indels
                                                                                                                                                                                                                                                                                                                                                                  119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                   Score 500; DB 2;
Pred. No. 9.9e-42;
6; Mismatches 9;
                                                                                                                                                                    Clin. Immunol. Immunopathol. 87:184-192 (1998)
EMBL; AF015041; AAD56277.1; -
PIR; PH0876; PH0876.
                                                                                                                                                                                                                                                                                           SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                         InterPro, IPR007110; Ig-like.
InterPro, IPR003596; Ig-v.
                                                                                                                                                                                                                                                                                                                                                                                                   80.0%;
82.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                            HSSP; P01820; 1G7J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                              NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                          fetus."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q6GMX7
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Q6GMX7
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Gaps

2

77

9 1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY

Gaps

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Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BC063384; AAH63384.1;
HSSP; P01820; 1A7N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 100; Conservative
                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
                                                                                                                                                            05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
 114 TVSS 117
                                  140 TVSS 143
                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                               IGHD protein.
                                                                                                                                                                                                                                   Name=IGHD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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                                                                                                                                            Q6P4I8;
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                                                                                       RESULT
                                                                                                       Q6P418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79
80 YNPSLKSRVIISVDISKNQFSLRLSSVTAADIAVYYCARLGMGAFDFWGHGTMVTVSS 137
                                                  61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGDG-YKYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 QLQLQESGPGLVKSSETLSLTCTVSGGSISSSSXYWGWIRQPPGKGLEWIANTYXSGITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strandard (OCT-2001) to the EMBL/GenBank/DDBJ databases. Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC016369; AAH16369.1; -. IMSP; DOB76; 10W0. InterPro; IPR0031097; Ig-cl. InterPro; IPR003597; Ig-cl. InterPro; IPR003596; Ig_MHC. InterPro; IPR003596; Ig_WHC. InterPro; IPR003596; Ig_WHC. InterPro; IPR003596; Ig_WHC. InterPro; IPR003596; Ig_V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
SEQUENCE 496 AA; $3391 MW; D346929849040D69 CRC64;
                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Pred. No. 6.2e-40;
6; Mismatches 15;
                                                                                                                                                                              496 AA.
                                                                                                                                                                                                               Created)
                                                                                                                                                                          PRT;
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77.4%;
                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.
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les 96; Conservative
                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                MGC27165 protein.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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TISSUE=Primary B-Cells;

XX MEDINE=2298825; PubMed=12477932; DOI=10.1073/pnas.242603899;

X Strausberg R.L., Felingold B.A., Grouse L.H., Derge J.G.,

X Strausberg R.L., Felingold B.A., Magner L.H., Derge J.G.,

X Alackul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Na plachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Nobes S.J., Marra M.A.,

Jones C.D., Marra M.A.,

Jones S.J., Marra M.B.,

Jones S.J., Marra M.A.,

Jones S.J., Marra M.B.,

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                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003506; Ig_d.
InterPro; IPR003506; Ig_WHC.
InterPro; IPR003596; Ig_V.
InterPro; IPR00479; Ig_1.
InterPro; IPR00409; IG; I.
InterPro; IPR09409; IG WHC; UNRAOWN 2.
IPROSITE; PS00899; IG WHC; UNRAOWN 2.
IPROSITE; PS00899; IG WHC; UNRAOWN 2.
IPROSITE; IPR09409; IG WHC; INTERPRO; IPR0949D720FIE CRC64;
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
Last sequence update)
Last annotation update)
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Pred. No. 7.2e-40;
3; Mismatches 13,
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Q96EY0 RESULT 9 Q96EY0

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60 ----YYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCA-----RGGDGY----KYW 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 OVOLOOSGPGLVKPSETLSLTCTVSGGSISSSXYWGWIRQSPGKGLEWIGSLXYSGSTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGST-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Human rectum tumor;
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
Flobo G., Han M., Wiemann S.;
Submitted (JUN-2013) to the EMBL/GenBank/DDBJ databases.
EMBL; BX538077; CAD98001.1; -.
HSSP; P01820; 1G7J.
                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 130;
                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Anti-thyroglobulin heavy chain variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 478.5; DB 2; Length Pred. No. 1.5e-39; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Jang Y.-J., Chung J., Park J.-Y.;
Jang Y.-J., Chung J., Park J.-Y.;
Submitrad (ANG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY145455; AAN64329.1;
HSSP; P01820; 1G7J.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 130 130 130 MW; 036131FC6EC1551E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2004 (TrEMBLrel. 25, Created)
01-MAR-2004 (TrEMBLrel. 25, Last sequence update)
Hypocherical procein DKFZp686C02218 (Fragment).
Name=DKFZp686C02218;
Homo sapiens (Human).
Bukaryota, Metazoa.
                                                                                                                                                                                               130 AA
                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50835; IG_LIKE; 1.
NON TER 13 130
SEQÜENCE 130 AA; 13901 MW;
                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 74.6%;
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR007110; Ig-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GOGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GQGFLVTVSS 130
                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                             SS 117
                                                                                                145 SS 146
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                                                                                                                                                                                                               Q8IZD7;
                                                                                                                                                        RESULT 10
Q81ZD7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A trausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alasher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heishe F.,
By Altschul S.P., Jordan H., Moore T., Max S.I., Wang J., Heishe F.,
By Carpleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKernan K.J., Malak J.A., Gunarane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
And J. Helton E., Ketreman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
McKrywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
86 YNPSLKSRVTISVDKSKNQFSLKLSSVTAADTAVYYCASLGDIYYYGMDVWGQGTTVTVS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR----GGDGYKYWGQGTLVTV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.8%; Score 486.5; DB 2; Length 620; 82.8%; Pred. No. 1.2e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BCO11857, AAH11857.2;
PIR, S15590, S15590.
                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.2e-39;
3; Mismatches 11
                                                                                                                                                                      620 AA.
                                                                                                                                                                                                             Created)
                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.
                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 82.8 Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                 IGHM protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P01820; 1G7J
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                       S 146
                                   S 117
                                                                                                                                                                                     Q96EYO;
01-DEC-2001 (
01-DEC-2001 (
                                                                         146
                                   117
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Gaps

13;

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61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGG-------DGYKYWG 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RLQLQESGPGLVKPSETLSLTCIVSGGPIRRTGYYWGWIRQPPGKGLEWIGGVYYTGSIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUB-Blood;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                              MEDIATE 8222225; PubMed=6806818; Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.; Tompolete amino acid sequence of the delta heavy chain of human immunoglobulin D."; Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854 (1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14117 MW; D5D53D47ABE51319 CRC64;
                                                                                                                                                                                                                                                                                                            protein.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; 1g; 1.
RMART; SM00406; IGv; 1.
PROSTIE; PS50835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin V region.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 453; DB 1;
Pred. No. 4.9e-37;
                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
19 heavy chain V-II region WAH.
                                  129 AA.
                                                                                                                                                                                                                                                                                                                                       PIR; A02099; D2HUWA.
HSSP; P01820; G77J.
G1ycoSulteDB; P01824; -.
G0; G0:0005576; C:extracellular; NAS.
G0; G0:0005955; F:antigen binding; NAS.
G0; G0:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 67.4%
                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 QGTLVTVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                  HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON TER
SEQUENCE
                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                          61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGDG----YKYWGQGTLVTVS 116
                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                              91
                                                                                                                                                                                                                                 1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY
                                                                                                                                                                                                                                                   QLQLQESGPGLVKPSETLSLTCTVSGGSVSNRNYYWGWIRQPPGKGLEWIGSIYYNENTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY
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                                                                                                                                                                                                      Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Full-length cDNA clone CSODLO04YM19 of B cells (Ramos cell line)
                                                                                                                                                                                                      4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 75.8%; Score 474; DB 2; Length 139; Local Similarity 93.9%; Pred. No. 4.4e-39; nes 93; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                     76.3%; Score 477; DB 2; Length 492; 75.2%; Pred. No. 8.4e-39;
                                                                                                                                                                                                   13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUBER cells,
Li W.B., Gruber C., Jessee J., Polayes D.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genoscope;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON TER 1 -1
SEQUENCE 139 AA; 15573 MW; 7DIE2302410E4F8C CRC64;
                                                                                                                                        492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 AA.
                                                                                                                                                                                                   13; Mismatches
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF07654; Cl-set; Z.
SMART; SM0406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human) (Fragment).
Homo sapiens (Human).
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InterPro; IPR001596; Ig v.
SWART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; BX248300; CAD62627.1;
HSSP; P01820; 1G7J.
                                                                                                                                                                                   Local Similarity 75.2%
les 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                        Hypothetical protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                        117 $ 117
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                                                                                                                                       SEQUENCE
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Matches
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko, L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Bratcheron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Rapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Nilalon D.K., Muzuy D.M., Sodesgrar B.J., Lu X., Gibbs R.A.,
Anilalon D.K., Muzuy D.M., Sodesgrar B.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Andriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,
Jones S.J., Marra M.A.;
T. Generation and initial analysis of more than 15,000 full-length human
RT. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 QVDLQESGPGLVKPSETLSLTCSVSGDSIAS--YYWSWIRKSPQGGMEWIGYIFHSGTTL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 71.2%; Score 445; DB 2; Length 478; Local Similarity 71.1%; Pred. No. 1.2e-35; les 86; Conservative 17; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC066594; AAH66594.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
SEQUENCE 478 AA; 51856 MW; 5F8B98F60F077256 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003599; IG.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig.c1.
InterPro; IPR003006; Ig.MHC.
InterPro; IPR003596; Ig.WHC.
InterPro; IPR003596; Ig.V.
Pfam; PP07654; Cl-8et; Z.
SWART; SW00400; IG; 4.
SWART; SW004007; IGC1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, Hypochetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                   HSSP; P01820; 1A7N
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                            rissum=Blood;
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Attachul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
A point R.F., Jordan H., Moore T., Max S.I., Wang J., Halteh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Uddin T.B., Toshiyuki S., Carninoi P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Halesley R.W., Touchman J.W., Gareen B.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Goneration and initial analysis of more than 15,000 full-length human
and mouse GDNA sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85 YNPSLKSRVTISVDTSKKQLSLKLSSVNAADTAVYYCARVITRASPGTDGRYGMDV#GQG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 QVQLQQWGAGLLKPSETLSLTCGVYGGSFSG--YYWSWIRQPPGKGLEWIGEINHSGSTN 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 595 AA; 65290 MW; 0D4B50776545714E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 69.4%; Score 434; DB 2; Local Similarity 71.7%; Pred. No. 1.9e-34; les 91; Conservative 5; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.; Strausberg R.; Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBar EMBL; BC019235, AAH19235.2; -. PIR; G34964; G34964. HSSP: P01861; 1ADQ. Pfam; PF070564; C1-8et; 4. SWART; SW00409; IG; 2. SWART; SW00409; IG; 2. SWART; SW00409; IG; 2. PROSITE; PS002995; IG LIKE; 5. PROSITE; PS002999; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLVTVSS 117
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Search completed: November 9, 2005, 13:05:47 Job time: 61.406 secs

145 TTVTVSS 151

(OTARU) XWAJO YBAY SIHT

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
               Copyright
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OM protein - protein search, using sw model

November 9, 2005, 11:43:32; Search time 74.6015 Seconds (without alignments) 627.306 Million cell updates/sec Run on:

US-10-660-357A-9 Title: Perfect score:

650 1 QVQLQESGPGLVKPSETLSL......WLLPDAPDIWGQGTMVTVSS 121 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2105692 Total number of hits satisfying chosen parameters:

2105692 seqs, 386760381 residues

Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

•• Database

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A_Geneseq_16Dec04:* 1: geneseqp1980s:* 2: geneseqp1990s:* geneseqp2000s:* geneseqp2001s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

	Description	Adc99780 Anti-huma	Add05384 Anti-MUC1			Adc99788 Anti-huma	Add05376 Anti-MUC1	Add05392 Anti-MUC1	Adf09814 Human ant	Adf09830 Human ant	Adc99808 Anti-huma	Add05412 Anti-MUC1	0	Ado58076 S9 cell d	Abg92884 Human imm	Abb07171 ebvHigM M	_		Adp03884 Murine-ex		Adp03889 Murine-ex	Aaw27554 Human Ab	Abj18676 Antibody	Adp22272 Human ant	Ada89258 Human ant	Adp03931 Murine-ex
	ΩI	ADC99780	ADD05384	ADF09822	ADC99772	ADC99788	ADD05376	ADD05392	ADF09814	ADF09830	ADC99808	ADD05412	ADF09850	AD058076	ABG92884	ABB07171	ADI26658	ADP03887	ADP03884	ADP03885	ADP03889	AAW27554	ABJ18676	ADP22272	ADA89258	ADP03931
	ength DB	121 7	121 7	121 7	121 7	121 7	121 7	121 7	121 7	121 7	121 7	121 7	121 7	243 8	121 5	121 5	121 8	122 7	122 7	122 7	122 7	119 2	119 6	118 8	123 6	122 7
æ	Query Match Length	100.0	100.0	100.0	98.9	98.9	98.9	98.9	98.9	98.9	92.0	92.0	92.0	87.2	84.3	84.1	84.1	84.1	4	83.9	H.	83.2	83.2	83.2	83.1	83.0
	Score	650	650	650	643	643	643	643	643	643	598	598	598	566.5	548	546.5	546.5	546.5	546.5	545.5	545.5	541	541	540.5	540	539.5
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Murine Murine Murine Murine Anti- Anti- Murine Human Human Murine Human Human Human Human Human Human Human	Ado39737 Human C-m
ADP03864 ADP03862 ADP03984 ADP03983 ADP03933 AAY15126 AAY1199 ADS19313 AMW90287 ABG22888 ADP03868 ADP03868 ADF03868	AD039737
0010000400000044004 	4.
1220 1220 1220 1220 1220 1220 1220 1220	47
88 82 2 4 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	91.6
537.55 537.55 537.55 537.55 532.55 53	230.5
272226666666666644444446666646646664666646666	4

ALIGNMENTS

anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast; Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 9. ADC99780 standard; protein; 121 AA. 26-DEC-2002; 2002WO-US041581. 28-DEC-2001; 2001US-0346299P. (first entry) (ABGE-) ABGENIX INC lung cancer; human. WO2003057838-A2. Homo sapiens 01-JAN-2004 17-JUL-2003. ADC99780; Gudas J; RESULT 1

New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.

WPI; 2003-587113/55.

N-PSDB; ADC99782

Claim 1; SEQ ID NO 9; 78pp; English.

The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the pancreatic or colorectal tumours, specifically melanoma, oesophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung canneer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody

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Gaps

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Length 121; Indels 9

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61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
                                                                                                                                                                                         61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
                                                                                                                          QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTNYN
                                                                                                          1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTTNYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell proliferation inhibition; MUC18 tumour antigen;
anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
carcinoma; cancer; malignancy; heavy chain; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human anti-MUC18 monoclonal antibody heavy chain #3.
                                          100.0%; Score 650; DB 7;
100.0%; Pred. No. 1.5e-47;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                               ADF09822 standard; protein; 121 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                         Matches 121; Conservative
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Matches 121; Conservative
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                                                            Best Local Similarity
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              Sequence 121 AA;
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                                                                                                                                                                                                                                                                  121
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                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gudas J;
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ID ADFC
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                                                                                                                                                                                       120
                                                                                                                                                                                                         61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGQWLLPDAFDIWGQGTWVTVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
                                                                                                                         1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTTNYN
                                                                                                                                              QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTTNYN
                                                                                                                                                                                       61 PSLKSRVTISVDTSKNOFSLRLSSVTAADTALYYCARDQGQWLLPDAFDIWGQGTMVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 9.
                                                                                             Gaps
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                                                          100.0%; Score 650; DB 7; Length 121; 100.0%; Pred. No. 1.5e-47; ive 0; Mismatches 0; Indels C
heavy chain protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 9; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                ADD05384 standard; protein; 121 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                         Local Similarity 100.
nes 121; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gudas J, Bar-Eli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ABGE-) ABGENIX INC.
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                             Sequence 121 AA;
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                                                                                                                                                                                                                                                                                 $ 121
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                                                          Query Match
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Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 650; DB 7; Length 121; 100.0%; Pred. No. 1.5e-47; ive 0; Mismatches 0; Indels C
                                                                                                                                                              English.
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The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to WUC18. The monoclonal antibody of the invention demonstrates cytostacic activity and may be useful for treating a disease or condition associated with the expression of WUC18 on the cell surface such as tumours, specifically melanoma, ossophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody heavy chain protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.
                                                                                                                                                                                                                                                                                                                                                                                                     anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSIKSRVTISVDTSKNOFSIRLSSVTAADTALYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
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      PSLKSRVTISVDTSKNOFSLRLSSVTAADTALYYCARDQGQWLLPDAFDIWGQGTMVTVS
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98.3%; Pred. No. 5.8e-47;
ive 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                  ADC99788 standard; protein; 121 AA.
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                                                                                                                                                                                                                                                                                                                     (first entry)
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Les 119; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lung cancer; human.
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                                                                                                                            s 121
                                                                                       121 S 121
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                                                                                                                                                                                                                                                                           ADC99788;
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                                                                                    120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUCIS. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUCIS on the cell surface such as tumours, specifically melanoma, oscophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUCIS monoclonal antibody heavy chain protein of the invention.
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                                                                                                      New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
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                              QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTTNYN
                                                                              PSLKSRVTISVDTSKNOFSLRLSSVTAADTALYYCARDQGQWLLPDAFDIWGQGTMVTVS
QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYMSWIRQPPGKGLEWIGYIXYTWTTNYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
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Pred. No. 5.8e-47;
2; Mismatches 0;
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                                                                                                                                                                                                                                                                                                              ADC99772 standard; protein; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer; human
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                                                                                                                                                                 S 121
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Matches 119;
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WO2003057006-A2.
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                                                                                                      ADD05392;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a menoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has cytostatic and can be used in the production of a vaccine. The monoclonal antibodies against the MUC18 antigen are useful for diagnosing and treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-MUC18 antibody heavy chain, variable region,
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                                                                                                                                                                                  monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                     Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 OVOLOESGPGLVKPSETLSLTCTVSGGSISSYYWSWIROPPGKGLEWIGYIYYTWTTNYN
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                                                                                                                                                            Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 1.
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Pred. No. 5.8e-47;
2; Mismatches 0; Indels
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                                                                                        ADD05376 standard; protein; 121 AA.
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ilarity 98.3%;
Conservative 2
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                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein of the invention.
                                                                                                                                                                                                                                                                                                                                         (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                               Bar-Eli M;
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les 119; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        metastatic tumor.
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          S 121
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                                                                                                                ADD05376;
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tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody antibodies against the MUC18 antigen are useful for diagnosing and treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or tumour metastasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-MUC18 antibody heavy chain, variable region,
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                                                                                                                                                                                                                     Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 17.
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                                                                                                                                                                                                                                                                                                monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccin:
antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
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ADD05392 standard; protein; 121 AA.
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Matches 119; Conserv
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cell proliferation inhibition; MUC18 tumour antigen; anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour; carcinoma; cancer; malignancy; heavy chain; human.
                                                                                            Human anti-MUC18 monoclonal antibody heavy chain #5.
ADF09830 standard; protein; 121
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Local Similarity 98.3%;
les 119; Conservative 2
                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention comprises a method for inhibiting cell proliferation associated with expression of MUCI8 tumour antigen. The method involves administering anti-MUCI8 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUCI8 tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting tumour metastasis. The method carcinomas, cancer and other malignancies. The present amino acid sequence represents a heavy chain from an MUCI8 tumour antigen-specific monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSLKSRVTISVDTSKNOFSLRLSSVTAADTALYYCARDQGQWLLPDAFDIWGQGTWVTVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTTNYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell proliferation inhibition; MUC18 tumour antigen; anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour; carcinoma; cancer; malignancy; heavy chain; human.
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Pred. No. 5.8e-47;
2; Mismatches 0; Indels
                                                                                                                                                                                        Human anti-MUC18 monoclonal antibody heavy chain #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 1; 83pp; English.
                                                                                            Ą.
                                                                                          ADF09814 Standard; protein; 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                    28-DEC-2001; 2001US-0346414P.
                                                                                                                                                         (first entry)
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Matches 119, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-598367/56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ADF09816.
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                                                                                                                                                                                                                                                                                                                   WO2003057837-A2
          s 121
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                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                         12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                     17-JUL-2003
                                                                                                                          ADF09814;
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             121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gudas J;
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                                                                                                                                                                                                                                    The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid sequence represents a heavy chain from an MUC18 tumour antigen-specific monoclonal antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMYTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTTNYN 60
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Inhibiting cell proliferation associated with expression of MUCI8 tumor antigen, involves incubating and inhibiting cell by administering anti-MUCI8 monoclonal antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 643; DB 7; Length 121;
Pred. No. 5.8e-47;
2; Mismatches 0; Indels
                                                                                                                                                                Claim 1; SEQ ID NO 17; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADC99808 standard; protein; 121 AA.
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ADF09830

RESULT

8 셤 ò 요 ò 원 us-10-660-357a-9.rag

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WO2003057006-A2
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                Homo sapiens,
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                                                            17-JUL-2003
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                                                                                                                                                        Gudas J,
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Matches
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                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain variable domain where the antibody binds to MCIB. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MCIB on the pancreatic or colorectal tunours, specifically melanoma, oesophageal, pancreatic or colorectal turnours, carcinomas, particularly cervical carcinomas and cervical intraeptithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUCIB monoclonal antibody
                      anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
                                                                                                                                                                                                                                                                                     New human anti-MUC18 monoclonal antibodies, useful for treating a disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQESGPGLVKPSETLSLTCTVSGGSISTYYWSWIRQPPGKGLEWIGYIYYTGNTYYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PSLKSRVIVSVDTSKNQFSLKLNSVTAADTAVYYCARDPGQWLVPDAFDIWGQGTWVSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTTNYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGQWLLPDAFDIWGQGTMVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                               or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.
Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 598; DB 7;
Pred. No. 3.8e-43;
7; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heavy chain protein of the invention.
                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 37; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADD05412 standard; protein; 121 AA.
                                                                                                                                                       26-DEC-2002; 2002WO-US041581
                                                                                                                                                                             28-DEC-2001; 2001US-0346299P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92.0%;
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Best Local Similarity 90.9
Matches 110; Conservative
                                                                                                                                                                                                                                                 WPI; 2003-587113/55.
                                                                                                                                                                                                     (ABGE-) ABGENIX INC
                                                           lung cancer; human.
                                                                                                                                                                                                                                                                N-PSDB; ADC99810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 121 AA;
                                                                                                        WO2003057838-A2
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                                                                                   Homo sapiens
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                                                                                                                                17-JUL-2003
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tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in hibited proliferation of the cells. The monoclonal antibody as antibodies against the WUC18 antigen are useful for diagnosing and reating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or tumour metastasis), inhibiting claim associated with melanoma, or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-MUC18 antibody heavy chain, variable region,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel monoclonal antibody used for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVQLQESGPGLVKPSETLSLTCTVSGGSISTYYWSWIRQPPGKGLEWIGYIYYTGNTYYN
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anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
carcinoma; cancer; malignancy; heavy chain; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 3.8e-43;
7; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 37; 87pp; English.
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26-DEC-2002; 2002WO-US041582
                                                                             28-DEC-2001; 2001US-0346460P
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Local Similarity 90.9%;
Local Similarity 90.9%;
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                                                                                                                                                                                                                                                 Bar-Eli M;
                                                                                                                                                                                                                                                                                                                              2003-577496/54.
                                                                                                                                                               (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ADD05414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            metastatic tumor
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27-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSLKSRVIISVDTSKNQPSLRLSSVTAADTALYYCARDQGQMLLPDAFDIWGQGTMVTVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                     Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B cell; surface immunoglobulin; Ig; binding site; antigen; human CD28; closed system; detection laser-beam; catcher tube; electrochemical device; fluorescence activated cell sorter; FACS;
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTTNYN
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                                                                                                                                                                                                                                                                                                                                                                                          92.0%; Score 598; DB 7; Length 121; ilarity 90.9%; Pred. No. 3.8e-43; Conservative 7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S9 cell derived human scFvVL-VH protein.
                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 37; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADO58076 standard; protein; 243 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibody variable region; human.
                                                                     26-DEC-2002; 2002WO-US041580.
                                                                                         28-DEC-2001; 2001US-0346414P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                        WPI; 2003-598367/56.
                                                                                                               (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                   monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 110; Conserv
                                                                                                                                                                  N-PSDB; ADF09852
                             WO2003057837-A2.
                                                                                                                                                                                                                                                                                                                                                                      Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2004044584-A1
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         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                  17-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                    Gudas J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADO58076
셤
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The invention relates to a novel method for identifying a B cell carrying a surface immunoglobulin (Ig) molecule having a binding site for an antigen of interest. The method comprises contacting a sample putatively containing the B cell with the antigen of interest and with a receptor specifically binding to the Ig molecule, and assessing the presence of the detectable signal. The invention further comprises: an antibody comprising an amino acid(s) sequence(s) given in the specification, and advice for assessing the presence of a detectable signal defined above, where the device for assessing the presence of a detectable signal defined above, where the device comprises a closed system for the signal defined above, where the device comprises a closed system for the carbor to laser-beam and a catcher tube, and where the B cell of interest can be collected as a single call by means of an electrochemical device, which is triggered by an electric signal generated by the fluorescence activated cell sorter (RACS) device, where the electrochemical device, which is triggered by an electric signal generated by the fluorescence of activated cell sorter (RACS) device, where the electrochemical device, covers the nozzle of the steady catcher tube liquid stream for a programmed time over a collecting tube, microtiter plate or other container after a B cell is sorted. The method is useful for identifying or antigen of interest. The method is also useful for cloning of antibodies or the capments or derivatives useful in therapeutic approaches. The method is susful and antibodies or its fragments. This sequence represents an S2 cell derived human contained the surface of the sequence represents an S2 cell derived human contained the surface of the sequence represents and S2 cell derived human contained the surface of the second solution of proteins and sanitable sequence represents and S2 cell derived by the second surface of the second surf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 PSLKSRVIISVDTSKNQFSLKLSSVTAADTAVYYCAREGGP-LIMGAFDIWGQGTMVTVS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying a B cell carrying a surface immunoglobulin molecule having binding site for an antigen of interest, useful for constructing therapeutic antibodies, comprises contacting a sample with the antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTTNYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Gaps
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Pred. No. 3.6e-40;
6; Mismatches 5; Indels 1;
                                                                                                                                                                                                                                                                                     Kischel R;
                                                                                                                                                                                                                                                                                     Weinberger S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 22; SEQ ID NO 76; 156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG92884 standard; protein; 121 AA.
12-NOV-2003; 2003WO-EP012664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   its fragments. This sequence polypeptide of the invention.
                                                                                          13-NOV-2002; 2002EP-00025335
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Best Local Similarity 90.1
Matches 109; Conservative
                                                                                                                                                                                                                                                                                     Baeuerle P, Hoffmann P,
                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-449579/42.
                                                                                                                                                                                     (MICR-) MICROMET AG
                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ADO58077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 243 AA;
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The invention describes an isolated polynucleotide encoding a first antibody at least 95-100% identical to a second antibody consisting of an amino acid sequence comprising at least one, two or three CDR regions of a variable heavy (VH) or variable light (VL) domain of the antibody expressed by a hybridoma cell line consisting of XF2.5F1, XF21.1F8, XF27/28.1088, XF27/28.1885, X
                                                                          Immunoglobulin, variable heavy chain, variable light chain, human, deprotein chemokine receptor; CCR5, HDGNR10; cancer; inflammation; immunologic deficiency syndrome; blood protein disorder; nephritis; ataxia telangiectasia; endocaxia lethality; inflammatory bowel disease; histiocytosis; chemotaxis; infectious disease; autoimmune disease; histiocytosis; chemotaxis; infectious disease; autoimmune disease; heaving disease; dermatitis; rheumatoid arthritis; allergy; neurodegenerative disorder; viral infection; poxvirus infection; HIV; human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma; pheumocystis carnii infection; cardiovascular disorder; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human G-protein Chemokine Receptor gene (HDGNR10) useful for treating, preventing, ameliorating or monitoring diseases or disorders associated with aberrant expression of HDGNR10 e.g. cancer.
                       Human immunoglobulin variable light domain #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 55; Fig 4; 562pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-FEB-2001; 2001WO-US004153.
12-JUN-2001; 2001US-0297257P;
08-AUG-2001; 2001US-0310458P;
12-OCT-2001; 2001US-0328447P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-DEC-2001; 2001US-0341725P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-FEB-2002; 2002WO-US003634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-643455/69.
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                                                                                                                                                                                                                                                                                                                                               lymphocytopenia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200264612-A2
                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-FEB-2001;
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12-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roschke V,
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                                                                                     sequence of human immunoglobulin sequence associated with the antibodies
cardiovascular disorders such as atherosclerosis, lymphocytopenias, or disease or disorder associated with aberrant expression of novel human protein chemokine receptor (CCRS) HDGNR10. This is the amino acid
                                                                                                                                                                                                                          Length 121;
                                                                                                                                                                                                                     Score 548; DB 5;
Pred. No. 6.6e-39;
8; Mismatches 9;
                                                                                                                                                                                                                        84.3%;
86.0%;
                                                                                                                                                                                                                  Query Match
Best Local Similarity
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The invention provides a neuromodulatory agent (1) capable of promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system (CNS). (I) is capable of inducing remyelination, promoting cellular proliferation of glial cells, and promoting Ca2+ signaling with oligodendrocytes. An humanised antibody to (I) can be selected from antibody sHIGM22 (LVM 22), ebvHigM MSI19D10, ebv HigM CB2DE12, CB2D68, AKJR4, CB2DE12, CB2DE7 or MSI19E5. (I) is useful for stimulating cremyelination of CNS axons, stimulating proliferation of glial cells in CNS axons, or treating demyelinating disease of CNS in a mammal in need cof such therapy. (I) is capable of binding to structures and cells within CNS. (I) is preferably useful for treating a demyelinating disease of CNS of a mouse infected with Strain DA of Theiler's murine encephalomyelitis (TMEV) or for treating a human being having multiple sclerosis, or a post-chuman or domestic animal with a viral demyelinating disease, or a post-consumption of GNS. (I) is also useful for an in vitro method of stimulating the proliferation of glial cells from mixed cell culture. (I) is also useful for an in vitro method of stimulating the proliferation of glial cells from mixed cell culture. (I) is also useful for preventing infection by a bacterium, virus or like pathogen that causes demyelination or other neurodegenerative condition con a subject. Methods where (I) is administered to a patient are useful for treating multiple sclerosis, parkinson's disease, Alzheimer's constructing disease, anyotrophic lateral sclerosis (ALS), a viral demyelinating disease, anyotrophic lateral sclerosis (ALS), a viral demyelinating are
                                                                                              61 PSLKSRVIMSVDTSKQRFSLKLSSVTAADTAVYYCARDRGSSWYPDAFDIWGGGTWVTVS 120
                                                                  61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
wover neuromodulatory agent (a human IgM monoclonal antibody), promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system, useful to treat post-infectious encephalomyelitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neuromodulatory; central nervous system; CNS; sHIgM22; LYM 22; AKJR4; ebvHigM Ms119D10; ebv HIgM CB2bGB; CB2iE12; CB2iE7; MS119E5; virucide; antiparkinsonian; neuroprotective; nootropic; vulnerary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ebvHigM MSI19D10 heavy chain variable region sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MAYO-) MAYO FOUND MEDICAL EDUCATION RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pease LR;
                                                                                                                                                                                                                                                                                                                    ABB07171 standard; protein; 121 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000; 2000WO-US014902.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAY-2000; 2000US-00568351.
                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rodriguez M, Miller DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002-066596/09.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200185797-A1.
                                                                                                                                                              121 S 121
                                                                                                                                                                                                      s 121
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                                                                                                                                                                                                                                                                                                                                                                                                              13-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                 ABB07171;
                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                          RESULT 15
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Conservative

Matches 104;

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9; Indels

Search completed: November 9, 2005, 12:55:25 Job time: 75.6015 secs

121 S 121 | | 120 S 120

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Title: Perfect score:

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Scoring table:

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Minimum DB Maximum DB

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us-10-660-357a-9.rai

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Sequence Seq
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Sequence
Sequence
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; Sequence 39, Application US/09025769B
; Patent No. 6300064
; GENERAL INPORMATION;
; APPLICANT: Knapplk, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ge, Liming
; APPLICANT: Morone, Simon
; APPLICANT: Plueckthun, Andreas
; APPLICANT: Plueckthun, Andreas
; TRILL OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
ZIP. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 541; DB 3; Length 119;
Pred. No. 5.2e-46;
5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

SOFTWARE: PACENTIN RELABSE #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILLING DATA: 18-FEB-1998

PRIOR APPLICATION NUMBER: EP 95 11 3021.0

FILLING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Janes F. Haley, Tr., EBQ.

REGISTRATION NUMBER: 27,794

TELEPHONE: (212)596-9090

INFORMATION: TELEPHONE: (212)596-9090

INFORMATION: CARACTERISTICS:

LENGTH: 119 anino acide

TTYPE: mino acide
                      US-08-450-578-5

US-09-017-628-5

US-09-017-628-5

US-09-017-80-5

US-08-450-363-5

US-08-652-816A-10

US-08-472-087-86

US-08-793-450-8

US-08-793-450-8

US-08-793-450-8

US-08-793-450-8

US-08-793-450-8

US-09-311-276-888

US-09-313-698-6

US-08-313-698-6

US-08-313-698-6

US-08-313-698-6

US-08-313-698-6

US-08-313-698-6

US-08-313-698-6

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US-08-313-698-6

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US-08-313-698-6
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.2%;
86.8%;
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Best Local Similarity 86.8
Matches 105; Conservative
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MOLECULE TYPE: protein
STRANDEDNESS:
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473.5
472.5
471.5
471.5
470.5
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                                                                                                                                                                            November 9, 2005, 11:29:55; Search time 18.802 Seconds (without alignments) 480.403 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 39
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650
1 QVQLQESGPGLVKPSETLSL.....WLLPDAFDIWGQGTMVTVSS
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                      GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-08-545-809A-140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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US-09-467-903-11
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
                                                                                                                               protein search, using
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Match Length
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Result No.

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STATE: D.C.
COUNTRY: USA
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                                                                                                                                     US-09-490-070A-39
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                                  PSLKSRVTISVDTSKNOFSLRLSSVTAADTALYYCARDQGQWLLPDAFDIWGQGTMVTVS
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COUNTRY: USA

CONFUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAMME: James F. Hal-ey, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 83.2%; Score 541; DB 3; Length 119; Best Local Similarity 86.8%; Pred. No. 5.2e-46; Matches 105; Conservative 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   c/o Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: 11ag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Pluckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: James F. Haley, Jr., Esq. STREET: 1251 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-025-769B-65; Sequence 65, Application US/09025769B; Patent No. 6300064
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APPLICANT: Knappi
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61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 83.2%; Score 541; DB 4; Length 119; Best Local Similarity 86.8%; Pred. No. 5.2e-46; Matches 105; Conservative 5; Mismatches 9; Indels
                                                                                                                                                                                  Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET UNDBER: 37629-0005
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-070A-39
Sequence 39, Application US/09490070A Patent No. 6696248 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
US-09-490-070A-65
; Sequence 65, Application US/09490070A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202) 912-2020
INFORWATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acid
TYPE: amino acid
                                                                                 APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
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                                                                                                                                                          Ge, Liming
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INFORMATION FOR SEQ ID NO: 39
SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Gaps
                                                                                                                                                                           ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                            ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DAIA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Indels
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protain/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 541; DB 4;
Pred. No. 5.2e-46;
5; Mismatches 9
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FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTONNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ge, Liming
Moroney, Simon
Plueckthun, Andreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 39, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 86.8%;
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 65
                                                                                                                                                                                                                                        CITY: Washington
                                                                                                                                                                                                                                                        STATE: D.C.
COUNTRY: USA
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US-09-490-153-39
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NUMBER OF SEQUENCES: 373

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61 PSLKSRVTISVDTSKNQPSLRLSSVTAADTALYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 65, Application US/09490324

Sequence 65, Application US/09490324

Patent No. 6828422

GENERAL INFORMATION:
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Pluckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas

CHTY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATH:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Indels
               CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 541; DB 4;
Pred. No. 5.2e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83.2%; Scor.
86.8%; Pred. No. 5...
5; Mismatches
                                                                                                                                                                                                                                NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REGISTRATION INDREME: 27,794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/025,769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212)596-9000
TELEFAX: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10021
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 83.2
Best Local Similarity 86.8
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYN 60
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                                                                              COMPOTER: I Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Halley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION NUMBER: AD. 7794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION NUMBER: MORPHO/5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

83.2%; Score 541; DB 4; Length 119;
Best Local Similarity 86.8%; Pred. No. 5.2e-46;
Matches 105; Conservative 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-153-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 39, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 119 amino acids
TYPE: amino acid
                                        ZIP: 10021
COMPUTER READABLE FORM:
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STATE: New York
COUNTRY: USA
ZIP: 10021
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9

Gaps

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ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                              TYPE: amino acids
STRANDEDNESS:
TOPOLOGY: ling
                                                                                                                                                                                                81.9%;
85.1%;
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                                                                                                                                                                                              Query Match 81.9°
Best Local Similarity 85.1°
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 118 amino aci
                                                                                                                            MOLECULE TYPE: protein US-09-025-769B-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 S 118
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                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 5;
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Pred. No. 5.2e-46;
5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: 11ag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Pluckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
CORRESPONDENCE ADDRESS:
                APPLICATION NUMBER: EP 95 11 3021.0 FILING DATE: 18-AUG-1995 ATTORNEY/AGENT INFORMATION:
                                                                       NAME: James P. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REPERENCE/DOCKET NUMBER: PORPHO/S TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUC-1995
ATTOCHEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27.794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25, Application US/09025769B Patent No. 6300064
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
REDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
FILING DATE: 18-FEB-1998
                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                       TELEFAX: (212)596-9090 INFORMATION FOR SEQ ID NO: 65:
                                                                                                                                                                                                                                                                                                                                                                      83.2%;
86.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (212) 596-9000
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 86.8°
Matches 105; Conservative
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61 PSLKSRVTISVDTSKNOFSLRLSSVTAADTALYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
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                                                                                                                                                    1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGEIYHSGSTNYN 60
                                                                                                                   1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTTNYN
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application US/09490070A

Sequence 25, Application US/09490070A

GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Lining
Moroney, Simon
Pluckhun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE: Colin G. Sandercock, Esq. c/o Heller Ehrman
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
      DB 3; Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                               8; Indels
Score 532.5; DB 3,
Pred. No. 3.5e-45;
7; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: BP 95 11 3021.0 FILING DATE: 18-AUG-1995 ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq. REGISTRATION NUMBER: 31,298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
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61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGQWLLPDAFDIWGQGTWVTVS 120
                                                                                                                                                   61 PSLKSRVŢISVDŢSKNQFSLKLSSVŢAADŢAVYYCARGRGG---GGVFDYWGQGŢLVŢVS 117
                                                      1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGEIYHSGSTNYN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 81.9%; Score 532.5; DB 4; Length Best Local Similarity 85.1%; Pred. No. 3.5e-45; Matches 103; Conservative 7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT Knappik, Achim
Pack, Peter
Tlag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: James F. Haley, Jr., Esq. STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-324-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: James F. Haley, Jr., REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                          Sequence 25, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 118 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10021
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
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                                                                                                                                                 1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTTNYN
                                                                                                                                                                             1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGEIYHSGSTNYN
                                                                                                                                                                                                                                                       Gaps
                                                                                                            <u>ب</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                   Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 118;
                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11arity 85.1%; Score 532.5; DB 4; Braity 85.1%; Pred. No. 3.5e-45; Conservative 7; Mismatches 8;
                                                            Score 532.5; DB 4
Pred. No. 3.5e-45;
7; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-3an-2000
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794 REFERENCE/DOCKET NUMBER: MORPHO/5
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-070A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence Description: SEQ ID NO: 25: US-09-490-153-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 118 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
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SEQUENCE CHARACTERISTICS:
                                                               81.9%;
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                                                          Query Match
Best Local Similarity 85.1
Matches 103; Conservative
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STATE: New York
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Best Local Similarity
Matches 103; Conserv
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Matches 102; Conservative
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US-09-138-091A-77
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3; Gaps
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Fatent No. 679038
GENERAL INFORMATION:
APPLICANT: BERCHCIG, Peter
APPLICANT: BERCHCIG, Peter
TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
FILE REFERENCE: 100564-09049
CURRENT APPLICATION NUMBER: US/09/424,840B
FRIOR APPLICATION NUMBER: DE 1980-663.1
PRIOR APPLICATION NUMBER: DE 19755227.7
PRIOR PILING DATE: 1998-05-08
PRIOR FILING DATE: 1999-12-12
PRIOR APPLICATION NUMBER: DE 19755227.7
PRIOR PILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: DE 19753904.8
PRIOR FILING DATE: 1997-06-06
SOFTWARE: PALENTIN DATE: 1997-06-15
FRIOR FILING DATE: 1997-06-16
SOFTWARE: PALENTIN OFFER DE 1973904.8
FRIOR FILING DATE: 1997-06-06
SOFTWARE: PALENTIN VERSION 3.1
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Pred. No. 3.6e-45;
6; Mismatches 10; Indels
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Patent No. 6342220
GENERAL INFORMATION:
APPLICANT: Adams, Camellia
APPLICANT: W.
APPLICANT: Gurter, Paul J.
APPLICANT: Gurter, Paul J.
APPLICANT: Gurter, Paul M.
APPLICANT: Gurter, Paul J.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
CURRENT APPLICATION NUMBER: US/08/918,148A
CURRENT FILING DATE: 1997-08-25
NUMBER OF SEQ ID NOS: 79
SERVINE SEQ ID NOS: 79
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84.4%;
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Best Local Similarity 84.4:
Matches 103; Conservative
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; ORGANISM: Homo sapiens
US-09-424-840B-20
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Best Local Similarity
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                                                                                                                                                                                                63 PSLKSRVIISVDISKSQFSLKLSSVTAADTAVYYCAR--GRY-----PDVWGRGTMVTVS 115
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                                                       1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTTNYN 60
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                                                                                          3 QVQLQQSGPGLVKPSETLSLTCTVSGDSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYN.
     7; Gaps
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Best Local Similarity 84.3%; Pred. No. 1.3e-44;
Matches 102; Conservative 10; Mismatches 2; Indels 7
2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: single chain antibody (8cFv) fragments
US-09-138-091A-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 77, Application US/09138091A

Batent No. 6737249

GENERAL INFORMATION:
APPLICANT: Adams, Camellia W.
APPLICANT: Carter, Paul J.
APPLICANT: Carter, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REPERENCE: 9491-013-27

CURRENT APPLICATION NUMBER: US/09/138,091A

CURRENT FILING DATE: 1998-08-21

FILE REPLICATION NUMBER: US 60/056,736

PRIOR FILING DATE: 1999-08-22

NUMBER OF SEQ ID NOS: 77

SOFTWARE: PRESEQ for Windows Version 4.0

SEQ ID NO 77
10; Mismatches
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Job time : 18.802 secs
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ORGANISM: Artificial Sequence
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5, Appli 5, Appli 178, App 102, App 71, Appl 90, Appl

Scoring table:

Searched:

Minimum DB Maximum DB

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5, Appli 26, Appl

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1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTTNYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/10330613
; Sequence 9, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFRENCE: ABGRNIX.022A
; CURRENT APPLICATION NUMBER: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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100.0%; Pred. No. 3.5e-49;
ive 0; Mismatches 0;
US-10-660-357-37
US-10-292-088-142
US-10-292-088-142
US-10-292-088-142
US-10-994-679-60
US-10-994-679-60
US-10-309-762-24
US-10-309-762-24
US-10-309-762-25
US-10-309-762-29
US-10-309-762-29
US-10-309-762-102
US-10-309-762-102
US-10-309-762-113
US-10-309-762-124
US-10-309-762-124
US-10-309-762-124
US-10-309-762-124
US-10-309-762-26
US-10-308-360-100
US-10-308-360-100
US-10-308-377-56
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Best Local Similarity 100.
Matches 121; Conservative
    TYPE: PRT
ORGANISM: Homo Sapiens
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                                                                                        9, 2005, 11:40:37; Search time 67.222 Seconds (without alignments) 753.137 Million cell updates/sec
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                                                                                                                                                                      QVQLQESGPGLVKPSETLSL........WLLPDAFDIWGQGTMVTVSS 121
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Sequence 3
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                                                                                                                                                                                                                                                                                                                                                                                         | Cgn2_6/ptodata1/lpubpaa/US07_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/lpubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata1/lpubpaa/US06_NEW_PUB.ppp:*
| Cgn2_6/ptodata1/lpubpaa/US06_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/lpubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata1/lpubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/lpubpaa/US108_PUBCOMB.ppp:*
             version 5.1.6
- 2005 Compugen Ltd.
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US-10-330-530-9
US-10-330-613-1
US-10-330-613-1
US-10-330-530-1
US-10-330-530-1
US-10-660-357-1
US-10-660-357-1
US-10-330-613-37
US-10-330-337-17
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Maximum Match 100%
Listing first 45 summaries
                                                                  using sw model
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Gapop 10.0 , Gapext 0.5
                GenCore (c) 1993
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Result No.

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                                                                                                                                                                     | Sequence 1, Application US/10330613
| Publication No. US20030147809A1
| GENERAL INFORMATION:
| APPLICANT: Gudas, Jean
| TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
| FILE REFERENCE: ABGENIX.022-
| CURRENT APPLICATION NUMBER: US/10/330,613
| CURRENT FILING DATE: 2002-12-26
| PRIOR PILING DATE: 2001-12-18
| NUMBER OF SEQ ID NOS: 40.012-18
| SOFTHARE: PastSEQ for Windows Version 4.0
| SEQ ID NO 1
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Sequence 17, Application US/10330613
Publication No. US20030147809A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUCIB ANTIGEN
FILE REFERENCE: ABGENIX.022A
CURRENT APPLICATION NUMBER: US/10/330,613
CURRENT FILING DATE: 2002-12-26
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Pred. No. 1.4e-48;
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98.3%; Pred. No. 1.4e-48;
iive 2; Mismatches 0;
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PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 98.3%;
Matches 119; Conservative
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US-10-330-613-1
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Best Local Similarity
                         121 $ 121
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LENGTH: 121
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US-10-330-613-1
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                                                                                                      Sequence 9, Application US/10330530; Publication No. US2030152514A1; GENERAL INFORMATION:

APPLICANT: GUAGA, Jean
TITLE OF INVENTION:

FILE REFERENCE: ABGENIX.031A
CURRENT APPLICATION NUMBER: US/10/330,530
CURRENT APPLICATION NUMBER: US/10/330,530
PRIOR APPLICATION NUMBER: US 60/346414
PRIOR APPLICATION NUMBER: US 60/346414
PRIOR APPLICATION NUMBER: US 60/346414
NUMBER OF SEQ ID NOS: 40

NUMBER OF SEQ ID NOS: 40

SOFTWARE: FastSEQ for Windows Version 4.0
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; Sequence 9, Application US/20040115205A1
; Gangard. INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USF OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: USF OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2003-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.0%; Pred. No. 3.5e-49;
Matches 121; Conservative 0; Mismatches 0;
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Best Local Similarity
Matches 121; Conserv
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LENGTH: 121
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Fublication No. US20040115205A1
GENERAL INFORMATION:
APPLICANT: Bar-Bil, Menashe
TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
TITLE OF INVENTION: WHITEN
FILE REFERENCE: AMGRNIX: 03001
CURRENT APPLICATION NUMBER: US/10/660,357
CURRENT APPLICATION NUMBER: 10/330,580
PRIOR APPLICATION NUMBER: 10/330,580
PRIOR FILING DATE: 2002-12-26
NUMBER OF SEQ ID NOS: 40
SEQ ID NO.
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Publication No. US20040115205A1

GENERAL INFORMATION:

APPLICANT: Bar-Bil, Menashe

TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18

TITLE OF INVENTION: ANTIGEN

TITLE OF INVENTION: ANTIGEN

CURRENT APPLICATION NUMBER: US/10/660,357

CURRENT APPLICATION NUMBER: 10/330,580

PRIOR FILING DATE: 2003-12-26
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98.9%; Score 643; DB 16;
Best Local Similarity 98.3%; Pred. No. 1.4e-48;
Matches 119; Conservative 2; Mismatches 0;
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98.3%; Pred. No. 1.4e-48;
iive 2; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 121
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Best Local Similarity 98.3
Matches 119; Conservative
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ORGANISM: Homo Sapiens
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61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
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Publication No. US20030152514A1
GENERAL INFORMATION:
APPLICANT: GUGAS, Jean
TITLE OF INVENTION:
FILE REFERENCE: ABGENIX.031A
CURRENT APPLICATION NUMBER: US/10/330,530
CURRENT APPLICATION NUMBER: US 60/346414
PRIOR APPLICATION NUMBER: US 60/346414
PRIOR APPLICATION NUMBER: US 60/346414
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FASESEQ for Windows Version 4.0
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Publication No. US20030152514A1;
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/330,530;
CURRENT FILING DATE: 2002-12-26;
PRIOR PAPLICATION NUMBER: US 60/346414;
PRIOR FILING DATE: 2001-12-18;
NUMBER OF SEQ ID NOS: 40;
SOFTWARE: FastSEQ for Windows Version 4.0
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98.9%; Score 643; DB 14; Length 121;
Best Local Similarity 98.3%; Pred. No. 1.4e-48;
Matches 119; Conservative 2; Mismatches 0; Indels
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Pred. No. 1.4e-48;
2; Mismatches 0;
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Best Local Similarity 98.3'
Matches 119; Conservative
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PRIOR APPLICATION NUMBER: 60/348,980 PRIOR FILING DATE: 2001-11-09 NUMBER OF SEQ ID NOS: 147 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 142
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US-10-660-357-37
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QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTTNYN
                      QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTTTSNYN
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| Publication No. US20030152514A1
| GENERAL INFORMATION:
| APPLICANT: Gudas, Jean
| TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
| FILE REPERENCE: ABGENIX.031A
| CURRENT APPLICATION NUMBER: US/10/330,530
| PRIOR PAPLICATION NUMBER: US 60/346414
| PRIOR FILING DATE: 2001-12-18
| NUMBER OF SEQ ID NOS: 40
| SEQ ID NO 37
| LENGTH: 121
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                                                                                                                                                                                                                                                              Sequence 37, Application US/10330613

Publication No. US20030147809A1

GENERAL INFORMATION:

APPLICANT: Gudas, Jean

TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN

FILE REFERENCE: ABGENIX.022A

CURRENT APPLICATION NUMBER: US/10/330,613

CURRENT FILING DATE: 2002-12-26

PRIOR PILING DATE: 2001-12-18

NUMBER OF SEQ ID NOS: 40

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 37

LENGTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
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Best Local Similarity 90.9'
Matches 110; Conservative
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Best Local Similarity 90.9
Matches 110; Conservative
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; ORGANISM: Homo Sapiens
US-10-330-613-37
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ORGANISM: Homo Sapiens
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Publication No. US20040115205A1

GENERAL INFORMATION:

APPLICANT: BAr-BIL, Menashe

TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18

TITLE OF INVENTION: ANTIGEN

FILE REFERENCE: ABGENIX.030C1

CURRENT APPLICATION NUMBER: US/10/660,357

CURRENT FILING DATE: 2003-09-10

PRIOR APPLICATION NUMBER: 10/330,580

PRIOR PILING DATE: 2002-12-26
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APPLICANT: GLADUE, RONALD P.
APPLICANT: GLADUE, RONALD P.
APPLICANT: GLADUE, RONALD P.
APPLICANT: JIA, XIAO-CHI
APPLICANT: FENG, XIAO
TITLE OF INVENTION: ANTIBODIES TO CD40
FILE REFERENCE: ABX-PF/3 US
CURRENT APPLICATION NUMBER: US/10/292,088
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 37
LENGTH: 121
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                                                                                                                                                                                      1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYN 60
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Sequence 60, Application US/10067800

Sequence 60, Application US/10067800

GENERAL SECTION:

APPLICANT: Roschke, Viktor

APPLICANT: Rosen, Craig A.

APPLICANT: Ruben, Steven, M.

TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10

FILE REFERENCE: 1488.1150001

CURRENT APPLICATION NUMBER: US/10/067,800
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                                                                           Query Match 85.3%; Score 554.5; DB 15; Length 118; Best Local Similarity 87.6%; Pred. No. 7.4e-41; Matches 106; Conservative 7; Mismatches 5; Indels 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches
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APPLICANT: GLADUE, RONALD P.
APPLICANT: GLADUE, RONALD P.
APPLICANT: GORVALAN, JOSE
APPLICANT: JIA, XIAO-CHI
APPLICANT: FENG, XIAO-CHI
APPLICANT: FENG, XIAO-CHI
APPLICANT: FENG, XIAO-CHI
CURRENT APPLICATION NUMBER: US/10/292,088
CURRENT FILIATION NUMBER: 00/348,980
PRIOR APPLICATION NUMBER: 60/348,980
PRIOR PILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PERCENTIN VET: 2.1
SOFTWARE: PERCENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 109, Application US/10292088
Publication No. US20030211100A1
GENERAL INFORMATION:
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87.68;
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Best Local Similarity 87.6
Matches 106; Conservative
                ; ORGANISM: Homo sapiens
US-10-292-088-142
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US-10-292-088-109
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61 PSLKSRVTWSVDTSKNRFSLKLSSVTAADTAVYYCARDRGSSWYPDAFDIWGQGTWVTVS 120
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Pred. No. 2.8e-40;
8; Mismatches 9; Indels
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Job time : 67.2222 secs
        APPLICATION NUMBER: PCT/US01/04153
PRIOR APPLICATION UNMER: PCT/USO1/0415
PRIOR FILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: 60/297,257
PRIOR APPLICATION NUMBER: 60/310,458
PRIOR APPLICATION NUMBER: 60/310,458
PRIOR PILING DATE: 2001-08-08
PRIOR PILING DATE: 2001-08-08
PRIOR PILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/328,447
PRIOR FILING DATE: 2001-11-12
PRIOR APPLICATION NUMBER: 60/341,725
PRIOR SEQ ID NOS: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 86.0%;
Matches 104; Conservative
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ORGANISM: Homo sapiens
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

November 9, 2005, 12:25:58; Search time 13.0401 Seconds (without alignments) 892.802 Million cell updates/sec Run on:

Title: Perfect score:

US-10-660-357A-9 650 1 QVQLQESGPGLVKPSETLSL......WLLPDAFDIWGQGTMVTVSS 121 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

S	ption	Id variable region	g heavy cha	g heavy chain -	g heavy chain -	g heavy chain V	σ	>	5	heavy chain V	heavy	heavy chain	lambda chain	heavy	heavy		heavy chain	heavy chain V		heavy chain V	heavy	heavy chain	Ig heavy chain V r		heavy chain pr	heavy chain	heavy chain V	heavy ch	gamma-1 heavy	Ig heavy chain V r
SUMMARIES	ID	137782	831690	831512	S31511	S31586	S30534	831676	S20780	S13519	S78052	S78051	S44125	S26906	S09711	B26340	S12416	S44113	A49045	831696	A26340	S44114	830530	S47010	S78055	S24443	S26802	S26803	A49444	PH0876
	DB	2	~	~	~	~	~	~	~	~	7	7	7	~	~	~	~	~	~	~	~	7	~	~	7	7	7	~	7	7
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	Score	544	534	532	w	2	5	513.5	2	ഹ	499.5	496	491	490	490	489	487	487	486	482	478	475.5	475		74.	469.5	468	468	9	467
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Ig heavy chain V r	Ig heavy chain V-I	heavy chain	heavy chain	Ig heavy chain V-I	heavy chain	heavy chair	heavy chain	heavy chair	heavy chair	heavy	otheti	Ig heavy chain V r	heavy	Ig heavy chain V-J	Ig Fab region IV-J
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S	B4	22	S												
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2 66	~	97 2	116 2			• •			•						
71.7 99 2	143 2	70.9 97 2	70.9 116 2	70.8	9.07	9.07	20.6	70.2	70.1	70.0	69.7	69.5	69.5	69.2	

ALIGNMENTS

RESULT 1 137782	Ig variable region (VDJ) (clone T23-9) - human (fragment) C;Species: Homo sapiens (man)	C:Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999 C:Accession: 137782: S25476	R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.	Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994	A; Title: Somatic diversification in the heavy chain variable region genes expressed l	Ajketegrance number: A36876; MUID:94119917; PMID:8290556 A.Accesion: T37782	A.Status: preliminary	A; Molecule type: mRN	A;Residues: 1-140 <res></res>	A; Cross-references: EMBL: X67906; NID: q33582; PIDN: CAA48104.1; PID: q33583	C; Superfamily: immunoglobulin V region; immunoglobulin homology	F;46-128/Domain: immunoglobulin homology <imm></imm>	Query Match 83.7%; Score 544; DB 2; Length 140;	Matches 104; Conservative 5; Mismatches 12; Indels 0; Gaps 0;	QY 1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTNYN 60	Db 20 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYN 79	Qy 61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGQWLLFDAFDIWGQGTWYTVS 120	Db RO PSIKSRVTISVITSVITSKITSKITSKITAANTAVYCABHNSSSWYGBYFDYWGGTIVIUS 139
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C;Accession: S31586
R;Culsinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: S31585
A;Accession: S31586
                                                                                                                                                                                                                                                               93 PPLKSRVTISVDTSKNQFSLKVSSVTAADTAVYYCARGGGISSWYDYYGMDVWGQGTTVT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 PSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCARG-GLGIRRGAFDIWGQGTMVTVS 138
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C.Date: 06-Jan-1995 #Bequence_revision 06-Jan-1995 #text_change 16-Aug-1996
C.Accession: S30534
R.Mariette, X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
                                                                                                                                                                                33 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTGSATYN
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                        Length 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 527.5; DB 2; Length
Pred. No. 1.9e-40;
6; Mismatches 10; Indels
                                                                         14; Indels
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                     Score 529; DB 2;
Pred. No. 1.6e-40;
5; Mismatches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain V region - human (fragment)
                           81.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 86.0%;
Matches 104; Conservative
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A;Molecule type: mRNA
A;Residues: 1-130 <MAR>
A;Cross-references: EMBL:218320
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                        Query Match
Best Local Similarity 82.9
Matches 102; Conservative
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A,Molecule type: mRNA
A,Residues: 1-139 <CUI>
                                                                                                                                                                                                                                                                                                                                                                              153 VSS 155
                                                                                                                                                                                                                                                                                                                                           119 VSS 121
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Richastagner, P., Demaison, C.; Theze, J.; Zouali, M.
Richastagner, P., Demaison, C.; Theze, J.; Zouali, M.
Richastagner, P., Demaison, C.; Theze, J.; Zouali, M.
Bubmitted to the EMBL Data Library, December 1992
A; Accession: S31512
A; Catual: preliminary
A; Molecule type: mRNA
A; Residues: L-155 CGHA-
A; Cross-references: EMBL; X69860; NID:g33082; PIDN:CAA49494.1; PID:g33083
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 47-129/Domain: immunoglobulin homology <IMM>
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R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
Submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autc
A;Reference number: S31509
A;Accession: S31511
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
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                                                                                                                                                                                                           65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species: Homo sapiens (man)
Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
Accession: S31512
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
                                                                                                                                                       1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTTNYN
                                                                                                                                                                                   QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYMSWSRQPPGKGLEWIGYIYYSGSTNYN
                                                                                                                                                                                                                                                            PSLKSRVTISVDTSKNOFSLRLSSVTAADTALYYCARDQGQWL----LPDAFDIWGQGTM
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A;Cross-references: EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PID:g33095
A;Cross-references: EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PID:g33095
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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                                                   Length 130;
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                                                                                                    11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.8%; Score 532; DB 2;
82.1%; Pred. No. 8.5e-41;
                                                Score 534; DB 2;
Pred. No. 4.7e-41;
5; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Mismatches
F;20-102/Domain: immunoglobulin homology <IMM>
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                                                82.2%;
ilarity 84.0%;
Conservative
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Matches 101; Conservative
                                              Query Match
Best Local Similarity
Matches 105; Conserv
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Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: 813519
R;Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.
Noticle Acids Res. 19, 673, 1991
A;Title: Immunoglobulin variable heavy chain CDNA sequence from a patient with X-linked A;Reference number: 813519
A;Accession: 813519
A;Accession: S13519
A;Accession: Preliminary
A;Accession: Preliminary
A;Residues: 1-147 <MOR>
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A;Reference number: $78051
A;Accession: $78052
A;Accession: $78052
A;Molecule type: mRNA
A;Residues: 1-140 <HAR>
A;Residues: Brition: $78052
A;Cross-references: B
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                                                                                             QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTTNYN
                                                                                                                                                                          1 QVQLQESGPGLVXPSETLSLTCTVSVGSISGHYWSWIRQPPGKGLEWIAFIRYTGSTHYN
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                 Gaps
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Pred. No. 1.7e-38;
7; Mismatches 11; Indels
            9; Indels
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            11; Mismatches
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A,Residues: 15-111 <HAW>
A,Cross-references: EMBL:X54441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 77.8
Best Local Similarity 82.1
Matches 101, Conservative
            98; Conservative
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R. Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
B. Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
B. Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
B. Course of the EMBL Data Library, June 1992
A. Description: Mchanisms that generate human immunoglobulin diversity operate from the A; Reference number: S31885
A. Accession: S31676
A. 
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RjMortari, F.; Wang, J.; Schroeder, H.W.
A)Description: Analysis of human cord blood Ig heavy chain IgA and IgG repertoire.
A;Reference number: $20764
A;Sccession: $20780
A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                        61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDKGGFWSGYYTRNSRAAFDIW 120
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                                                                                                                                                                          1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGSYWSWIRQPAGKGLEWIGRIYTSGSTN 60
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Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
                                                                                                                                1 QVQLQESGPGLVKPSETLSLTCTVSGGSIS--SYYWSWIRQPPGKGLEWIGYIYYTWTTN
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A; Residues: 1-118 <MOR>
A; Cross-references: EMBL: Z11958; NID: 933893; PIDN: CAA78015.1; P: C; Superfamily: immunoglobulin v region; immunoglobulin homology C; Keywords: heteroterramer; immunoglobulin F: 15-97/Domain: immunoglobulin homology <IMM>
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81.0%; Pred. No. 5.4e-39;
        Pred. No. 9.4e-40;
                                          Mismatches
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81.5%;
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        Best Local Similarity 81.5
Matches 106; Conservative
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Ritawakins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K. submitted to the EMBL Data Library, March 1994
submitted to the EMBL Data Library, March 1994
submitted to the EMBL Data Library, March 1994
A; Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable A; Reference number: S44105
A; Reference number: S44105
A; Reference number: DNA
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-105 cHAW>
A; Cross-references: EMBL: Z31383; NID: 9472978; PIDN: CAA83258.1; PID: 9940535
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 15-97/Domain: immunoglobulin homology < IMM>
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A,Reference number: S09421; MUID:90059975; PMID:2511001
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Cjates 22.Nov-1993 Hacquence revision 10-Nov-1995 #text_change 23-Jul-1999
Cjatession: S26906; S09421; S12415
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Tile: The repertoire of human germline V(H) sequences reveals about fifty
A;Reference number: S26885; MUID:93021117; PMID:1404388
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <TOM>
A;Cross-references: EMBL:Z12371; NID:g32962; PIDN:CAA78241.1; PID:g32963
A;Cross-references: EMBL:X12371; NID:g32962; PIDN:CAA78241.1; PID:g32963
A;Note: designated DP-71
R;Sanz, 1: Kelly, P:; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A;Title: The smaller human V(H) gene families display remarkably little p
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Pred. No. 3e-37;
4; Mismatches 1; Indels
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llarity 94.8%;
Conservative
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A;Note: designated 4.11
A;Accession: S12415
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                                                                                                                                                                                                                                                                                                                                                                                                                                       92; Conservative
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Best Local Similarity
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A; Residues: 1-97 <SA2>
  844125
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A; Residues: 1-135 <HARA:
A; A; Actionse: 1-135 <HARA:
A; Cross-references: ENBL:X54437; NID:g37814; PIDN:CAA38306.1; PID:g930117
B; Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Tht. Immunol. 3, 865-875, 1991
A; Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and beatient.
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                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Dates: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S?8051; S23716
R;Harindranath, N.
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
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A;Accession: S23716
A;Molecule type: mRNA
A;Residues: 13-111 A:BAN.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
C;F:1-13/Domain: signal sequence (fragment) #status predicted <SIG>F;14-13/Product: Ig heavy chain (fragment) #status predicted <MAT>F;27-111/Domain: immunoglobulin homology <IMM>
                         C;Keywords: immunoglobulin
F;I-14/Domain: signal sequence (fragment) #status predicted <SIG>
F;I5-140/Product: Ig heavy chain (fragment) #status predicted <MAT>
F;29-111/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                  Length 140;
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C; Superfamily: immunoglobulin V region; immunoglobulin homology
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                                                                                                                                                            76.8%; Score 499.5; DB 2; llarity 77.0%; Pred. No. 6.3e-38; Conservative 9; Mismatches 15;
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A;Accession: S78051
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A;Title: Organization and evolution of variable region genes of the human immunoglobulin A;Reference number: A26340; MUID:87061007; PMID:3097326
                                                                                                                                                                                                                                                        R; Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990
A; Title: Nucleocide sequences and three-dimensional modelling of the VH and VL domains
A; Reference number: $809710; MUID:90262535; PMID:2111699
A; Recession: $809710; MUID:90262535; PMID:2111699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 QVQLQESGPGLVKPSETLSVTCTVSGGSVSSGLYWSWIRQPPGKGPEWIGYIYYSGSTN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTTNYN 60
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                                                                                                            Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C;Accession: S09711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Species: Homo sapiens (man)
C.bate: 05-Jun-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLQESGPGLVXPSETLSLTCTVSGGSISS -- YYWSWIRQPPGKGLEWIGYIYYTWTTN
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A Molecule type: DNA
A Molecule type: DNA
A Molecule type: DNA
A Residues: 1-116 < KOD>
A Cross-references: GB:X05711; NID:g33602; PIDN:CAA29183.1; PID:g296660
A;Note: the authors translated the codon GAG for residue 25 as Gln
A;Note: the authors translated the codon GAG for residue 25 as Gln
A;Note: the authors translated the codon GAG for residue 25 as Gln
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <NGT>
F;20-116/Product: Ig heavy chain V region 71-4 #status predicted <MAT>
F;34-116/Domain: immunoglobulin homology <IMM>
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-146 <HUG>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 34-118/ Domain: immunoglobulin homology <IMM>
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GenCore version 5.1.6
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62.7
62.3
60.8
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59.6
58.2
57.7
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509.5
502.5
499.5
494.5
478.5
473.5
473.5
473.5
                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                       Scoring table:
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417.5
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392.5
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374.5
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                                                                                                         Run on:
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        32
        364.5
        56.1
        116
        1 HV60_MOUSE
        P18531 mus musculu

        33
        358
        55.1
        117
        1 HV62_MOUSE
        P18533 mus musculu

        34
        357.5
        55.0
        116
        1 HV43_MOUSE
        P18532 mus musculu

        36
        348.5
        53.6
        121
        2 Q9MG4
        P01819 mus musculu

        37
        348.5
        53.6
        135
        1 HV02_XENLA
        Q99mG4

        38
        345.5
        53.2
        118
        2 Q81105
        Q91145
        mus musculu

        39
        344
        52.9
        118
        2 Q9UL74
        Q91174
        Q91174
        D01174

        40
        331
        50.9
        121
        2 Q9UL96
        Q91174
        Q91174
        Q91174

        41
        326.5
        50.2
        118
        2 Q9UL94
        Q91914
        D00191
        D00191

        43
        326.5
        50.2
        118
        2 Q9UL91
        Q9191
        D000 Sapien

        43
        326.5
        50.2
        113
        2 Q9UMYI
        Q6GMYZ
        Q6GMYZ
        Q6GMYZ

        45
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ALIGNMENTS

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Local Similarity
                                                                                                     SEQUENCE FROM N.A
                                                                                 NCBI_TaxID=9606;
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                                                                                                              59 YNPSLKSRVTISVDTSKNOPSLRLSSVTAADTALYYCARDOGOW----LLLPDAFDIWGO 113
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                                                                     1 QVQLQESGPGLVKPSETLSLTCTVSGGSISS -- YYWSWIRQPPGKGLEWIGYIYYTWTTN
                                                                                  QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGDYYWSWIRQPPGKGLEWIGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTTNYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSLKSRVTISVDTSKNOFSLRLSSVTAADTALYYCARDQGQWLLPDAFDIWGQGTMVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PSLKSRVTISVDRSKNQFSLKLTSLTAADTAVYFCAR-LSNW-GPYYFDYWGQGTLVTVS
                                                    Gaps
                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
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80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
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                             Length 476;
                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                   Hypothetical protein. S2286 MW; 622AABASC62DDE9D CRC64; SEQUENCE 476 AA; 52286 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   Ciin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035041; AAD56277.1; -.
PIR; PH0876; PH0876.
HSSP; P01820; 124416.
HSSP; P01820; 1G7J.
InterPro; IPR007110; Ig-like.
InterPro; IPR005596; Ig_v.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                               119 AA.
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                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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                                       Best Local Similarity 79.7% Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                        GTMVTVSS 121
                                                                                                                                                                            GTMVTVSS 146
                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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                              Query Match
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Q9UL73;
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The Girl. 1904 (TreMistrel. 27, Last eagence update)

The Girl. 2004 (TreMistrel. 27, Last eagence update)

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Q6GMX7;
                  Q6GMX7
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WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

METARUSPERR R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Astapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketreman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Norley A., Marra M.A.,

Marra M.A., Schalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 123
| TISSUE=Primary B-Cells;
| SEQUENCE FROM N.A.
| SEQUENCE FROM N.A.
| SINDABAGE R.;
| Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
| Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
| EMBL; SISSOB, SISSOB.
| RICEPTO; IPRO01359; IG.
| InterPro; IPRO01359; IG. I.
| InterPro; IPRO01359; IG. I.
| RICEPTO; IPRO01359; IG. I.
| R. SWART; SMO0409; IG.; IG. I.
| SWART; SMO0406; IG; I.
| SWART; SMO0406; IG; I.
| R. SWART; SMO0406; IG.; I.
| R. SWART; SMO0406; IG.; I.
| R. SWART; SMO0406; IG. I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 502.5; DB 2;
Pred. No. 6.4e-42;
6; Mismatches 13;
  620 AA
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.3%;
                        01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 82.0°
Matches 100; Conservative
 PRELIMINARY;
                                                               IGHM protein.
Homo sapiens (Human)
                                                                                                                                              SEQUENCE FROM N.A.
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Q96EY0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 76.8%; Score 499.5; DB 2; Length I Similarity 81.0%; Pred. No. 9.7e-42; 98; Conservative 8; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein. -
SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CFF85 CRC64;
                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
477 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                   Created)
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, BC073765; AAH73765.1; -...
InterPro; IPR003599; Ig. InterPro; IPR003597; Ig-like.
InterPro; IPR003597; Ig-like.
InterPro; IPR003596; Ig-MHC.
InterPro; IPR003596; Ig-WHC.
Pfam; PP07654; C1-eet; Z.
Pfam; PP0047; ig; 3.
                               05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00409; IG; 4.
SMART; SM00407; IGc1; 3.
SMART; SM00406; IGv; 1.
 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
                                                                                 Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                    NCBI_TaxID=9606;
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Best Local 8
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DB 2; Length 478;
                                                    76.1%; Score 494.5; DB 2; Lenguary 77.2%; Pred. No. 3.1e-41; Bridels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sub C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF103795; ARC79084.1; -.
PIR, S31673; S31673.
PIR, S78056; S78056.
HSSP; P01820; 1G7J.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SWART; SM00406; IGv.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150 150
150 AA; 16315 MW; 85664E04938AA7C9 CRC64;
                                        478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                        01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
VH4 heavy chain variable region precursor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              576 AA.
                                                                                                                                                                                                                                                                                                                                150 AA
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PROSITE; PS00290; IG_MHC; UNKNOWN_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                              Local Similarity 77.23
tes 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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20 >150
150 150
           Hypothecical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                           136 VSS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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                                                                                                                                                                                                                                  119 VSS 121
                           NON TER
SEQUENCE
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal.
SIGNAL
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                                                                                                                                                                                                                                                                                                                                095973
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                                                                                 Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
                                                                                                                                                                                                                                                                                                      RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q6P418
ID 06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Human rectum tumor;
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
Fobo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX538066; CAD97996.1; -.
HSSP; P01820; 1G7J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                  01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MRR-2004 (TrEMBLrel. 26, Last annotation update)
Full-length cDNA clone CSODL004YM19 of B cells (Ramos cell line)
                                                                                                                             Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                         'Match 76.3%; Score 496; DB 2; Length 139; Local Similarity 94.9%; Pred. No. 5.8e-42; les 93; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUEs calls;
Li W.B., Geber C., Jessee J., Polayes D.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                       Genoscope;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL: BX248300; CAD62627.1; --
HSSP; P01820; 1G7J.
InterPrc; JPR007110; 1g-1ike.
InterPrc; JRR005156; 1g-v.
SWART; SM00406; ICV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  NON TER 1 1
SEQÜENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARD 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-DAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp686K04218 (Fragment).
Name-DKFZp686K04218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PSLKSRVTISVDTSKNOFSLRLSSVTAADTALYYCARD 98
                           139 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  478 AA.
                                                                                                         Homo sapiens (human) (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR007110; I9-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF07654; C1-set; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                    ROSITE, PS50835, IG LIKE, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                           PRELIMINARY;
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE=B cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Q72379;
                         Q86SX2
Q86SX2;
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            Q7Z379
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59 YNPSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGQWLLPDAFDIWGQGTMVT 118
                                                                                  19 QVQLQESGPGLVKPSQTLSLTCTVSGGSIGSGDYFWSWIRQAPGRGLEWMGYIYYSGSTY 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLQESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYTWTTN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 QLQLQESGPGLVKPSETLSLSCTVSGGSISSTNYYWGWIRQPPEKGLEWIGSLHNSGSDY 79
                                                        1 QVQLQESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYTWTTN
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Match 73.6%; Score 478.5; DB 2; Length 150; Local Similarity 78.9%; Pred. No. 3.6e-40; les 97; Conservative 7; Mismatches 12; Indels 7.
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95; Conservative
                    PRELIMINARY;
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                                                                                                                 Name=DKFZp686C02218;
                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147 LVTVSS 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 MVTVSS 121
                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                               NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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Q96KX8
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                                                                                                                                                                   TISSUE FROM N.A.

TISSUE-Primary B-Cells,

A TISSUE-Primary B-Cells,

MEDINE-2138257; PubMed=12477932, DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausherg R.L., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Strausher R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Dischul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

A Dischul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

B Discherko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Rapleton M., Soares M.B., Bonaldo M.F., Cashant T.L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

R Richards S.W. Worley D.M., Sodergren B.J., Lu X., Gibbs R.A.,

A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

A Nilating M.M., Shalska U., Schmutz J., Myers R.M., Butterfield Y.S.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Wones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

"A man mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLQESGPGLVKPSETLSLTCTVSGGSI-SSYYMSWIRQPPGKGLEWIGYIYYTWTTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 QVQLQESGPGLVKPSGTLSLTCAVSGGSISSSNWWSWVRQPPGKGLEWIGEIYHSGSTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 NPSLKSRVTISVDTSKNOPSLRLSSVTAADTALYYCARDQGQWLLPDAF----DIWGQGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC063384; AAH63384.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG WHC; UNKNOWN 2.
SEQUENCE 576 AA; 63363 MW; FBB97C949D720FIE CRC64;
             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 72.8%; Score 473.5; DB 2; Best Local Similarity 76.2%; Pred. No. 4.9e-39; Matches 96; Conservative 9; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P01820; 1A7N.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003006; Ig.MC.
InterPro; IPR003596; Ig.MC.
Pfam; PF07554; Cl.eqt; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig; 1.
SMART; SM00409; IG; 1.
SMART; SM00407; IGc1; 3.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
                                                                                             Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 MVTVSS 121
                                                                 IGHD protein.
                                                                              Name=IGHD;
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RESULT 10

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59 YNPSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARD-QGQ--WLLPDAFDIWGQGT 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQESGPGLVXPSETLSLTCTVSGGSIS -- SYYWSWIRQPPGKGLEWIGYIYYTWTTN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Lung;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Felingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                           TISSUE-Human rectum tumor;
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
Fobo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX538077; CAD98001.1;
HSSP; P01820; IG7J.
                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;
                                          01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp686C02218 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 473; DB 2;
Pred. No. 4.6e-39;
9; Mismatches 12;
492 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        INCEPPO: JPR00710; 19-like.
INCEPPO: JPR003597; 1g_c1.
INCEPPO: JPR003506; 1g_MHC.
INCEPPO: JPR003506; 1g_v.
Pfam; PF07654; C1-set; 2.
PROSITE; SM0406; IGv.
PROSITE; PS00359; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.8%;
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
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InterPro; IPR003599; Ig
                                                                                      146
117
127
146
115
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                                                                    1
20
10
118
128
128
142
146
146 AA;
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                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                    DISULFID
NON TER
SEQUENCE
                                                                                                                                                                                                                                                           Query Match
Best Local 9
                                                                                                                                                                                                                                                                                      Local
                                                                                      CHAIN
DOMAIN
DOMAIN
                                                                  SIGNAL
                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q6NYH3
                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 YNPSLKSRVTISVDTSKNQLSLKVRSVTAADTAVYFCARHGYSRSGR---TGAIDYWGQG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLQESGPGLVKPSETLSLTCTVSGGSI -- SSYYWSWIRQPPGKGLEWIGYIYYTWTTN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 QLQLQESGPGLVKSSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIANTYYSGITY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=85205332; PubMed=3922855; DOI=10.1016/0378-1119(85)90092-7; MEDLINE=85205332; PubMed=3922855; DOI=10.1016/0378-1119(85)90092-7; A Kudo A., Ishihara T., Nishimura Y., Watenabe T.; A cloned human immunoglobulin heavy chain gene with a novel directrepeat sequence in 5' flanking region."; Cone 3:181-189(1985).

It dene 3:181-189(1985).

R SP; PO1825; 7FAB.

RSP; PO1825; 7FAB.

RO; GO:0005576; C:extracellular; NAS.

RO; GO:00038276; F:antigen binding; NAS.

RO; GO:0005855; P:immune response; NAS.

RO; GO:0005855; P:immune response; NAS.
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergen E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S., Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 496;
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                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO16369; AAH16369.1; -.
HSSP; P01876; 10W0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;
                                                                                                                                                                                                                                       Proc. Nat1. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 71.0%; Score 461.5; DB 2; Best Local Similarity 74.0%; Pred. No. 6.7e-38; Matches 94; Conservative 8; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
11-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V-II region ARH-77 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 AA.
                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR003596, Ig_V.
Pfam; PF07654; C1-8et; Z.
                                                                                                                                                                                                                   and mouse cDNA sequences.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; 1g; 1.
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137 TLVTVSS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00406; IGV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 TMVTVSS 121
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                       LISSUE=Lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HV2I HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P06331;
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HV2I_HUMAN
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*** Strausberg**: PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Zebebrg B., Buerow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zebebrg B., Buerow K.H., Schaefer C.F., Bhat N.K., A strausberg R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F., Diatchenko, L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.A., McEwan R.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Bakealey R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Touchman J.W., Green E.D., Myers R.M., Butterfield Y.S., Jones S.J., Marra M.A., Jones S.J., Marra M.A., Soneilus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., Tones S.J., Marra M.A., Tones S.J., Marra M.A., Stalska U., Smailus D.E., Schnerch A., Schein J.E., Grimwood J., Schmutz J., Myers R.M., Goreration and initial analysis of more than 15,000 full-length human and mouse CDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PSLKSRVTISVDTSKNOFSLRLSSVTAADTALYYCARD--OGOWLLPDAF---DIWGQGT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 QVQLQQWGAGLVKPSETLSLTCAVFGGSFSGYYWSWIRQPPGRGLEWIGEINHSGSTNYK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTTNYN
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                      Ig heavy chain V-II region ARH-77. V segment. D segment. J segment. By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 455.5; DB 1; Length 146; Pred. No. 7.3e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO66594; AAH66594.1; -.
HSSP; P01820; 1A7N.
                                                                                                                                                                                                                                                                                                                              146
16228 MW; 8D7FD52BB218171F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                       70.1%;
72.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91; Conservative
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SEQUENCE FROM N.A.
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bahar N.K.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bahar N.K.,
Antschenk L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Rapleton M., Soares M.B., Bonaldon M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toohiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Rachards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Jones A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
Jones S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PSLKSRVTISVDTSKNOFSLRLSSVTAADTALYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 QVDLQESGPGLVKPSETLSLTCSVSGDSIASYYWSWIRKSPQGGMEWIGYIFHSGTTLYN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTTNYN
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                        69.7%; Score 453; DB 2; Length 478; 71.9%; Pred. No. 4.6e-37; ive 16; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019235; AAH19235.2; -.
PIR; G34964; G34964.
                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 478 AA; 51856 MW; 5F8B98F60F077256 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
1-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
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               InterPro; IPR003597; 1g cl.
InterPro; IPR003597; 1g cl.
InterPro; IPR00306; 1g MHC.
InterPro; IPR003596; 1g WHC.
InterPro; IPR003596; 1g W.
Pfam; PF07654; Cl-set; 2.
SWART; SW00409; 1G; 4.
SWART; SW00406; 1G; 1.
PROSITE; PS50835; 1G LIKE; 4.
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InterPro; IPR007110; Ig-like.
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les 87, Conservative
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**X STANDELLYME-2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

**Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

**Rausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

**Altschul S.F., Zeeberg B., Buetov K.H., Schaefer C.F., Bhat N.K.,

**Altschul S.F., Zeeberg B., Buetov K.H., Schaefer C.F., Bhat N.K.,

**Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heishe F.,

**Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

**Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

**Stapleton M., Soares M.B., Deshiyuki S., Carninci P., Prange C.,

**Robert S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

**Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

**Villaton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

**Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

**Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

**A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

**Richards S.J., Marra M.A.;

**Generation and initial analysis of more than 15,000 full-length human

**Tores S.J., Marra M.A.;

**Tores S.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PSLKSRVTISVDTSKNQPSLRLSSVTAADTALYYCAR-----DQGQWLLPDAFDIWG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                             86
                                                                                                                                                                                                                                                                                                                                                                                                                     QVQLQQWGAGLLKPSETLSLTCGVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTTNYN
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                       Length 595;
                                                                                                                                                                                                                                                                    ; Score 452; DB 2; Length 595; Pred. No. 7.4e-37; 10; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg_R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, BC073/767; AAH73767.1; -.
InterPro; IPR001599; Ig.
InterPro; IPR001597; Ig.cl.
InterPro; IPR001597; Ig.cl.
InterPro; IPR003507; Ig.cl.
InterPro; IPR003006; Ig_MHC.
Pfam; PP07654; Cl-set; 4.

SMART; SM00409; IG; 2.

SMART; SM00406; IGc1, 4.

SMART; SM00406; IGv1, 1.

PROSITE; PS00299; IG_MIC; UNKNOWN_3.

Hypothetical protein.

SPQUENCE 595 AA; 65290 MW; 0D4850776545714E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  597 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                       69.5%;
69.8%;
                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 69.84
Matches 90; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 QGTMVTVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OGTTVTVSS 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein. Homo sapiens (Human).
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DR InterPro; IPR003596; 1g_v.

DR Pfam; PP00647; 1g_v.

DR SMART; SM00409; 1G; 2.

DR SMART; SM00406; 1Gv; 1.

DR PROSITE; PS50835; 1G_LIKE; 5.

SQUENCE 597 AA; 65304 MW; ZAIE75F6AED85230 CRC64;

Query Match

69.5%; Score 452; DB 2; Length 597;

RW Hypothetical protein.

69.5%; Score 452; DB 2; Length 597;

Best Local Similarity 69.8%; Pred. No. 7.4e-37;

Achieve 90; Conservative 10; Mismatches 17; Indels 12; Gaps 2;

OV | 1 QVQLQESGPGLVKPSETLSLTCGVSGSFSSYWSWIRQPPGKGLEWIGEINSGSTNYN 79

OY | 1 QVQLQESGPGLVKPSETLSLTCGVSGSFSGYWSWIRQPPGKGLEWIGEINSGSTNYN 79

OY | 61 PSLKSRVIISVDTSKKQLSLKLSSVNAADTALYYCARVITRASPGTDGRY----GMDVWG 135

OY | 113 QGTWVTVSS 121

Db | 136 QGTTVTVSS 144

Search completed: November 9, 2005, 13:05:47

Job time: 62.4712 secs
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November 9, 2005, 11:43:32; Search time 72.1353 Seconds (without alignments) 627.306 Million cell updates/sec
                                                                                                                                                                                                                              1 QVQLQESGPGLVKPSQTLSL.....AREGDGFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                       2105692
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                            2105692 segs, 386760381 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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geneseqp2003as:*
geneseqp2003bs:*
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Maximum DB seq length: 2000000000
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624
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Perfect score:
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                                                                          OM protein
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                                                                                                               Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Adc99784 Anti-huma	Add05388 Anti-MUC1	Adf09826 Human ant	Adc99776 Anti-huma	Add05380 Anti-MUC1	Adf09818 Human ant	Adp03968 Murine-ex	Adp03870 Murine-ex	Adp03974 Murine-ex	Adp03873 Murine-ex	Adp03935 Murine-ex	Adp03868 Murine-ex	Adp03876 Murine-ex	Adj80377 Antibody	Adp03977 Murine-ex	Adp03981 Murine-ex	Aab62775 Human HIV	Adp03871 Murine-ex	Adc99804 Anti-huma	Add05408 Anti-MUC1	Adf09846 Human ant	Adp03982 Murine-ex	Aab62765 Human HIV	Adp03970 Murine-ex	Abp45608 Human BLy
	ΔI	ADC99784	ADD05388	ADF09826	ADC99776	ADD05380	ADF09818	ADP03968	ADP03870	ADP03974	ADP03873	ADP03935	ADP03868	ADP03876	ADJ80377	ADP03977	ADP03981	AAB62775	ADP03871	ADC99804	ADD05408	ADF09846	ADP03982	AAB62765	ADP03970	ABP45608
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	Length	117	117	117	117	117	117	118	123	120	120	124	125	125	121	122	121	120	125	117	117	117	121	122	119	253
* Query	Match	100.0	100.0	100.0	94.1	94.1	94.1	93.8	95.8	92.2	92.2	92.1	91.7	91.7	91.6	91.4	91.3	91.2	91.2	91.0	91.0	91.0	90.9	90.9	90.7	90.7
	Score	624	624	624	587	587	587	585.5	579	575.5	575.5	574.5	572	572	571.5	570.5	570	569	569	568	568	268	567	567	995	266
Result	No.	-	7	e	4	ស	9	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

	Adc99796 Anti-huma Add05400 Anti-MUC1 Adf09838 Human ant Adp03877 Murine-ex Adp03874 Murine-ex
ADG96435 ADK52356 AAR62745 ADP03872 ADP038973 AAW78433 AAW78433 AAW733869 ADP03869 ADP22124 ADP22124 ADP22104 ADP222096 ADP22096	ADC99796 ADD05400 ADF09838 ADF03877 ADF03874
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 4 4 4 4 4 4 4 4 7

ALIGNMENTS

RESULT 1 ADC99784

anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast; Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 13 ADC99784 standard; protein; 117 AA. 26-DEC-2002; 2002WO-US041581. 28-DEC-2001; 2001US-0346299P. (first entry) WPI; 2003-587113/55. (ABGE-) ABGENIX INC lung cancer; human. N-PSDB; ADC99786 WO2003057838-A2 Homo sapiens 01-JAN-2004 17-JUL-2003. ADC99784; Gudas J;

New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.

Claim 1; SEQ ID NO 13; 78pp; English.

The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to WUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the pancreatic or colorectal tumours, specifically melanoma, oesophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody

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Best Local Similarity
Matches 117; Conserv
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ADF09826
ID ADF0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
                                                                                                                                                                                                                          YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGDGFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
                                                                                                                                                     1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY
                                                                                                                                                                          QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 13.
                                                                                                                    Gaps
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0
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                                                                         100.0%; Score 624; DB 7;
100.0%; Pred. No. 3.1e-48;
ive 0; Mismatches 0;
   heavy chain protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                          ADD05388 standard; protein; 117 AA.
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                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-577496/54.
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                                                                                         Local Similarity
nes 117; Conserv
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                                    Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003057006-A2.
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                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                               ADD05388;
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                                                                         Query Match
                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                      RESULT 2
ADD05388
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DB 7; Length 117;

100.0%; Score 624;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid sequence represents a heavy chain from an MUC18 tumour antigen-specific
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                                                                                                                                                                                                                                          61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGDGFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                         61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGDGFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 YNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCAREGDGFDYWGQGTLVTVSS 117
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                                                                                                                                                          QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYWTWIRQHPGKGLEWIGFIYYSGSTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell proliferation inhibition; MUC18 tumour antigen; anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour; carcinoma; cancer; malignancy; heavy chain; human.
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                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human anti-MUC18 monoclonal antibody heavy chain #4.
                              Pred. No. 3.1e-48;
Mismatches 0;
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100.0%; Pred. No. 3.1e-48;
ive 0; Mismatches 0;
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100.0%; Pr
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Best Local Similarity 100.0%; P.
Matches 117; Conservative 0;
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                                                             117; Conservative
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monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
                                                                                                                                                                                                                                                                                                                                                         Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
                              Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 5; 87pp; English.
                                                                                                                                                                                          26-DEC-2002; 2002WO-US041582
                                                                                                                                                                                                                         28-DEC-2001; 2001US-0346460P
01-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                  Gudas J, Bar-Eli M;
                                                                                                                                                                                                                                                                                                                WPI; 2003-577496/54.
                                                                                                                                                                                                                                                     (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                         metastatic tumor.
                                                                                                                                                                                                                                                                                                                               N-PSDB; ADD05382.
                                                                                                                                   WO2003057006-A2.
                                                                                                       Homo sapiens.
                                                                                                                                                                17-JUL-2003.
   임
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                                                                                                                                                                      anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUCIS. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUCIS on the cell surface such as tumnours, specifically melanoma, oscophageal, pancreatic or colorectal tumnours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUCIS monoclonal antibody heavy chain protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCAREGDGFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGDGYKYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY
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                                                                                                                                              Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 5.
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Pred. No. 6.4e-45;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 5; 78pp; English.
                                                         ADC99776 standard; protein; 117 AA.
                                                                                                                                                                                                                                                                                                                                        26-DEC-2002; 2002WO-US041581.
                                                                                                                                                                                                                                                                                                                                                                       28-DEC-2001; 2001US-0346299P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 94.0%;
Matches 110; Conservative 4
                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-587113/55.
                                                                                                                                                                                                                                                                                                                                                                                                   (ABGE-) ABGENIX INC
                                                                                                                                                                                                                        lung cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADC99778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 117 AA;
                                                                                                                                                                                                                                                                               WO2003057838-A2.
                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                  01-JAN-2004
                                                                                                                                                                                                                                                                                                             17-JUL-2003
                                                                                    ADC99776;
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                           RESULT 4
                                           ADC99776
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The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has cytostatic and can be used in the production of a vaccine. The monoclonal antibodies against the MUC18 antigen are useful for diagnosing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                  treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or tumour metastaais), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-MCL8 antibody heavy chain, variable region,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGDGFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY
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0
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Pred. No. 6.4e-45;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell proliferation inhibition; MUC18 tumour antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human anti-MUC18 monoclonal antibody heavy chain #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADF09818 standard; protein; 117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 94.0
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 117 AA;
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ID ADF0
XX
AC ADFC
XX
XX
DY
DE HUME
XX
XX
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ADD05380 standard; protein; 117 AA.

RESULT 5 ADD05380 ADD05380

SXXX

Gallo M;

Handa M,

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New anti-CA IX monoclonal antibody, useful for treating a tumor e.g., colorectal neoplasms, colorectal tumors, cervical
              02-DEC-2002; 2002WO-US038550
                                     03-DEC-2001; 2001US-0337275P
                                                                                   Foltz I,
                                                                                                         WPI; 2003-523295/49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
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                                                                                   Gudas J,
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ADP03870
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                                                                                                                                                                                                                                                                                                 The invention comprises a method for inhibiting cell proliferation associated with expression of MUCIB tumour antigen. The method involves administering anti-MUCIB monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUCIB tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid sequence represents a heavy chain from an MUCIB tumour antigen-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen; cytostatic; colorectal neoplasm; renal cell carcinoma; cervical intraepithelial squamous neoplasia; cervical intraepithelial glandular neoplasia; oesophageal; breast cancer; gene therapy; murine; mouse; human; heavy chain variable domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 138.
                                                                                                                                                                                                                                Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGDGFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QVQLQESGPGLVKDSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY
anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour; carcinoma; cancer; malignancy; heavy chain; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 587; DB 7; L
Pred. No. 6.4e-45;
4; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 6.4e
4; Mismatches
                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 5; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADP03968 standard; protein; 118 AA.
                                                                                                      26-DEC-2002; 2002WO-US041580
                                                                                                                            28-DEC-2001; 2001US-0346414P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                 2003-598367/56.
                                                                                                                                                   (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                             monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
es 110; Conserv
                                                                                                                                                                                                             N-PSDB; ADF09820
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 117 AA;
                                                        WO2003057837-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003048328-A2
                                   Homo sapiens
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                                                                               17-JUL-2003
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                                                                                                                                                                         Gudas J;
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The invention relates to a novel isolated monoclonal antibody (mAb) comprising a heavy chain polypeptide and light chain polypeptide having a sequence chosen from one of 53 fully defined amino acid sequences given in the specification, where the antibody specifically binds carbonic anhydrase IX (CA IX) tumour antigen. The antibody of the invention shuhydrase IX (CA IX) tumour antigen. The antibody of the invention such as colorectal activity and may be useful for treating a tumour, such as colorectal neoplasm, renal cell carcinoma, cervical intraepithelial squamous and glandular neoplasia, oesophageal tumour or breast cancer, possibly via gene therapy. The current sequence is that of a murine-expressed anti-human CA IX monoclonal antibody VH (heavy chain variable domain) protein of the invention. The protein was generated via the introduction of the human CA IX protein into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YNPSLKSRVTISVDTSKNQPSLKLSSVTAADTAVYYCARYYGSGSDYWGQGTLVTVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY
colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical intraepithelial squamous and glandular neoplasia or esophageal tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 585.5; DB 7;
Pred. No. 8.8e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                    Example 2; SEQ ID NO 138; 89pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transgenic mouse strain.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 118 AA;
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WPI; 2003-523295/49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
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ADP03873
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                                                                                                                                                     The invention relates to a novel isolated monoclonal antibody (mab) comprising a heavy chain polypeptide and light chain polypeptide having a sequence chosen from one of 53 fully defined amino acid sequences given in the specification, where the antibody specifically binds carbonic anhydrase IX (CA IX) tumour antigen. The antibody of the invention such as colorectal activity and may be useful for treating a tumour such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma, cervical intraepithelial squamous and glandular neoplasm, ossophageal tumour or breast cancer, possibly via gene therapy. The current sequence is that of a murine-expressed anti-human CA IX monoclonal antibody WH (heavy chain variable domain) protein of the invention. The protein was generated via the introduction of the human CA IX protein into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 YNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCARAGKYYGSGSYLDYWGOGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGDGF-----DYWGQGTLVT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                   New anti-CA IX monoclonal antibody, useful for treating a tumor e.g., colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical intraepithelial squamous and glandular neoplasia or esophageal tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen; cytostatic; colorectal neoplasm; renal cell carcinoma; cervical intraepithelial squamous neoplasia; cervical intraepithelial glandular neoplasia; oesophageal; breast gene therapy; murine; mouse; human; heavy chain variable domain.
                                                                                                                                                                                                                                                                                                                                                                                                                         . 9
                                                                                                                                                                                                                                                                                                                                                                                           Length 123;
                                                                                                                                                                                                                                                                                                                                                                                        Score 579; DB 7; Length 12
Pred. No. 3.5e-44;
3; Mismatches 3; Indels
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                                                                                                                            Claim 1; SEQ ID NO 10; 89pp; English.
                Gallo
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              Handa M,
                                                                                                                                                                                                                                                                                                                                                                                         92.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 90.2
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                  transgenic mouse strain.
             Foltz I,
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              Gudas J,
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                                                                                                                               The invention relates to a novel isolated monoclonal antibody (mAb) comprising a heavy chain polypeptide and light chain polypeptide having a sequence chosen from one of 53 fully defined amino acid sequences given in the specification, where the antibody specifically binds carbonic anhydrase IX (CA IX) tumour antigen. The antibody of the invention anhydrase IX (CA IX) tumour antigen. The antibody of the invention such as colorectal activity and may be useful for treating a tumour, such as colorectal neoplasm, renal cell carcinoma, cervical intraepithelial squamous and glandular neoplasia, osesophageal tumour or breast cancer, possibly via gene therapy. The current sequence is that of a murine-expressed anti-human CA IX monoclonal antibody VH (heavy chain variable domain) protein of the invention. The protein was generated via the introduction of the human CA IX protein into
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New anti-CA IX monoclonal antibody, useful for treating a tumor e.g., colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical intraepithelial squamous and glandular neoplasia or esophageal tumors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen; cytostatic; colorectal neoplasm; renal call carcinoma; cervical intraepithelial squamous neoplasm; cervical intraepithelial glandular neoplasm; oesophageal; breast gene therapy; murine; mouse; human; heavy chain variable domain.
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                                                                                          Example 2; SEQ ID NO 144; 89pp; English.
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Best Local Similarity
Matches 110; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen; cotostatic; colorectal neoplasm; renal cell carcinoma; cervical intraepithelial squamous neoplasia; cervical intraepithelial glandular neoplasia; oesophageal; breast cancer; gene therapy; murine; mouse; human; heavy chain variable domain.
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                                                                      invention relates to a novel isolated monoclonal antibody
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                  SEQ ID NO 13; 89pp; English
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91.7%;
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Best Local Similarity
Matches 110; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 120 AA;
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in the specification, where the antibody specifically binds carbonic anhydrase IX (CA IX) tumour antigen. The antibody of the invention demonstrates cytostatic activity and may be useful for treating a tumour, such as colorectal neoplasm, renal call carcinoma, cervical carcinoma, cervical intraepithelial squamous and glandular neoplasia, oesophageal tumour or breast cancer, possibly via gene therapy. The current sequence is that of a murine-expressed anti-human CA IX monoclonal antibody VH (heavy chain variable domain) protein of the invention. The protein was generated via the introduction of the human CA IX protein into
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                                                                                                                                                                                                                                                                                                                              3; Mismatches
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                                                                                                                                                                                                                                                                                     92.1%;
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Matches 111, Conservative
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demonstrates cytostatic activity and may be useful for treating a tumour, such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma, cervical intraepithelial squamous and glandular neoplasm, oesophageal tumour or breast cancer, possibly via gene therapy. The current sequence is that of a murine-expressed anti-human CA IX monoclonal antibody VH Gheavy chain variable domain) protein of the invention. The protein was generated via the introduction of the human CA IX protein into a transgenic mouse strain.
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                                                                                                                                                                                                                                                                                                                                                                                        61 YNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCARTYYDILTGYPDAFDIWGQGTM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               breast cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New anti-CA IX monoclonal antibody, useful for treating a tumor e.g., colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical intraepithelial squamous and glandular neoplasia or esophageal tumors.
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen; cytostatic; colorectal neoplasm; renal call carcinoma; cervical intraepithelial squamous neoplasia; cervical intraepithelial glandlar neoplasia; oesophageal; breast gene therapy; murine; mouse; human; heavy chain variable domain.
                                                                                                                                                                                                                                           8;
                                                                                                                                                                                                     Length 125;
                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                   Score 572; DB 7; L
Pred. No. 1.5e-43;
2; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallo M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 16; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADP03876 standard; protein; 125 AA.
                                                                                                                                                                                                   91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-DEC-2002; 2002WO-US038550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-DEC-2001; 2001US-0337275P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Handa M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                              Query Match
Best Local Similarity 88.0
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-523295/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ABGE-) ABGENIX INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                              117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                VIVSS 125
                                                                                                                                                                 Sequence 125 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003048328-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                              VTVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
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ID ADPC
   8888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method of producing a hybrid antibody or hybrid antibody fragment by: (1) providing an initial antibody having specificity for a target; (i1) determining the sequence of a variable region of the initial antibody; (iii) selecting a first component of the variable region consisting of FR1, FR2, FR3 and FR4; (iv) comparing the sequence of the first component to sequencers contained in a reference database of antibody sequences or antibody fragment sequences from a target species; (v) selecting a sequence from an antibody in the database which demonstrates a high degree of homology to the first component; (vi) selecting a second component of the variable region which is different than the first component, the second component selected from the group consisting of FR1, FR2, FR3 and FR4; (vii) comparing the sequence of the second component to sequence second component in a reference database of
cervical intraepithelial squamous and glandular neoplasia, oesophageal tumour or breast cancer, possibly via gene therapy. The current sequence is that of a murine-expressed anti-human CA IX monoclonal antibody VH (heavy chain variable domain) protein of the invention. The protein was generated via the introduction of the human CA IX protein into a
                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibody variable heavy chain with homology to mouse anti-human antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Producing a hybrid antibody or hybrid antibody fragment by operatively linking the selected framework sequences to one or more complementarity determining regions of the initial antibody.
                                                                                                                                                                                                                                                                          QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWNWIRQHPGKGLEWIGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                             YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARE-----GDGFDYWGQGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hybrid antibody; antibody; framework region; homology; immunogenicity.
                                                                                                                                                                                                                                                    QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                .,
8
                                                                                                                                                                           Length 125;
                                                                                                                                                                                                                Indels
                                                                                                                                                                         Score 572; DB 7; L
Pred. No. 1.5e-43;
2; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; SEQ ID NO 137; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADJ80377 standard, protein; 121 AA.
                                                                                                                                                                                                              2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-DEC-2001; 2001US-0336591P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-DEC-2002; 2002WO-US038450.
                                                                                                                                                                         91.7%;
88.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ALEX-) ALEXION PHARM INC
                                                                                                                                                                                                                Conservative
                                                                                                  transgenic mouse strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-513753/48.
                                                                                                                                                                   Query Match
Best Local Similarity
Matches 110; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                        VTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                           VTVSS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wu D;
                                                                                                                                      Sequence 125 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003048321-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
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antibody sequences or antibody fragment sequences from the target species (vii) selecting a sequence from the database which demonstrates a high degree of homology to the second component and which is from a different antibody than the selected antibody; and (ix) operatively linking the selected framework sequences to one or more complementarity determining regions (CRBs) of the initial antibody to produce a hybrid antibody or hybrid antibody fragment. The method is useful for producing a hybrid antibody fragment (claimed). The antibody and fragments are useful for therapeutic and diagnostic purposes. The method traspent sare useful for therapeutic and diagnostic purposes. The method cuses entire framework regions from a single antibody variable heavy or variable light chain to receive the CDRs. This produces antibodies that are highly homologous and exhibit reduced immunogenicity while maintaining an optimum binding profile. This sequence represents an entibody variable heavy chain which has good homology to an initial murine anti-human mannose binding lectin antibody (AbJ80371). The sequence was used to generate a hybrid antibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NPSLKSRVTISVDTSKNQPSLKLSSVTAADTAVYYCARGLKWGSNHYEDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen; cytostatic; colorectal neoplasm; renal cell carcinoma; cervical intraepithelial squamous neoplasia; cervical intraepithelial glandular neoplasia; oesophageal; breast cancer; gene therapy; murine; mouse; human; heavy chain variable domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWNWIRQHPGKGLEWIGYIYYSGSTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NPSLKSRVIISVDISKNOFSLKLSSVIAADIAVYYCAR----EGDGFDYWGQGTLVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTYY
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    s.
                                                                                                                                                                                                                                                                                                                                                               Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                             Score 571.5; DB 7
Pred. No. 1.6e-43;
1; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallo M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADP03977 standard; protein; 122 AA.
                                                                                                                                                                                                                                                                                                                                                             91.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-DEC-2002; 2002WO-US038550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-DEC-2001; 2001US-0337275P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-523295/49.
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                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003048328-A2.
                                                                                                                                                                                                                                                                                                                         Sequence 121 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                Matches 110;
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New anti-CA IX monoclonal antibody, useful for treating a tumor e.g., colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical intraepithelial squamous and glandular neoplasia or esophageal tumors.

Example 2; SEQ ID NO 147; 89pp; English.

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The invention relates to a novel isolated monoclonal antibody (mAb) comprising a heavy chain polypeptide and light chain polypeptide having a sequence chosen from one of 53 fully defined amino acid sequences given in the specification, where the antibody specifically binds carbonic anhydrase IX (CA IX) tumour antigen. The antibody of the invention shupdrase IX (CA IX) tumour antigen. The antibody of the invention such as colorectal activity and may be useful for treating a tumour, such as colorectal acquamous and glandular neoplasia, oesophageal tumour or breast cancer, possibly via gene therapy. The current sequence is that of a murine-expressed anti-human CA IX monoclonal antibody WH (heavy chain variable domain) protein of the invention. The protein was generated via the introduction of the human CA IX protein into a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YNPSLKSRVTISVDISKNOFSLKLSSVTAADTAVYYCAR----EGDGFDYWGQGTLVTV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 YNPSLKSRVTISVDTSKNQPSLKLSSVTAADTAVYYCARYYDILTGYGMDV#GQGTTVTV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTY
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2
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 570.5; DB 7; Length 122;
Pred. No. 2e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  completed: November 9, 2005, 12:55:25
ne : 72.1353 secs
                                                                                                                                                                                                                                                                                                                                                                                                                  91.4%;
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                                                                                                                                                                                                                                                                                                                        transgenic mouse strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                         Sequence 122 AA;
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Job time
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Sequence Sequence Sequence Sequence Sequence

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APPLICANT: Saiko HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5767246ihiko ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
TITLE OF INVENTION: Cell Membrane
TITLE OF INVENTION: Cell Membrane
TOWNESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
                     US-09-720-493-2

US-08-545-809A-116

US-08-918-148-79

US-09-138-091A-77

US-09-138-091A-77

US-09-471-276-888

US-09-471-276-888

US-08-480-774A-2

US-08-545-809A-142

US-08-545-809A-123

US-09-260-527-3

US-09-260-527-3

US-09-260-537-14

US-08-748-450-4

US-08-748-450-4

US-08-793-450-4

US-08-793-755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,125
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 5, Application US/08360125
; Patent No. 5767246
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION UNDRER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington
                          US-08-360-125-5
525.5
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                                                                                                                                                                November 9, 2005, 11:29:55 ; Search time 18.1805 Seconds (without alignments) 480.403 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 55, Sequence 65, Sequence 65, Sequence 65, Sequence 39, Sequence 65, Sequence 67, Sequence 145, Sequence 25, Sequence 25, Sequence 25, Sequence 11, Sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5,
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                                                                                                                                                                                                                                                                      US-10-660-357A-13
624
1 QVQLQESGPGLVKPSQTLSL.....AREGDGFDYWGQGTLVTVSS
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                     GenCore version 5.1.6
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US-09-017-628-5

US-09-014-080-5

US-09-025-769B-39

US-09-490-025-769B-65

US-09-490-025-769B-65

US-09-490-153-65

US-09-490-153-65

US-09-490-153-65

US-09-490-153-65

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US-09-490-153-65

US-09-490-070A-45

US-09-490-070A-25

US-09-490-070A-25

US-09-490-153-25

US-09-490-153-25

US-09-490-153-25

US-09-490-153-25

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US-09-490-153-25

US-09-490-153-25

US-09-490-153-25

US-09-490-153-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fotal number of hits satisfying chosen parameters:
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US-09-472-087-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                         513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                        - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Issued Patents AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match Length DB
                                                                                                                                                                                                                                                                        Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
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Maximum DB E
                                                                                                                     OM protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Result
No.
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Score 550; DB 2; Length 119;
Pred. No. 1.3e-48;
COMPUTER EADABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: In Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,578
FILING DATE: May 25, 1995
CLASSIFICATION TOWAR: 08/360,125
RIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPRANE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL TYPE: antibody GAH
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) DOCUMENT NUMBER:

; FILING DATE:

; PUBLICATION DATE:

; RELEVANT RESIDUES IN SEQ ID NO:

US-08-450-578-5
                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 119 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANELLE:
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VOLUME:
ISSUE:
PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSCGFYWNWIRQHPGKGLEWIGYIYYSGSTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 OVOLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREG--DGFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Monoclonal Antibody
Specifically Binding to Surface Antigen of Cancer
Cell Membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 88.1%; Score 550; DB 1; Length 119; Best Local Similarity 88.2%; Pred. No. 1.3e-48; Matches 105; Conservative 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Voko HIRAKAWA
APPLICANT: Noko HIRAKAWA
APPLICANT: No. 58378451hiko ITO
APPLICANT: No. 58378451hiko ITO
APPLICANT: Naxuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                         TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL TYPE: antibody GAH
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-450-578-5; Sequence 5, Application US/08450578; Patent No. 5837845
                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
LDCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                               CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
                                                                                                  INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                       ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
  ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                             ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSCGFYWNWIRQHPGKGLEWIGYIYYSGSTY 60
                                                                                                                                            61 YNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCAREG--DGFDYWGOGTLVTVSS 117
                                                                                                                                                                         61 YNPSLKSRVTISLDTSKSQFSLKLSSLTAADTAVYYCARSTRLRGADYWGQGTWVTVSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: Saiko HOSOKAWA et al.

APPLICANT: Saiko HOSOKAWA et al.

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY

TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE

TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE

TORRESPONDENCE ADDRESS.

ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.

STREET: 2033 K Street, N.W., #800

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.
  2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: TAGAWA, Saiko
APPLICANT: TAGAWA, Toshiaki
APPLICANT: TAGAWA, Toshiaki
APPLICANT: TAGAWA, Toshiaki
APPLICANT: HITRKAWA, Yoko
APPLICANT: HITO, NO. 5990287ihiko
APPLICANT: NAGAIKE, Kazuhiro
TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
FILE REPERENCE: 177/527361KH
CURRENT APPLICATION NUMBER: US/09/017,628
EARLIER APPLICATION NUMBER: US/360,125
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 119;
6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Hybridoma producing human antibody GAH
US-09-017-628-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 550; DB 2;
Pred. No. 1.3e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diskette, 3.5 inch, 1.44 mb
6; Mismatches
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                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09017628
Patent No. 5990287
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09014880
Patent No. 5990297
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MEDIUM TYPE: Diskette, 3.5
COMPUTER: IBM Comparible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDER-EGE. 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 88.1%;
Best Local Similarity 88.2%;
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Ver. 2.0
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 5
LENGTH: 119
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Sequence 5, Application US/08450363

Sequence 5, Application US/08450363

Pacent No. 6436434

GENERAL INFORMATION:
APPLICANT: Saiko HISAKAWA

APPLICANT: Toshiaki TAGAWA

APPLICANT: No. 6436434ihiko ITO
APPLICANT: No. 6436434ihiko ITO
APPLICANT: No. 6436434ihiko ITO
APPLICANT: No. 626434ihiko ITO
APPLICANT: ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSCGFYWNWIRQHPGKGLEWIGYIYYSGSTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREG--DGFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 550; DB 2;
Pred. No. 1.3e-48;
6; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Wenderoth, Lind & Ponack
805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette, 5.25 inch, 500 COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 5.1 CURREMY APPLICATION DATA: APPLICATION NUMBER: US/08/450,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CELL TYPE: Hybridoma producing human CELL TYPE: antibody GAH
       CLASSIFICATION: 536
PRIOR APPLICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/450,578
FILING DATE: MAY 25, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION NUMBER: 07/905,534
PRIOR APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: WARTEN M. CHEEK, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELEPHONE: 202-721-8200
January 28, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.1%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 119 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-014-880-5
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TITLE OF INVENTION: Human Monoclonal Antibody
Specifically Binding to Surface Antigen of Cancer
         61 YNPSLKSRVTISLDTSKSQFSLKLSSLTAADTAVYYCARSTRLRGADYWGQGTMVTVSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDIVIDUAL ISOLATE: «Unknown»
DEVELOPWENTAL STAGE: «Unknown»
HAPLOTYPE: «Unknown»
TISSUE TYPE: «Unknown»
CELL TYPE: Hybridoma producing human
CELL LINE: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2. Dec-1999
CLASSIFICATION: CUNKnown>
PRIOR APPLICATION DATA: 2. Dec-1999
PRIOR DATE: CANDER: 08/450,363
FILING DATE: May 25, 1995
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
APPLICATION NUMBER: JP58859/1991
FILING DATE: June 28, 1991
APPLICATION NUMBER: JP158860/1991
FILING DATE: June 28, 1991
APPLICATION NUMBER: JP158861/1991
APPLICATION NUMBER: JP158861/1991
APPLICATION NUMBER: JP158861/1991
APTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS,
ADDRESSEE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 2033 K Street, N.W., #800
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/467,903
                                                                                                                Sequence 5, Application US/09467903
Patent No. 6787153
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
YOKO HIRAKAWA
YOKO HIRAKAWA
NO. 67871531hiko ITO
Kazuhiro NAGAIKE
                                                                                                                                                                                                                                                                                                                                             Cell Membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Warren M.Cheek Jr. REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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STRAIN: <Unknown>
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ANTI-SENSE: <Unknown>
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
                                                                         RESULT 6
US-09-467-903-5
         엄
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREG--DGFDYWQQGTLVTVSS 117
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Pred. No. 1.3e-48;
6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human CELL TYPE: antibody GAH
CELL TYPE: antibody GAH
CELL TYPE: ALIBODY GAH
LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
FILING DATE: May 25, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTONNEY/AGENT INPORMATION:
NAME: Warren M. Check, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-371-8850
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PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 88.1%;
Best Local Similarity 88.2%;
Matches 105; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: ANTI-SENSE: PRAGMENT TYPE: ORIGINAL SOURCE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION:
PUBLICATION INFORMATION:
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CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
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DATE:
DOCUMENT NUMBER:
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NAME/KEY:
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JOURNAL:
VOLUME:
ISSUE:
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59 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARWGGDGFYAMDYWGQGTLVTVS 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLQESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYSGSTN 58
                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                            Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDITAL TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPANDER: PatentIn Release #1.0, Version #1.30 (EPO)
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 55, Application US/09025769B
Patent No. 630064
GENERAL INFORMATION:
APPLICANT: Fack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Plueckthun, Andreas
ITTLE OF INVENTION: Procein/(Poly)peptide libraries
VINDER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
                                                                                                                                                                                                                                                                                                                          87.0%; Score 543; DB 3;
90.1%; Pred. No. 6.6e-48;
iive 3; Mismatches 3;
  NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REPERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
                                                                                                    TELEFAX: (212)596-9990
INFORMATION FOR SEQ ID NO: 39-SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 90.13
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (212) 596-9090
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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7
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88.2%; Pred. No. 1.3e-48;
live 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1251 Avenue of the Americas CITY: New York STATE: New York COUNTY: USA 2TO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 39, Application US/09025769B
Fatent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knapplek, Achim
APPLICANT: 11ag, Vic
APPLICANT: Ge, Liming
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
           IMMEDIATE SOURCE:
LIBRARY: «Unknown»
CLONE: «Unknown»
POSITION IN GENOME:
CHROMOSOME/SEGMENT: «Unknown»
MAP POSITION: «Unknown»
UNITS: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                         LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
AUTHORS:
ORGANELLE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 88.2
Matches 105; Conservative
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                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                              JOURNAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS-09-025-769B-39
                                                                                                                                                                 FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-467-903-5
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59 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARWGGDGFYAMDYWGQGTLVTVS 118
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                                                                                1 QVQLQESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYSGSTN 58
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        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe STRBET: 1666 K Street, N.W., Suite 300
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 243n-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 543; DB 4; Length 119;
Pred. No. 6.6e-48;
3; Mismatches 3; Indels
        3; Indels
                                                                                                                                                                                                                                                                                                                          Sequence 65, Application US/09490070A
Patent No. 6665248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Pluckthum, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: EP 95 11 3021.0 FILING DATE: 18-AUG-1995
ATTORNEY/AGNT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (202) 912-2000
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 65
SEQUENCE CHARACTERISTICS
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90.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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Matches 109; Conservative
        109; Conservative
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                                                                                                                                                                                                                                                      61 YNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCAR-EGDGF---DYWGQGTLVTVS 116
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                                                                                                                                                                          1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe STREET: 1666 K Street, N.W., Suite 300
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                                                                                                    Length 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 39, Application US/09490070A

Patent No. 6696248

GENERAL INFORMATION:

APPLICANT Rappik, Achim

Fack, Peter

Ilag, Vic

Ge, Liming

Moroney, Simon

Pluckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES:
                                                                                                                                      3; Indels
                                                                                                  Score 543; DB 3;
Pred. No. 6.6e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Colin G. Sandercock, Esq. REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: protein
DESCRIPTION: SEQ ID NO: 39:
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INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 119 amino acids
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90.1%;
                                                                                            Query Match
Best Local Similarity 90.1%;
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington STATE: D.C.
                                MOLECULE TYPE: protein
amino acid
GY: linear
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Best Local Similarity
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SEQUENCE
US-09-490-070A-39
                                                      US-09-025-769B-65
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59 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARWGGDGFYAMDYWGQGTLVTVS 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.0%; Score 543; DB 4; Length 119; 90.1%; Pred. No. 6.6e-48;
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                                                                                                                                                                                                                                                                                Ge, Liming
Moroney, Simon
Plueckthun, Andreas
INVENTION: Protein/(Poly)peptide libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PACENTIN Release #1.0, CURRIN APPLICATION DATA: APPLICATION NUMBER: US/09/490,153 FILING DATE: 24-Jan-2000 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                                                                                                                   Sequence 39, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                                         APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Prote NUMBER OF SEQUENCES: 373 CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
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Matches 109; Conservative
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                                     $ 117
                                                                           S 119
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61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-EGDGF---DYWGQGTLVTVS 116
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                                                                                                                                                        Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.0%; Score 543; DB 4;
90.1%; Pred. No. 6.6e-48;
                                                                                                                                                                                                                                                                                                   ADDRESSEE: James F. Haley, Jr., Esq. STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
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SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-153-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                   Sequence 65, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
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APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (212)596-9000
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                                                                                         APPLICANT: Knappik, Achim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
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STATE: New York
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                                                                                                                                     Ilag,
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US-09-490-153-65
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59 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYÇARWGGDGFYAMDYWGQGTLVTVS 118
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    CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lai, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Au-Voung, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Goegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 87.0%; Score 543; DB 4; Length 119; Best Local Similarity 90.1%; Pred. No. 6.6e-48; Matches 109; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 65: US-09-490-324-65
                                                                                                                                      ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09049672A Patent No. 6135941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 65
SEQUENCE CHARACTERISTICS
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                                                                        CITY: New York
STATE: New York
COUNTRY: USA
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CORRESPONDENCE ADDRESS:
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APPLICANT: Hillma
APPLICANT: Lal, P
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US-09-049-672A-4
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION NUMBER: US/09/490,324

FILING DATE: 24-Jan-2000

PRIOR APPLICATION NUMBER: US/09/025,769

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0
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                                                                                                                                                              ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
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90.1%; Pred. No. 6.6e-48;
tive 3; Mismatches 3; Indels
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
CORRESPONDENCE ADDRESS:
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Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794 REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-900
INFORMATION FOR SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 65, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 90.11
Matches 109; Conservative
                                                                                                                                                                                                          CITY: New York
STATE: New York
COUNTRY: USA
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US-09-490-324-65
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COMPTER: CA
COUNTER: USA
COMPTER: USA
COMPTER: USA
COMPUTER READABLE FORM:
MUDIUM TIPE: Disketete
MUDIUM TIPE: Disketete
MUDIUM TIPE: Disketete
MUSURENT APPLICATION DATA:
MARE: CETTON NUMBER: US/09/049,672A
FILING DATE: MINCHARTION:
MARE: CETTON NUMBER: PP-0497 US
FILING DATE: MINCHARTION:
MARE: CETTON NUMBER: PP-0497 US
FERERENCE/DOCKET NUMBER: PP-0497 US
FERERENCE/DOCKET NUMBER: PP-0497 US
FELERAX: 650-845-4166
FELEX: MARACTERISTICS:
LENGTH: 473 amino acids
FTRANDEDNESS: shingle
TYPE: amino acids
FTRANDEDNESS: shingle
TYPE: amino acids
FTRANDEDNESS: shingle
TYPE: MINCHARTION:
MARCHART SHING SHORE:
MUS-09-049-672A
US-09-049-672A

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US-09-049-672A

US-09-049-672A

US-09-049-773 Anito acids
MUS-09-049-672A

US-09-049-672A

US-09-049-672A

US-09-049-672A

US-09-049-672A

US-09-049-672A

US-09-049-672A

US-09-049-773 Match
Best Local Similarity 84.7%; Pred. 7; Indels 7; Gaps 1;
Matches 105; Conservative 5; Mismatches 7; Indels 7; Gaps 1;
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Db 80 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDDVGLRGGNYGMDVWGQGTLV 139
Qy 114 TVSS 117
Db 140 TVSS 143

Search completed: November 9, 2005, 11:46:38 Job time: 19.1805 secs

61 YNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCARE-----GDGFDYWGQGTLV 113

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Consider the service and the

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RESULT
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Sequence 13, Appl
Sequence 20, Appl
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 138, App
Sequence 138, Appl
Sequence 10, Appl
Sequence 10, Appl
                                                                                                                          9, 2005, 11:40:37; Search time 65 Seconds (without alignments) 753.137 Million cell updates/sec
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624
1 QVQLQESGFGLVKPSQTLSL.....AREGDGFDYWGQGTLVTVSS
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/ cgn2_6/ptodata///pubpaa/US07_NEW_PUB.pep:*
/ cgn2_6/ptodata///pubpaa/US06_NEW_PUB.pep:*
/ cgn2_6/ptodata///pubpaa/US06_PUBCOMB.pep:*
/ cgn2_6/ptodata///pubpaa/US07_NEW_PUB.pep:*
/ cgn2_6/ptodata///pubpaa/US08_NEW_PUB.pep:*
/ cgn2_6/ptodata///pubpaa/US08_NEW_PUB.pep:*
/ cgn2_6/ptodata///pubpaa/US08_PUBCOMB.pep:*
/ cgn2_6/ptodata///pubpaa/US08_PUBCOMB.pep:*
/ cgn2_6/ptodata///pubpaa/US09_PUBCOMB.pep:*
/ cgn2_6/ptodata///pubpaa/US00_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US60_PUBGOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-310-530-13
US-10-660-357-13
US-10-984-960A-20
US-10-330-613-5
US-10-330-530-5
US-10-309-762-138
US-10-309-762-10
US-10-309-762-10
US-10-309-762-10
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                                                                                                                                                                                                                                                                                                                                                                           1867879 segs, 418409474 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published_Applications_AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length
                                                                                                                               November
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Perfect score:
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Maximum DB seq
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                                                                                                                                                                                                                                                              Sequence:
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                                                                                                                               Run on:
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No.
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	Sequence 6, sequence 13, sequence 13, sequence 13, sequence 13, sequence 11, sequence 11, sequence 11, sequence 12, sequence 13, sequence 12, sequence 13, sequen	th 117; ls 0; Gaps 0;
US-10-309-762-144 US-10-984-960A-56 US-10-309-762-75 US-10-309-762-96 US-10-309-762-8 US-10-309-762-16 US-10-309-762-16 US-10-309-762-16 US-10-309-762-147 US-10-309-762-151	US-10-310-901-6 US-10-330-613-33 US-10-330-613-33 US-10-330-613-33 US-10-660-357-33 US-10-693-576-410 US-10-693-576-410 US-10-693-576-140 US-10-693-576-140 US-10-693-576-140 US-10-693-576-140 US-10-644-277-62 US-10-649-8 US-10-706-689-8 US-10-707-155-10 US-10-330-613 US-10-330-61	Score 624; DB 14; Length; Pred. No. 1e-47; 0; Mismatches 0; Indels
575.5 92.2 120 1574.5 92.1 124 1574.5 92.1 124 1574.5 92.1 124 1572 1572 1572 1572 1572 1572 1572 1572	9 91.2 480 18 9 91.2 480 18 91.0 117 18 91.0 117 18 91.0 117 18 91.0 117 19 90.9 120 118 18 90.7 18 90.5 123 18 90.5 123 18 90.5 123 18 90.5 123 18 90.5 123 18 90.5 123 18 90.5 123 18 90.5 123 18 90.5 123 18 90.5 123 18 90.5 123 18 90.5 128 18 90.5 128 18 90.5 128 18 90.5 128 18 90.5 128 18 90.5 128 18 90.5 128 18 90.1 128 90.1 128 90	Query Match Best Local Similarity 100.0%; Matches 117; Conservative

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TYPE: PRT
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US-10-330-530-13
; Sequence 13, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
    APPLICANT: Gudas, Jean
; TILLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR PELLING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SEQ ID NO 13
; LENGTH: 117
; TYPE: PRI

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Publication No. US20040115205A1

GENERAL INFORMATION:

APPLICANT: BAT-Eli, Menashe

APPLICANT: BAT-Eli, Menashe

TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18

TITLE OF INVENTION: ANTIGEN

FILE REFERENCE: ABGENIX.03001

CURRENT FILING DATE: 2003-09-10

PRIOR APPLICATION NUMBER: 10/330,580

PRIOR APPLICATION NUMBER: 10/330,580

PRIOR PLING DATE: 2002-12-26

NUMBER OF SEQ ID NOS: 40

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 624; DB 16; Length
100.0%; Pred. No. 1e-47;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Pred. No. 1e-47;
0; Mismatches 0;
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US-10-984-960A-20
Sequence 20, Application US/10984960A
Publication No. US20050142137A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 117; Conservative 0
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Best Local Similarity 100.
Matches 117; Conservative
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                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo Sapiens
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LENGTH: 117
TYPE: PRT
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APPLICANT: Zhong, Haihong
APPLICANT: Ara, Gulshan
APPLICANT: Ara, Gulshan
APPLICANT: LaRochelle, William J.
ITILE OF INVENTION: ANTIBODIES AGAINST SECRETORYLEUKOCYTE PROTEASE INHIBITOR
FILE REFERENCE: Cura 970
CURRENT APPLICATION NUMBER: US/10/984,960A
CURRENT FILING DATE: 2004-11-08
PRIOR PPLICATION NUMBER: 60/518,275
PRIOR FILING DATE: 2003-11-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
94.2%; Score 587.5; DB 18; Length 122;
Best Local Similarity 91.8%; Pred. No. 1.9e-44;
Matches 112; Conservative 4; Mismatches 1; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 117;
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Publication No. US20030147809A1
GENERAL INFORMATION:
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
FILE REFREENCE: ABGRINS. 022A
CURRENT APPLICATION NUMBER: U5/10/330,613
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: 60/346299
PRIOR PILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FRASESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.1%; Score 587; DB 14; Length 1
94.0%; Pred. No. 2e-44;
tive 4; Mismatches 3; Indels
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                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 112
SOFTWARE: CuraSequist version 0.1
SEQ ID NO 20
LENGTH: 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 94.0
Matches 110; Conservative
Chui, Daniel
                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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US-10-330-613-5
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US-10-330-530-5
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TVSS 124
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Pred. No. 2e-44;
4; Mismatches 3; Indels (
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APPLICANT: Foltz, Ian
APPLICANT: Handa, Machael
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
              TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES FILE REFERENCE: ABGENTX.031A.
CURRENT APPLICATION NUMBER: US/10/330,530
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: US 60/346414
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bar-Ell, Menashe
APPLICANT: Green, Larry L.
TITLE OF INVENTION: USE OF ANTIBODIES ACAINST THE MUC18
TITLE OF INVENTION: ANTIGEN
FILE REFERENCE: ABGENIX.030C1
CURRENT APPLICATION NUMBER: US/10/660,357
CURRENT FILING DATE: 2003-09-10
PRIOR PRING DATE: 2003-12-26
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 138, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/10660357
Publication No. US20040115205A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           94.1%;
94.0%;
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 94.0°
Matches 110; Conservative
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                                                                                                                                                                                                                                             ; ORGANISM: Homo Sapiens
US-10-330-530-5
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GRGANISM: Homo Sapiens
US-10-660-357-5
APPLICANT: Gudas, Jean
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APPLICANT: Tee, Kam Fai
APPLICANT: Tee, Kam Fai
APPLICANT: Jeffers, Michael
APPLICANT: Jeffers, Michael
APPLICANT: Mesti, Mehdi
APPLICANT: Starling, Gary
APPLICANT: Starling, Gary
APPLICANT: Starling, Gary
APPLICANT: Khramtsov, Nikolia
TITLE OF INVENTION: DOMAIN AND MUCIN DOMAIN 1 (TIM-1) ANTIGEN AND USES THEREOF
TITLE OF INVENTION: DOMAIN AND MUCIN DOMAIN 1 (TIM-1) ANTIGEN AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/805,177
CURRENT APPLICATION NUMBER: 600456,652
PRIOR APPLICATION NUMBER: 600456,652
PRIOR FILING DATE: 2003-03-19
NUMBER OF SEQ ID NOS: 141
SEQ ID NO 53
SEQ ID NO 53
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                                                                                                                                                                                                                                                                                                                                                                                                                    Score 585.5; DB 15; Length
Pred. No. 2.7e-44;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
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89.5%; Pred. No. 6.5e-44;
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT APPLICATION NUMBER: US/10/309,762
PRICH APPLICATION NUMBER: 60/337275
PRICH APPLICATION NUMBER: 60/337275
PRICH FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 138
LENGTH: 118
TUDE: ....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 53, Application US/10805177; Publication No. US20050084449A1; GENERAL INFORMATION: APPLICANT: Landes, Gregory M.; APPLICANT: Bezabeh, Binyam; APPLICANT: Bezabeh, Binyam; APPLICANT: Tse, Kam Fai; APPLICANT: Use, Kam Fai; APPLICANT: Use, Kam Fai;
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Best Local Similarity 94.9%;
Matches 112; Conservative
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CRGANISM: Homo sapiens
US-10-309-762-138
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TYPE: PRT
ORGANISM: Homo Sapiens
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Query Match
Best Local Similarity 91.7%;
Matches 110; Conservative
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Best Local Similarity 89.3
Matches 109; Conservative
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ORGANISM: Homo sapiens
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US-10-309-762-144
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                              Sequence 10, Application US/10309762
| Publication No. US20040018198A1
| GENERAL INFORMATION:
| APPLICANT: Gudas, Jean
| APPLICANT: Foltz, Jan
| APPLICANT: Handa, Masahisa
| APPLICANT: Handa, Masahisa
| APPLICANT: Handa, Masahisa
| APPLICANT: Grids, Jean
| APPLICANT: Handa, Masahisa
| TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
| TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
| TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
| TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
| TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
| CURRENT FILING DATE: 2002-12-02
| PRIOR FILING DATE: 2001-12-03
| NUMBER OF SEQ ID NOS: 246
| SOFTWARE: FastSEQ for Windows Version 4.0
| LENGTH: 123
| TYPE: PRT
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| Sequence 13, Application US/10309762
| Publication No. US20040018198A1
| GENERAL INFORMATION:
| APPLICANT: Godds, Jean
| APPLICANT: Foltz, Ian
| APPLICANT: Gallo, Michael
| TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
| TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
| TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
| CURRENT APPLICATION NUMBER: US/10/309,762
| CURRENT APPLICATION NUMBER: 06/337275
| PRIOR APPLICATION NUMBER: 60/337275
| PRIOR PELIAG DATE: 2001-12-03
| NUMBER OF SEQ ID NOS: 246
| SEQ ID NO 13
| LENGTH: 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
92.8%; Score 579; DB 15; Length 123;
Best Local Similarity 90.2%; Pred. No. 1.1e-43;
Matches 111; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .le-43;
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4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-10-309-762-10
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ORGANISM: Homo sapiens
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RESULT 10
US-10-309-762-10
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US-10-309-762-13
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GENERAL INFORMATION:

APPLICATION OF US20050142137A1

GENERAL INFORMATION:

APPLICANT: Gallo, Michael

APPLICANT: Callo, Michael

APPLICANT: Callo, Michael

APPLICANT: Ara, Gulshang

APPLICANT: LARCohelle, William J.

TITLE OF INVENTION: ANTIBODIES AGAINST SECRETORYLEUKOCYTE PROTEASE INHIBITOR

TITLE OF INVENTION: ANTIBODIES AGAINST SECRETORYLEUKOCYTE PROTEASE INHIBITOR

CURRENT FILING DATE: 2004-11-08

PRIOR PILICATION NUMBER: 60/518,275

PRIOR FILING DATE: 2003-11-07

NUMBER OF SEQ ID NOS: 112

SOFTWARE: CuraSeqList version 0.1
                           61 YNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCARDGYNYWYFDLWGRGTLVTVSS 120
61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGDG---FDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGDG---FDYWGQGTLVTVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 15; Length 120;
                                                                                                                                                                                                                                                                                                               APPLICANT: Tall, Tan
APPLICANT: Folic, Tan
APPLICANT: Handa, Magahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: 105/10/309,762
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 575.5; DB 15; Length
Pred. No. 2.1e-43;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 144
                                                                                                                                                                                                  ; Sequence 144, Application US/10309762; Publication No. US20040018198A1; GENERAL INFORMATION: APPLICANT: Gudas, Jean
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YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGD-----GFDYWGQGTLVTV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARENYDILTGFNWFDPWGQGTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREG-----DGFDYWGQGTLV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTY 60
1 QVQLQESGPGLVKPSQTLSLTCTVSGGSIKSGDYYWSWVRQLPGKGLEWIGYIYYSGSTY 60
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                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gudas, Jean
APPLICANT: Gudas, Jean
APPLICANT: Holtz, Ian
APPLICANT: Holtz, Ian
APPLICANT: Holtz, Ian
APPLICANT: Holts, Michael
TITLE OF INVENTION: ANTHODIES AGAINST CARBOXIC ANHYDRASE IX
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: ABGENIX. 027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 96, Application US/10309762
| Publication No. US20040018198A1
| GENERAL INFORMATION:
| APPLICANT: Handas, Masahisa |
| APPLICANT: Handa, Masahisa |
| TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN |
| TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN |
| FILE REPRENCE: ABGRIX.027A |
| CURRENT APPLICATION NUMBER: US/10/309,762 |
| CURRENT FILING DATE: 2002-12-02 |
| PRIOR FILING DATE: 201-12-03 |
| NUMBER OF SEQ ID NOS: 246 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| LEWOTH: 143 |
| TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.1%; Score 574.5; DB 15; Length 124; 89.5%; Pred. No. 2.7e-43; tive 3; Mismatches 3; Indels 7;
                                                                                                                                                                                                                                                                         US-10-309-762-75
Sequence 75, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
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Matches 111, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
CORGANISM: Homo sapiens
US-10-309-762-75
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61 YNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCAREG------DGFDYWGQGTLV 113
                                                                                                                                                                                                     80 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARENYDILTGFNWFDPWGQGTLV 139
                                                                                                                                                  20 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTY
                                                                                    Gaps
                                                                                  7;
                                                   Length 143;
                                                                                  3; Indels
                                                 Score 574.5; DB 15;
Pred. No. 3.1e-43;
                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                         Search completed: November 9, 2005, 12:42:59 Job time : 66 secs
                                                 92.1%;
                                             Query Match
Best Local Similarity 89.5
Matches 111; Conservative
, ORGANISM: Homo sapiens
US-10-309-762-96
                                                                                                                                                                                                                                                       114 TVSS 117
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79

(OTTEN) MUNICE SEARCH SHIT

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

November 9, 2005, 12:25:58; Search time 12.609 Seconds (without alignments) 892.802 Million cell updates/sec Run on:

US-10-660-357A-13
624
1 QVQLQESGFGLVKPSQTLSL.....AREGDGFDYWGQGTLVTVSS 117 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

. 283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:* Database :

1: pirl: * 2: pir2: * 3: pir3: * 4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Iq heavy chain V r	g variab	heavy cha	q heavy chain	σ	ס	וסו	Ig heavy chain V r	g mu cha	5	q heavy chain V	q heavy	heavy chain V	g V-D-J region	g heavy	g heavy chain V	g heavy chain V	וט	b	g heavy	5	b	heavy chain	Ig heavy chain V r		heavy chain V	Ig heavy chain V-D	heavy	heavy chain
ID	S13519	3778	_	44	S30534				S37456				S31586			S31676		N	830530	o	C	S78055	26	A49045	S19668	26	4411	7805	S31696
DB	2	~	~	~	~	~	7	0	7	~	0	~	~	~	~	~	~	~	7	~	7	~	~	~	0	~	~1	~	~
Length	1 4	4	135	2	\sim	m	2	66	н	S	4	ß	139	2	66	137	2	99	2	4	118	4	1	140	2	99	110		139
* Query Match	. &	9	84.9	4	84.1	83.8	83.0	82.9					81.2				9.6							78.2	78.0		77.8	•	77.4
Score	549	537	530	525	524.5	523	518	517	517	509	507	507	506.5	503.5	200	499.5	496.5	495	495	494	493.5	488.5	488	488	487	486	485.5	483.5	483
Result No.		8	e	4	ហ	9	7	œ	0	10		12		14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

Ig neavy	Ig heavy	Ig lambd	Ig heavy	PI PI	Ig heavy	1g heavy	Ig heavy	Ig heavy	70370 Ig mu chain precur	3 Ig heavy o					
S124	PH16	8316	8315	S470	S265	S26	S441	8316	A41287	S124	S26	B263	S124	PT02	S2444
~	7	7	7	7	7	7	~	7	~	~	~	N	7	7	7
66	109	135	137	126	97	66	105	124	139	66	66	116	97	120	118
٦.	o.	9.	4.	۲.	9.	७.	9.	9.	75.6	s.	s.	'n	'n.	'n.	۲.
77	16	16	16	75	75	75	75	75	75	75	75	75	75	75	75
481	480	478	476.5	472.5	472	472	472	472	471.5	471	471	471	470	470	468.5
		٠.	_	_	35		_	m	_	0	_	42	_		

ALIGNMENTS

RESULT 19 heav	RESULT 1 S1319 Glade heavy chain V region precursor - human C;Gpecies: Homo sapiens (man) C;Accession: S1319 C;Accession: S1319 C;Accession: S1319 Nucleic Acids Res. 19, 673, 1991 A;Atitle: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked A;Accession: S13519 A;Accession: S135
A, Cro C, Sup C, Key F, 41-	A,Cross-references: EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PID:g37725 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;41-125/Domain: immunoglobulin homology <imm></imm>
Que Besi Mat	Query Match 88.0%; Score 549; DB 2; Length 147; Best Local Similarity 88.4%; Pred. No. 7.3e-42; Matches 107; Conservative 3; Mismatches 7; Indels 4; Gaps 1;
\$ 8 8	1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY 60 -
ර සි	61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGDGFDYWGQGTLVTVS 116
δλ	\$ 117
qa	147 \$ 147

INSULE 1

INSULE 2

INSULE 3

INSULE 3

INSULE 4

INSULE 5

INSULE

N

9

Gaps

4.

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Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: 831690
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
Submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: 831585
A;Accession: 831690
                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 YNPSLKSRVTLSVDTSKNQFSLKLSSVTAADTGVYYCSRLSGGYYSDFDYWSQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                        61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGDG----FDYWGQGTLVTVS 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;bate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
C;Accession: S30534
R;Mariette, X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGSYYWSWIRQPAGKGLEWIGRIYTSGSTN
                                                                                                                                                                                                                                                                                                                                                       1 QVQLQESGPGLVKPSETLSLTCTVSGGYISSSSYYWGWTRQPPGKGLEWIGSIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY
                                                                                                                                                                                                                                                                                                                               1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY
                                                                                                                         PID:9940524
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                                                                                                                                                                                                                                       DB 2; Length 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Nocate 1710 (AMR)
A; Cross-references: BMBL: 218320
C; Superfamily: immunoglobulin v region; immunoglobulin homology
C; Keywords: heteroterramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology < NM>
                                                                                                                       12967; PIDN:CAA83264.1; immunoglobulin homology
                                                                                                                                                                                                                                                                                  12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 524.5; DB 2;
                                                                                                                                                                                                                                                             8e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.1%; Scc. 80.9:0.8%; Pred. No. >...
A;Reference number: S44105
A;Accession: S44113
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-121 < HAW>
A;Cross-references: EMBL:231389; NID:9472967; PIIC
C;Superfemily: immunoglobulin V region; immunogloC;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin P;15-99/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, October 1992
                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                       Score 525;
                                                                                                                                                                                                                                                               Pred. No.
                                                                                                                                                                                                                                     84.1%;
                                                                                                                                                                                                                                                          Best Local Similarity 84.3
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 80.8
Matches 105; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Accession: S30534
A, Status: preliminary
A, Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 S 117
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Igheavy chain precursor V-D-J region (clone mAB 61VH) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Accession: S78051; S23716
R;Harindranath, N.
A;Reference number: S78051
A;Residues: 1-135
A;Residues: 1-137
A;Residues: 1-137
A;Residues: 1-113/Product: Rimunoglobulin homology 
C;Superfamily: immunoglobulin v region; immunoglobulin homology 
C;Superfamily: immunoglobulin homology 
C;Superfamily: immunoglobulin homology 
C;Superfamily: immunoglobulin homology 
C;Superfamily: immunoglobulin homology 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig heavy chain V region - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001 C;Caccession: S4H13 R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K. submitted to the EMBL Data Library, March 1994 A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable
                                                                                               ;;
                                                                                                                                                                                                                                                          YNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCARE-----GDGFDYWGQGTLVT 114
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                                                                                                                                                                    QVQLQESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYSGSTN
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                                                                                                                                        1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY
                                                                                               Gaps
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                                                  Length 140
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83.7%; Pred. No. 3.2e-40;
ive 5; Mismatches 9; Indels
                                                                                               Indels
                                                                                          2;
                                               86.1%; Score 537; DB 2;
87.0%; Pred. No. 8e-41;
                                                                                          3; Mismatches
  F;46-128/Domain: immunoglobulin homology <IMM>
                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 83.77
Matches 103; Conservative
                                                                  Best Local Similarity
Matches 107; Conser
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                                                                                                                                                                                                                                                                                                                                                                        138 VSS 140
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                                               Query Match
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9

Gaps

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C;Accession: S37456
R;McIntosh, R.S.; Tandon, N.; Weetman, A.P.
RimCintosh, R.S.; Tandon, N.; Weetman, A.P.
RimCintosh, R.S.; Tandon, N.; Weetman, A.P.
Rimcintosh: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from A;Reference number: S37453
A;Accession: S37456
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-116 cMCI>
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Ig heavy chain - human

Ig heavy chain - human

Ig heavy chain - human

C;Species: Homo sapiens (man)

C;Accession: Siisil

R;Charcession: Siisil

R;Charcagner, P.; Demanison, C.; Theze, J.; Zouali, M.

Submitted to the EMBL Data Library, December 1992

A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA aut

A;Reference number: Siiso

A;Recession: Siisil
A; Molecule type: DNA
A; Residues: 1-99 cwEn.
A; Residues: 1-99 cwEn.
A; Cross-references: EMBL:Z14237; NID:g37706; PIDN:CAA78606.1; PID:g1335372
A; Cross-references: EMBL:Z14237; Narks, J.D.; Llewelyn, M.B.; Winter, G.
B; Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A; Tomlinson, T.W.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A; Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A; Reference number: S26885; MUID:93021117; PMID:1404388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig mu chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISVDTSKNQFSLKLSSVTAADTAVYYCAREGDGFDY------WGQGTLVTVSS 117
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                                                                                                                                                                                                                                                                                           A,Cross-references: EMBL:Z12365; NID:g32948; PIDN:CAA78235.1; PID:g32949 (S.Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: hererotetramer; immunoglobulin F;15-99/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 517; DB 2;
Pred. No. 3.9e-39;
4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 517; DB 2;
Pred. No. 3.3e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;6-90/Domain: immunoglobulin homology <IMM>
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98.0%;
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Best Local Similarity 85.3%;
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 97; Conserv
                                                                                                                                                                                   A; Accession: S26900
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-99 < TOM>
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Datession: S31514
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A;Reference number: S31509
                                                                                                                                                                                                                                                                    7
                                                                                                                                                                                                                                                                                                                                                                                                                               YNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCAREGD------GFDYWGQG 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 YNPFLKSRVIISVDTSENQFSLRLTSVTPADTAVYYCARIGYNFGYGFDPWGQGTLVTVS 127
                                                                                                                                                                                                                                                                                                                          9
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CiSpecies: Homo sapiens (man)
CiSpecies: Li Marcus, D.M.

Riweng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.

Riweng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.

A; Title: Polymorphism of human immunoglobulin V(H) 4 germ-line genes.
A; Reference number: S268001
A; Accession: S268001
                                                                                                                                                                                                                                                                                                                    1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY
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                                                                                                                                                                                                                                                                    Gaps
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                                                                      A;Cross-references: EMBL:214199; NID:g30984; PIDN:CAA78568.1; PID:g30985 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;20-102/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X69862; NID:g33086; PIDN:CAA49496.1; PID:g33087
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;22-106/Domain: immunoglobulin homology <IMM>
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Pred. No. 3.5e-39;
7; Mismatches 10; Indels
                                                                                                                                                                                                               Length 130;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                               Score 523; DB 2;
Pred. No. 1.3e-39;
                                                                                                                                                                                                                                                               3; Mismatches
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82.6%;
                                                                                                                                                                                                               83.8%;
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Best Local Similarity 82.7
Matches 105; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 TLVTVSS 130
                      A; Molecule type; mRNA
A; Residues: 1-130 <CUI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-128 < CHA>
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Status: preliminary
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Best Local Simi
Matches 100;
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A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-122 <SAH>
                                                                                                                                                                                        81.2%;
                                                                                                                                                                                     Query Match
Best Local Similarity 80.0
Matches 100; Conservative
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S31586
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S31512
Gybeavy chain - human
Gybeavy chain - hyps #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
Gybeavy chain - hyps #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
Gybeavy chain control con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: 50970
R; Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
B; Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
B; Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
B; Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
B; Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
B; Reference number: 509710
A; Reference number: 509710
A; Accession: 509710
A; Residues: preliminary
A; Molecule type: mRNA
A; Residues: 1-146 < HUG>
A; Residues: Inmunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 34-118/Domain: immunoglobulin homology < IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGDG-------FDYWGQG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 YNPSLKSRVIISVDTLKNNFSLKLSSVTAADTAVYYCTRPGYGDTSVRKRVMNMDLWGQG 139
                                                                                                                                                                                                                                                                                                                                                        1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY 60
                                                                                                                                                                                                                                                                                                                                                                                                  33 QVQLQESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYTGSAT 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) heavy chain V region - human
Species: Homo sapiens (man)
Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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                                                                                                                                                                                                                                                                                    10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Gaps
A;Readues: 1-155 «CHA»
A;Cross-references: BMBL:X69866; NID:933094; PIDN:CAA49500.1; PID:933095
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;47-129/Domain: immunoglobulin homology <IPMN>
                                                                                                                                                                                                                    Length 155;
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                                                                                                                                                                                                                    Score 509; DB 2; L
Pred. No. 2.7e-38;
5; Mismatches 9;
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                                                                                                                                                                                                             Query Match
Best Local Similarity 80.8%;
Matches 101; Conservative
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Cyaccosion: 831586
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
Bubmitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: 831585
A;Recession: 831586
A;Accession: S11586
A;Accession: Preliminary
A;Molecule type: mRNA
A;Residues: 1-139 <CUI>
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R;Sahota, S.; Hamblin, T.; Oscier, D.G.; Stevenson, F.K.
Leukemia 8, 1285-1289, 1994
A;Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of mult: A;Reference number: S69909; MUID:94335315; PMID:8057663
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                                                                                                                                                                                                                                                                                                                                                                                                                                         61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGD-----GFDYWGQGTL 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 YNPSLKSRVTISVDTSKNQPSLKLSSVTAADTAVYYCAREGDG-----PDYWGQGTLVTV 115
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                                                                                                                                                                                                                                                                                                                                              33 QVQLQESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYTGSAT 90
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C;Species: Homo sapiens (man)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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A;Cross-references: EMBL:X69860; NID:g33082; PIDN:CAA49494.1; PID:g33083 (S.Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin P;47-129/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:Z14196; NID:g30978; PIDN:CAA78565.1; PID:g30979 (S.Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;34-116/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                        Length 155;
                                                                                                                                                                                                                                           9; Indels
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84.4%; Pred. No. 4.1e-38;
iive 4; Mismatches 8;
                                                                                                                                                                     Score 507; DB 2;
Pred. No. 4.1e-38;
                                                                                                                                                                                                                                        6, Mismatches
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A;Cross-references: EMBL:Z33398; NID:g871347; PIDN:CAA83849.1; PID:g887460 A.Note: Lhe sequence of residues 108-122 and the corresponding nucleic acid sequence are C;Superfamily: immunoglobulin V region; immunoglobulin homology Fi15-99/Domain: immunoglobulin homology < IMM:
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C; Species: Homo sapiens (man)
C; Date: 13-3an-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C; Accession: 326803
R; Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Eur. J. Immunol. 22, 1075-1082, 1992
A; Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A; Reference number: S26803
A; Status: prellminary
A; Rocession: 326803
A; Status: prellminary
A; Molecule type: DNA
A; Residues: 1-99 «WENA
A; Residues: 1-99 «WENA
C; Superferences: EMBLE: Z14238; NID: 937710; PIDN: CAA78607.1; PID: 91335374
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 15-99/Domain: immunoglobulin homology <INM>
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                                                                                                                                                                                                                                                                                1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGPIYYSGSTY 60
                                                                                                                                                                                                                                                                                                                 1 RVQLQESGPGLVKPSQTLSLTCSVSGGSISSDGHFWNWIRQHPGKGLEWIGNIYFSGSSY 60
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                                                                                                                                                                                                                            5; Gaps
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                                                                                                                                                   Query Match 80.7%; Score 503.5; DB 2; Length 122; Best Local Similarity 79.5%; Pred. No. 6.5e-38; Matches 97; Conservative 11; Mismatches 9; Indels 5
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Best Local Similarity 96.04
Matches 95; Conservative
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Search completed: November 9, 2005, 13:08:02 Job time : 12.609 secs

1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGDYYWSWIRQPPGKGLEWIGYIYYSGSTY 60

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THE BOOK BINNK (NESTO)

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SEQUENCE FROM N.A.
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NCBI_TaxID=9606;
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Copyright (c) 1993 - 2005 Compugen Ltd.
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HV46 MOUSE
Q6LBQ5
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Q65ZI1
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HV47 MOUSE
Q6MZX7
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Q6GMX6
Q9UL73
Q95973
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Q6GMX7
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Q6P4I8
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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Perfect score:
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TISSUE-PILIMARY B-Cells;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=2838257; PubMed=12500 full-length human parageness of the pubmed=124779;

MEDLINE=2838257; PubMed=12477932;

MEDLINE=2838257; PubMed=125000 full-length human parageness of the pubmed=124779;

MEDLINE=2838257; PubMed=12477932;

MEDLINE=2838257; PubMed=125000 full-length human parageness of the pubmed=124779;

MEDLINE=2838257; PubMed=12477932;

MEDLINE=2838257; PubMed=125000 full-length human parageness of the pubmed=124779;

MEDLINE=2838257; PubMed=125000 full-length human parageness of the pubmed=124779;

MEDLINE=2838257; PubMed=12477932;

MEDLINE=2838257; PubMed=124793257;

MEDLINE=2838257; PubMed=124793257;

MEDLINE=2838257; PubMed=124793257;

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                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (UTN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073766; AAH73766.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.
InterPro; IPR003506; Ig.
InterPro; IPR003506; Ig.
InterPro; IPR003596; Ig.
InterPro; IPR003596; Ig.
Pfam; PF07654; C1-set; J.
Pfam; PF00047; ig. 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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Best Local Similarity 87.33
Matches 103; Conservative
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SMART; SM00407; IGC1; 3.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.
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465 AA; 5
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                                 (Human)
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                                                                                                      NCBI_TaxID=9606;
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SEQUENCE 46
                                 Homo sapiens
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                                                                                                                                                                      1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Human rectum tumor;
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX518066; CAD97996.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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80.0%; Pred. No. 2.2e-44;
live 14; Mismatches 7; Indels 3.
                                                                            Length 476;
                                                                                                                        4; Indels
Hypothetical protein.
SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp686K04218 (Fragment).
Name=DKFZp686K04218;
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Last annotation update)
                                                                       88.5%; Score 552; DB 2;
82.7%; Pred. No. 8.3e-48;
ive 8; Mismatches 4
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PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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Interpro; IPR003597; Ig_cl.
Interpro; IPR003065; Ig_MHC.
Interpro; IPR0035965; Ig_V.
Pfam; PF007654; Cl-set; Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 27, C
(TrEMBLrel. 27, I
(TrEMBLrel. 27, I
                                                                                            Best Local Similarity 82.7
Matches 105, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                       TLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                        TMVTVSS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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05-JUL-2004
05-JUL-2004
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                                                                          Query Match
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Q72379;
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MEDILINE-228825; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDILINE-228825; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Riausher R.D., Collins F.S., Wagner L., Shanman C.M., Schuler G.D., Altschul S.F., Zeeberg B. Buetcw K.H., Schaefer C.F., Bhat N.K., Diatchanko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Diatchanko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Saress M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKerran K.J., Malek J.A., Gunaratne P.H., Narlahon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A., Rhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., Markeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriquez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Kzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schner Ch.M., Schein J.E., Schner 
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                                                                          1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 QLQLQESGPGLVKSSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIANTYYSGITY 79
                                                                                                                                                                                                              61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGDG-FDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                     80 YNPSLKSRVTISVDTSKNQFSLRSSVTAADTAVYYCARLGMGAFDFWGHGTWVIVSS 137
                                                                                                                     20 QLQLQESGPGLVKPSETLSLSCTVSGGSISSTNYYWGWIRQPPEKGLEWIGSLHNSGSDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY
              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2004 (TrEMBLrel. 26, Last annotation update)
MGC27A65 protein
MGC27A67 MGC37A67 MGC3
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Pred. No. 2e-42;
4; Mismatches 15; Indels 7
              11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO16369; AAH16369.1; -.
HSSP; P01876; 10W0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00406; IGv; 1.
PROSITE; PSS0835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sci. U.S.A. 99:16899-16903(2002)
              8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_C1.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PP07654; C1-8et; Z
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Best Local Similarity 79.0%;
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences."
              98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Q96KX8;
              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 YTPSLKSRVIISVDRSKOOPSLKIISLTAADIAVYPCARLSNWGPYYPDYWGOGTLVTVS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCAREGDG----FDYWGQGTLVTVS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQESGPGLVKPSETLSLTCTVSGGSICS--YYWSWIRQPPGKGLEWIGYIYYSGSTN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY
Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                          "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 9
                                                                                                                                   SEQUENCE FROM N.A. MEDINE-9814; DOI=10.1006/clin.1998.4531; MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Wub X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potential.
VH4 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sub C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AP103795, ARC79084.1; -.
PIR; S31673, S31673.
PIR; S78056; S78056.
HSSP, P01820; 1G7J.
InterPro; IPR001710; 1g-like.
InterPro; IPR001596; 1g-v.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16315 MW; 85664E04938AA7C9 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
VH4 heavy chain variable region precursor (Fragment)
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Pred. No. 2.1e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 506; DB 2; L
Pred. No. 9.1e-44;
7; Mismatches 8;
                                                                                                                                                                                                                                                                                               fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035041; AAD56277.1; ...
PIR; PH0876; PH0876.
HSSP; PO1820; 1677.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
RSMART; SW00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 82.6
Matches 100; Conservative
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>150
   Eukaryota; Metazoa;
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                                                                   NCBI_TaxID=9606;
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78 YNPSLKSRVTLSLDTSKNOFSLRLNSVTAADTAVYYCAHGSSWDFAFDYWGQGTLVTVSS 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85 YNPSLKSRVTMSVDTSKNQPSLKLSSVTAADTAVYYCASQPWELPTVGLFYWGQGTLVTV 144
    61 YNPSLKSRVTISVDISKNQFSLKLSSVTAADIAVYYCAREGD---GFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 QVQLQESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPAGKGLEWIGRIYTSGSTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY
                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 492.5; DB 2; Length 620;
Pred. No. 1.3e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Erdmi, Frovest, ...
SMART; SM00409; IG; 2.
SMART; SM00406; IGc1; 4.
SMART; SM00406; IGv; 1.
FROSITE; PS50835; IG LIKE; 5.
PROSITE; PS00290; IG_MHC; UNKNOWN 3.
                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                       620
                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.9%;
                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (JUL-2001) to the
EMBL; BC011857, AAH11857.2;
PIR; S15590, S15590.
HSSP, P01820; 1G7J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003597; Ig cl.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig v.
Pfam; PF07654; Cl-set; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 82.8
Matches 101; Conservative
                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Primary B-Cells;
                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                            GHM protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse
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                                                                         RESULT 8
Q96EY0
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WEDINE-21388257; PubMed=12477912; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.H., Rubin G.M., Hong L.,

A Diatchenko L., Warusina K., Parmer A.H., Rubin G.M., Hong L.,

A Diatchenko L., Warusina K., Parmer A.H., Rubin G.M., Hong L.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S.W. Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bourfard G.G.,

A Hakeeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

""Generation and initial analysis of more than 15,000 full-length human
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80 YNPSLKSRVIISVDTSKNQLSLKVRSVTAADTAVYFCARHGYSRSGRTGAIDYWGQGTLV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77
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                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Primary B-Cells;
Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51631 MW; 9FE59C09C50CFF85 CRC64;
                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.7%; Score 497.5; DB 2;
81.7%; Pred. No. 3e-42;
ive 8; Mismatches 9;
                                                                                                                                              477 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
                                                                                                                                                                            Created)
                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EWBL. BC073765, AAH73765.11.
InterPro; IRR003199; Ig.
InterPro; IRR003109; Ig. linterPro; IRR003109; Ig. linterPro; IRR003106; Ig_MHC.
InterPro; IRR003186; Ig_WHC.
Pfam; PF07664; C1-8et; Z.
Pfam; PF07664; Ig. 3.
SMART; SM00407; IG; 4.
SMART; SM00400; IG; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 81.7%;
Matches 98; Conservative
                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.
                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                 Hypothetical protein.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                           114 TVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                       TVSS 143
                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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                                                                                                                                              O6GMX7
                                                                                                                   RESULT 7
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9 84

Gaps

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146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 QLOLOGESGPGLVKPSETLSLTCTVSGGSVSNRNYYWGWIRQPPGKGLEWIGSIYYNENTY 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Human rectum tumor;
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
Bloo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX538077; CAD98001.1; -.
HSSP; P01820; 1G7J.
                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.
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TISSUE=Primary B-Cells;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 78.8%; Score 492; DB 2; Length 492; Best Local Similarity 77.7%; Pred. No. 1.1e-41; Matches 94; Conservative 11; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;
                                                                                                                                                                                                      01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp686C02218 (Fragment).
Name=DKFZp686C02218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL_2004 (TrEMBLrel. 27, Created)
05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                  492 AA.
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PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypothetical protein.
1 1
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InterPro; IPR003597; Ig_c1.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PP07654; C1-set; Z
                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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               SS 117
                                                       145 SS 146
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                 116
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                                                                                                                                                              Q72374
Q72374;
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Q6P4I8;
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                                                                                                                      RESULT 9
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1D 06 P0 1D 06 06 DT 05 DDT 05 DDT 05 DDT 05 DD 10 
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61 YNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCAREGD----GFDYWGQGTLVTVS 116
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
10-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Anti-thyroglobulin heavy chain variable region (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 488.5; DB 2; Length Pred. No. 3.1e-41; Aismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Primary B-Cells,
Strausberg R.;
Submitted (DEC-2013) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO631984; AAH63184.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DWN 2.
FBB97C949D720F1E CRC64;
                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN
SEQUENCE 576 AA; 63363 MW; FBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jang Y.-J., Chung J., Park J.-Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF07654; Cl.set; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 81.00,
                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam, PF07654; C1-set;
Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00409; IG; 1.
SMART; SM00407; IGc1; 3
SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
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NCBI_TaxID=9606
                                                     HV2F HUMAN
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SEQUENCE
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                                                        셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SGSPYYAPSLRSRVIISVDTSKNQLSLRLSSVTAADTAVYYCASPTHCSGGGCYAFFOHW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 ----YYNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCAR----EGDG----FDYW 107
                                                                                                                                                                                                                                                                                                                                                             29
                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLQQSGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQSPGKGLEWIGSLYYSGSTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGST-
                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
11-Ength CDNA clone CSODL004XM19 of B cells (Ramos cell line) of Homo sapiens (Human) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                               13;
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2
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89.5%; Pred. No. 1.8e-40;
iive 4; Mismatches 2; Indels 5.
                                                                                                                                                                                                                                                                   Length 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARE---GD 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY14445; AAN64329.1; -.
HSSP; PO1820; 1G7J.
InterPro; IPR007110; 1g-like.
InterPro; IRR003596; 1g_v.
SMART; SM00406; 1Gv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUBE cells;
Li W.B., Gruber C., Jessee J., Polayes D.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genoscope;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX248300; CAD62627.1; --
HSSP; P01820; 1G7J.
                                                                                                                                                                                                               130 AA; 13901 MW; 036131FC6EC1551E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;
                                                                                                                                                                                                                                                              Query Match 77.2%; Score 481.5; DB 2; Best Local Similarity 75.4%; Pred. No. 3.2e-41; Matches 98; Conservative 6; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00406; IGv; 1.—
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 89.5.
Best Local Similarity 89.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 GOGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ĠĠĠFĽVŤVŠŠ 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. TISSUE=B cells;
                                                                                                                                                                 NON TER
NON TER
SEQUENCE
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Q86SX2
    STTRACKETES
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120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 YNPSLRGRVTISVDTSRNQFSLNLRSMSAADTAMYYCARGNPPPYYDIGTGSDDGIDVWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY
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TISSUB-BLOOG;
MEDLINB-22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;
StraubDerg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Butheria; Primates, Catarrhini, Hominidae, Homo.
NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                           Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.; "Complete amino acid sequence of the delta heavy chain of human immunoglobulin D."; D."; Sci. U.S.A. 79:2850-2854(1982).
-!- MISCELLANEOUS: This chain was isolated from an IgD myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.5%; Score 465; DB 1; Length 129; 69.0%; Pred. No. 1.5e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 AA; 14117 MW; D5D53D47ABE51319 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig; 1.
SNART; SN0606; IGv; 1.
SNSTE; PS5035; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin V region.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                            annotation update)
129 AA
                                                               Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A02099; DZHUWA.
HSSP; P01820; 1G7J.
GlycoSultebb; P01824; -.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007100; IG-like.
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                                                                                                                                                                                                                                                SEQUENCE.
MEDLINE=82222235; PubMed=6806818;
                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seque
05-JUL-2004 (Rel. 44, Last annot
IG heavy chain V-II region WAH.
Homo sapiens (Human).
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nes 89; Conservative
STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
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Search completed: November
Job time : 61.406 secs
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Ditchenko, L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Vilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
M. Halkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Andriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcerfield Y.S.,
Jones S.J., Marra M.A.,
Jones S.J., Marra M.J., M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 YNPSLESRVTMSVDTSKDQFSMKLTSVTAADTAIYYCARGYGGKSRYFDLMGRGVPVTVS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 QVDLQESGPGLVKPSETLSLTCSVSGDSIAS--YYWSWIRKSPQGGMEWIGYIFHSGTTL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.3%; Score 445; DB 2; Length 478; 71.1%; Pred. No. 7e-37; tive 17; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC066594; AAH66594.1; -.
HSSP; P01820; 1A7N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00230; IG_MHC; UNKNOWN_2.
WYDCHbetical protein.
SEQUENCE 478'AA; 51856 MW; 5F8B98F60F077256 CRC64;
                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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Interpro; IPR003106; 19-1ike.
Interpro; IPR003597; 19_C1.
Interpro; IPR003596; 19_V.
Pfam; PF07654; C1-set; 2.
SMART; SM00407; IG5; 4.
SMART; SM00407; IG6; 3.
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01-MAR-2002 (TrEMBLrel. 20, C.
01-MAR-2004 (TrEMBLrel. 26, L.
01-MAR-2004 (TrEMBLrel. 26, L.
Hypothetical protein.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003599; Ig.
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                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Blood
                                                                                                                                                                                                                                                                                                                                        and mouse
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9, 2005, 13:05:48

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Atlachur R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Raha S.S., Loquellano M.A., Peters G.J., Abramson R.D., Mullahy S.J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A., Raha J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Touchman J.W., Green E.D., Dickson M.C., Abalseley R.W., Touchman J.W., Green E.D., Dickson M.C., Abalseley R.W., Touchman J.W., Green E.D., Dickson M.C., Abalseley R.W., Salaka U., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., T., Goberzation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-----EGD-GFDYWGQG 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO19235; AAH19235.2; -.
PIR; G34964; G34964.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
SEQUENCE 595 AA; 65290 MW; 0D4B50776545714E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.2%; Score 444; DB 2; 73.2%; Pred. No. 1.1e-36; tive 6; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP, PO1861; 1ADQ.
Pfam; PF07654; C1-set; 4.
SMART; SM00409; IG; 2.
SMART; SM00406; IG21; 4.
SMART; SM00406; IG97; 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS00299; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.
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(CLED) 10 16 20 20 10 12

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein November 9, 2005, 11:43:32; Search time 74.6015 Seconds (without alignments) 627.306 Million cell updates/sec Run on:

US-10-660-357A-17

649 1 QVQLQESGPGLVKPSETLSL......WLLPDAFDIWGQGTMVTVSS 121 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2105692 seqs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*

geneseqp2003as:* geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

Description	1 1	-		Add05376 Anti-MUC1	Add05392 Anti-MUC1	Adf09814 Human ant	Adf09830 Human ant	Adc99780 Anti-huma	Add05384 Anti-MUC1	Adf09822 Human ant	Adc99808 Anti-huma	Add05412 Anti-MUC1	Adf09850 Human ant		Abg92884 Human imm	Abb07171 ebvHigM M		Adp03887 Murine-ex	Adp03884 Murine-ex	_		Aaw27554 Human Ab	Abj18676 Antibody	Adp22272 Human ant	Ada89258 Human ant	Adp03931 Murine-ex
ID		ADC33112	ADC99788	ADD05376	ADD05392	ADF09814	ADF09830	ADC99780	ADD05384	ADF09822	ADC99808	ADD05412	ADF09850	ADO58076	ABG92884	ABB07171	ADI26658	ADP03887	ADP03884	ADP03885	ADP03889	AAW27554	ABJ18676	ADP22272	ADA89258	ADP03931
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% Query Match		2	100.0	100.0	100.0	100.0	100.0	99.1	99.1	99.1	92.0	92.0	92.0	87.1	84.3	84.1	84.1	84.1			٠	•	æ.	83.1	83.1	83.0
Score	0.00		649	649	649	649	649	643	643	643	597	597	597	565.5	547	545.5	545.5	545.5		4.	544.5	540	540	539.5	539	538.5
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ADP03864 ADP03862	ADP03973	ADP03871 AAY15126	ADP03933	ABP43199	ADS19313	AAW90287	ABG92888	ADP03868	ADP03876	ABG97827	ABG35304	ABG97829	ABG35331	AAY06718	AD039737
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536.5	536	536 535.5	534.5	533.5	532.5	531.5	531.5	531	531	529.5	529.5	529.5	529.5	529.5	529.5
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ALIGNMENTS

anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast; Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 1. ADC99772 standard; protein; 121 AA. (first entry) lung cancer; human. 01-JAN-2004 ADC99772; RESULT 1 ADC99772

Homo sapiens

WO2003057838-A2

17-JUL-2003.

26-DEC-2002; 2002WO-US041581.

28-DEC-2001; 2001US-0346299P.

(ABGE-) ABGENIX INC

Gudas J;

WPI; 2003-587113/55. N-PSDB; ADC99774. New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.

Claim 1; SEQ ID NO 1; 78pp; English.

The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the pancreatic or colorectal tumours, specifically melanoma, oesophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung canneer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody

Length 121;

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Query Match 100.
Best Local Similarity 100.
Matches 121; Conservative
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                                                                                                                                        PSIKSRVIISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTWVTVS 120
                                                                                                                                                      anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g.
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                                                                                            1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
                                                                                                           QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                           Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 17
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0
                                                Length 121;
                                                                     Indels
                                                DB 7;
                                             100.0%; Score 649; DB 7;
100.0%; Pred. No. 6.4e-46;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumors, cancers, and other malignancies.
heavy chain protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 17; 78pp; English.
                                                                                                                                                                                                                                                                     ADC99788 standard; protein; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-DEC-2001; 2001US-0346299P
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                                                                      Conservative
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N-PSDB; ADC99790.
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                                                         Local Similarity
les 121; Conserv
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                       Sequence 121 AA;
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                                                                                                                                                                                                                                                                                                                           PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
                                                                                                                                                                                                                                                                                                                                                                61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQCQWLLPDAFDIWGQCTWVTVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
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                                                                                                                                                                                                                         QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
                                                                                                                                                                            1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
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                                                                                                         Gaps
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                              ; DB 7;
6.4e-46;
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N-PSDB; ADD05378.
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us-10-660-357a-17.rag

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a menoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds MUCI8, and contacting the tumour with the antibody resulting in thibited proliferation of the cells. The monoclonal antibody has cytostatic and can be used in the production of a vaccine. The monoclonal antibodies against the MUCI8 antigen are useful for diagnosing and antibodies against the MUCI8 antigen are useful for diagnosing and treating tumours, inhibiting cell invasion associated with melanoma, or tumour metastasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-MUCI8 antibody heavy chain, variable region,
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                                                                                                               PSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
                                                                                                PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
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                                                                                                                                                                                                                                                                                                                                                monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
                                                                                                                                                                                                                                                                                                                      Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 17.
                                                                        QVQLQESGPGLVKPSETLSLTCTVSGGS1SSYYWSW1ROPPGKGLEW1GY1YYTWTSNYN
                                                QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
                        Gaps
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                        Indels
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         Pred. No. 6.4e-46;
                      Mismatches
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100.08;
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                     Matches 121; Conservative
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          Best Local Similarity
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Length 121;

Score 649; DB 7; Pred. No. 6.4e-46;

100.0%; 100.0%;

Query Match Best Local Similarity

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                                                                                                                                                    61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
9
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                                      QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
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                                                                                                                       61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell proliferation inhibition; MUC18 tumour antigen; anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour; carcinoma; cancer; malignancy; heavy chain; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human anti-MUC18 monoclonal antibody heavy chain #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 1; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADF09814 standard; protein; 121 AA
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Best Local S
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anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g.
                                                                                                                                              Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumors, cancers, and other malignancies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 9; 78pp; English
                                                                  ADC99780 standard; protein; 121 AA.
                                                                                                                                                                                                                                                                                                                    26-DEC-2002; 2002WO-US041581
                                                                                                                                                                                                                                                                                                                                           28-DEC-2001; 2001US-0346299P.
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ilarity 98.3%;
Conservative
                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-587113/55.
                                                                                                                                                                                                                 lung cancer; human.
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  S 121
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Best Local Simi
Matches 119;
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                                                                                            ADC99780;
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                                                      ADC99780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid sequence represents a heavy chain from an MUC18 tumour antigen-specific
PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTWVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTWVTVS 120
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                                                                                                                                                                                                                                                  cell proliferation inhibition; MUC18 tumour antigen; anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour; carcinoma; cancer; malignancy; heavy chain; human.
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                                                                                                                                                                                                                         Human anti-MUC18 monoclonal antibody heavy chain #5.
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                                                                                                                                            ADF09830 standard; protein; 121 AA.
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MUC18 monoclonal antibody.
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Matches 121; Conservative
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N-PSDB; ADF09832.
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                                                                            S 121
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The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain variable domain where the antibody binds to MUCLB. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUCLB on the pancreatic or colorectal tumours, especially melanoma, oseophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intrappithalial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUCLB monoclonal antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS
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Pred. No. 2e-45;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                 current sequence is that of the anti-
heavy chain protein of the invention.
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ADF09822 standard; protein; 121
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                        ADF09822;
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                                                                                                                                                                                                                                                                                                                                                                                                                             tumour growth in an animal. The tumour inhibition process comprises belecting an animal in need of treatment for a tumour, providing a monimal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has cytostatic and can be used in the production of a vaccine. The monoclonal antibodies against the WUC18 antipogn are useful for diagnosing and treating tumours, inhibiting cumour growth (e.g. melanoma, lung tumour of tumour metastasis), inhibiting cell invasion associated with melanoma, or sequence represents an anti-WUC18 antibody heavy chain, variable region, protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN 60
                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel monoclonal antibody used for inhibiting
                                                                                                   monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
                                                                                                                                                                                                                                                                                                                                      Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 9.
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Pred. No. 2e-45;
2; Mismatches 0; Indels
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          ADD05384 standard; protein; 121 AA.
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                                                                                                                                                                                                        26-DEC-2002; 2002WO-US041582
                                                                                                                                                                                                                                28-DEC-2001; 2001US-0346460P
                                                       01-JAN-2004 (first entry)
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Matches 119; Conservative
                                                                                                                                                                                                                                                                                                    WPI; 2003-577496/54.
N-PSDB; ADD05386.
                                                                                                                                                                                                                                                       (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                              Bar-Eli M;
                                                                                                                                                                                                                                                                                                                                                                         metastatic tumor.
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                                                                                                                                                           WO2003057006-A2.
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                                                                                                                                      Homo sapiens
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                                ADD05384;
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ADD05384
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The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid sequence represents a heavy chain from an MUC18 tumour antigen-specific
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYMSWIRQPPGKGLEWIGYIYYTWTSNYN
                                                                                                                                                                                                                             cell proliferation inhibition; MUC18 tumour antigen;
anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
carcinoma; cancer; malignancy; heavy chain; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                         Human anti-MUC18 monoclonal antibody heavy chain #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 643; DB 7;
Pred. No. 2e-45;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 9; 83pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-DEC-2002; 2002WO-US041580.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-DEC-2001; 2001US-0346414P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUC18 monoclonal antibody.
                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 98.3
nes 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-598367/56.
N-PSDB; ADF09824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                             WO2003057837-A2
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                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-2004
                                                                                                              12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JUL-2003.
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RESULT 9 ADF09822

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Homo sapiens.
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                                                                                     17-JUL-2003
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                                                                                                                                                                                                                             Gudas J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADF09850;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the pancreatic or colorectal tumours, specifically melanoma, oesophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                              New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.
                                anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PSLKSRVTVSVDTSKNQFSLKLNSVTAADTAVYYCARDFGGWLVPDAFDIWGQGTWVSVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVQLQESGPGLVKPSETLSLTCTVSGGSISTYYWSWIRQPPGKGLEWIGYIYYTGNTYYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSIKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-MUC18 antibody heavy chain variable region protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 597; DB 7;
Pred. No. 1.2e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            heavy chain protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 37; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADD05412 standard; protein; 121 AA.
                                                                                                                                                                                                                          26-DEC-2002; 2002WO-US041581.
                                                                                                                                                                                                                                                            28-DEC-2001; 2001US-0346299P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.0%;
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                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-587113/55.
                                                                                                                                                                                                                                                                                            (ABGE-) ABGENIX INC
                                                                                     lung cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 110; Conserv
                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ADC99810.
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                                                                                                                                                        WO2003057838-A2
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                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADD05412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                              Gudas J;
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tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds WUCIS, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has cytostatic and can be used in the production of a vaccine. The monoclonal antibodies against the WUCIS antigen are useful for diagnosing and treating tumours, inhibiting cumour growth (e.g. melanoma, lung tumour or tumour metastasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-MUCIS antibody heavy chain, variable region, protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PSLKSRVTVSVDTSKNQFSLKLNSVTAADTAVYYCARDPGQMLVPDAFDIWGQGTMVSVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel monoclonal antibody used for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIXYTWTSNYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQESGPGLVKPSETLSLTCTVSGGSISTYYWSWIRQPPGKGLEWIGYIYYTGNTYYN
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anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
carcinoma; cancer; malignancy; heavy chain; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 1.2e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human anti-MUC18 monoclonal antibody heavy chain #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.26
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 37; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADF09850 standard; protein; 121 AA.
                                                                                                                                                             26-DEC-2002; 2002WO-US041582
                                                                                                                                                                                                                                             28-DEC-2001; 2001US-0346460P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.0%;
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Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               Bar-Eli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-577496/54.
                                                                                                                                                                                                                                                                                                                              (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ADD05414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             metastatic tumor.
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WO2003057006-A2.
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Kischel R;

Weinberger S,

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Identifying a B cell carrying a surface immunoglobulin molecule having binding site for an antigen of interest, useful for constructing therapeutic antibodies, comprises contacting a sample with the antigen
                        12-NOV-2003; 2003WO-EP012664.
                                                2002EP-00025335
                                                                                              Baeuerle P, Hoffmann P,
                                                                                                                    2004-449579/42.
                                                                      (MICR-) MICROMET AG
                                                                                                                                N-PSDB; ADO58077
                                                                                                                                                                                          and a receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         $ 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S 121
                                               13-NOV-2002;
  27-MAY-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG92884;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                               The invention comprises a method for inhibiting cell proliferation associated with expression of MUCIB tumour antigen. The method involves administering anti-MUCIB monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUCIB tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting ocal proliferation in patients with tumours, cancer and other malignancies. The present amino acid sequence represents a heavy chain from an MUCIB tumour antigen-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PSLKSRVTVSVDTSKNQFSLKLNSVTAADTAVYYCARDPGQMLVPDAFDIWGQGTMVSVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTWVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQESGPGLVKPSETLSLTCTVSGGSISTYYWSWIRQPPGKGLEWIGYIYYTGNTYYN 60
                                                                                                                                                                                                            Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B cell; surface immunoglobulin; Ig; binding site; antigen; human CD28; closed system; detection laser-beam; catcher tube; electrochemical device; fluorescence activated cell sorter; FACS; antibody variable region; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGY1YYTWTSNYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 597; DB 7; Length 121; Pred. No. 1.2e-41; 7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S9 cell derived human scFvVL-VH protein.
                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 37; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADO58076 standard; protein; 243 AA.
                                                                                                     28-DEC-2001; 2001US-0346414P.
                                                                                                                                                                                                                                                                                                                                                                                                                                         92.0%;
90.9%;
                                                                               26-DEC-2002; 2002WO-US041580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                            WPI; 2003-598367/56.
                                                                                                                              (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                             monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                       N-PSDB; ADF09852
                                 WO2003057837-A2
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 121 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 $ 121
            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                        17-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Sime
Matches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADO58076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                    Gudas J;
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The invention relates to a novel method for identifying a B cell carrying a surface immunoglobulin (Ig) molecule having a binding site for an antigen of interest. The method comprises contacting a sample putatively containing the B cell with the antigen of interest and with a receptor specifically binding to the Ig molecule, and assessing the presence of the detectable signal. The invention further comprises: an antibody generated by the method above which is specific for human CD28 or comprising an amino acid(8) sequence(8) also given in the specification, and advice for assessing the presence of a detectable signal defined above, where the device comprises a closed system for the detection laser-beam and a catcher tube, and where the B cell of interest can be collected as a single cell by means of an electrochemical device, which is triggered by an electric signal generated by the fluorescence activated cell sorter (FACS) device, where the electrochemical device contains the nozzle of the steady catcher tube liquid stream for a programmed time over a collecting tube, microtiter plate or other contains a surface Ig molecule having a binding site for an programmed time over a collecting tube, microtiter plate or other contains a fere a B cell is sorted. The method is useful for identifying a B cell carrying a surface Ig molecule having a binding site for an employed in the construction of proteins such as antibodies or its fragments or derivatives useful in therapeutic approaches. The method is also useful as an altérnative to phage display for the gain of antibodies or its fragments. This sequence represents an S2 cell derived human contains the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 8; Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 565.5; DB 8; Length Pred. No. 9.5e-39; Mismatches 5; Indels
Claim 22; SEQ ID NO 76; 156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG92884 standard; protein; 121 AA.
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90.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 243 AA;
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syndromes such as blood protein disorders and ataxia telangiectasia, inflammation associated disorders such as endotoxin lethality, nephritis and inflammation bowled disease, conditions associated with an increase in certain haematopoietic cells such as hisriocycosis, defective or aberrant chemotaxis of immune cells or T-cell antigen presenting cell interaction an infectious disease, an autoimmune disease such as Addison's disease, dermetitis and rheumatoid arthritis, allergies, a neurodegenerative disorder, a viral infection arthritis, allergies, a neurodegenerative poxvirus infection, a Pneumocystis carnii infection, Kaposi's sarcoma, cardiovascular disorder such as atherosclerosis, Iymphocytopenias, or a disease or disorder associated with aberrant expression of novel human Gprotein chemokine receptor (CRS) HDGNRIO. This is the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes an isolated polynucleotide encoding a first antibody at least 95-100% identical to a second antibody consisting of an amino acid sequence comprising at least one, two or three CDR regions of a variable heavy (VH) or variable light (VL) domain of the antibody expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8, XF3.6A2, XF3.1088, XF22.3C9.6, XF27.28.3F1, XF27/28.3F31, XF27/28.3F31,
                                                                                                                                                                                                                      histiocytosis, chemotaxis, infectious disease, autoimmune disease, Addison's disease; dermatitis; rheumatoid arthritis, allergy, neurodegenerative disorder; viral infection; poxvitus infection, HIV, human immunodeficiency virus, cytomegalovirus; Kaposi's sarcoma; Pneumocystis carnii infection; cardiovascular disorder; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence of human immunoglobulin sequence associated with the antibodies
                                                                                      Immunoglobulin, variable heavy chain, variable light chain, human, G-protein chemokine receptor, CCR5, HDGNR10; cancer, inflammation, immunologic deficiency syndrome; blood protein disorder, nephritis; ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treating, preventing, ameliorating or monitoring diseases or disorders associated with aberrant expression of HDGNR10 e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human G-protein Chemokine Receptor gene (HDGNR10) useful
                               Human immunoglobulin variable light domain #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 55; Fig 4; 562pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; 2001WO-US004153.
; 2001US-0297257P.
; 2001US-0310458P.
; 2001US-0328447P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001US-0341725P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-FEB-2002; 2002WO-US003634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-643455/69.
N-PSDB; ABS68607.
                                                                                                                                                                                                                                                                                                                                                                                                   lymphocytopenia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-AUG-2001;
12-OCT-2001;
21-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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The invention provides a neuromodulatory agent (1) capable of promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system (CNS) (I) is capable of inducing remyelination, promoting cellular proliferation of glial cells, and promoting Ca2+ signaling with oligodendrocytes. An humanised antibody to (1) can be selected from antibody sHIGAZ (LYM 22), ebvHigM MSI19D10, ebv HIGM CB2G8, AXM74, CB2IB12, CB2IB2 (LYM 22), ebvHigM MSI19D10, ebv HIGM CB2G8, AXM74, CB2IB12, CB2IB2 (LYM 22), ebvHigM MSI19D10, ebv HIGM CB2G8, AXM74, CB2IB12, CB2IB2 (LYM 22), ebvHigM MSI19D10, ebv HIGM CB2G8, AXM74, CB2IB12, CB2IB2 (LYM 22), ebvHigM MSI19D10, ebv HIGM CB2G8, AXM74, CB2IB12, CB2IB2 of CMSI19ES (I) is capable of binding to structures and cells in consume in fected with Strain DA of Theiler's murine encephalomyelitis of a mouse infected with Strain DA of Theiler's murine encephalomyelitis (TMWY) or for treating a human being having multiple sclerosis, or a human or domestic animal with a viral demyelinating disease, or a post-charmal disease of CNS. (I) is also useful for an in vitro method of standaring the proliferation of glial cells from mixed cell culture. (I) is also useful for preventing infection by a bacterium, virus or like care useful for preventing infection by a bacterium, virus or like pathogen that causes demyelination or other neurodegenerative condition in a subject. Methods where (I) is administered to a patient are useful for tracting multiple sclerosis, Parkinson's disease, Alzheimer's clease, amyotrophic lateral sclerosis, Parkinson's disease, Alzheimer's clease, amyotrophic lateral sclerosis (ALS), a viral demyelinating conditions in the CNS where nerves are
                                                                                          61 PSLKSRVTMSVDTSKNRFSLKLSSVTAADTAVYYCARDRGSSWYPDAFDIWGOGTWVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system, useful to treat post-infectious encephalomyelitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neuromodulatory; central nervous system; CNS; sHIgM22; LYM 22; AKJR4; ebvHigM MsI19D10; ebv HIgM CB2bGB; CB2iE12; CB2iE7; MSI19E5; virucide; antiparkinsonian; neuroprotective; nootropic; vulnerary.
PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTWVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ebvHigM MSI19D10 heavy chain variable region sequence.
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                                                                                                                                                                                                                                                                                                                       ABB07171 standard; protein; 121 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000; 2000WO-US014902.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAY-2000; 2000US-00568351
                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Miller DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002-066596/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABA94218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200185797-A1.
                                                                                                                                                            121 S 121
                                                                                                                                                                                                       $ 121
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                                                                                                                                                                                                                                                                                                                                                                                                               13-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rodriguez M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                    ABB07171;
                                                                    61
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Query Match

84.3%; Score 547; DB 5;
Best Local Similarity 86.0%; Pred. No. 1.6e-37;
Matches 104; Conservative 8; Mismatches 9;

Length 121; Indels

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CC damaged as by trauma. The present sequence represents the ebvHigM CC MSI19D10 heavy chain variable region amino acid sequence XX XX SQ Sequence 121 AA;

Query Match 84.1%; Score 545.5; DB 5; Length 121;

Best Local Similarity 87.6%; Pred. No. 2.1e-37;

Matches 106; Conservative 6; Mismatches 8; Indels 1; Gaps 1;
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	1;	09	60	120	119		
	1; Gaps	WYNSTW	GSTNYN	TMVTVS	TLVTVS		
121;	1,	GYIYYT	GYIYYS	DIWGOG	DYWGOG		
rengrn	Indels	PGKGLEWI	PGKGLEWI	QWLLPDAF	OOLV-YYF		
DB 5;	8	WSWIROP		CARDOG	CARSAQ		
84.1%; SCOIE 545.5; DB 5; Length 121; 87.6%; Pred. No. 2.1e~37;	smatches	1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN 60	1 QVQLQESGPGLVKPSETLSLTCTVSGGSIS8YYWSWIRQPPGKGLEWIGYIYYSGSTNYN 60	TAADTAVY	61 PSLKSRVIISVDISKNQFSLKLSSVTAADTAVYYCARSAQQQLV-YYFDYWGQGTLVTVS 119		
; score	6; Mi	LSLTCTVS	LSLTCTVS	FSLRLSSV	FSLKLSSV		
87.68	ative	SLVKPSET	SLVKPSET	VDTSKNO	VDTSKNO		
nilarity	Conser	OLOESGPO	/OLOESGPC	LKSRVTI	LKSRVTIS	121	120
al Sin	106;	10-	-6	61 PS	61 PS	121 \$ 121	120 S 120
Query Maccii Best Local Similarity 87.6%; Pred. No. 2.1e-37:	Matches 106; Conservative 6; Mismatches 8; Indels						
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Search completed: November 9, 2005, 12:55:26 Job time: 75.6015 secs

CLES MANTE BANK (SELO)

142, App 8, Appli 2, Appli

Sequence Sequence Sequence Sequence

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Scoring table:

Searched:

Database

Perfect score:

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Run on:

Sequence Sequence

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Sequence

Sequence 5 Sequence 5 Sequence 5 Sequence 1 Sequence 7

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83.2%; Score 540; DB 3; Length 119;
86.8%; Pred. No. 7.3e-45;
ive 5; Mismatches 9; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30 (EPO)
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY-AGENT INFORMATION:
NAME: James F. Haley, Jr., E8q.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 39, Application US/09025769B

Patent No. 6300064

GENERAL INFORMATION:
APPLICANT: Rangpik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
US-08-360-125-5
US-09-1017-628-5
US-09-011-628-5
US-09-014-880-5
US-09-467-903-5
US-09-467-903-5
US-09-472-081-7
US-09-472-081-7
US-09-472-081-8
US-08-545-809A-142
US-08-545-809A-142
US-09-203-768A-2
US-09-203-768A-2
US-09-203-768A-2
US-09-203-768A-2
US-09-203-768A-2
US-09-203-768A-2
US-09-333-598-6
US-08-335-955-6
US-08-335-955-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212)596-9000
TELEPAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 amino acids
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Best Local Similarity 86.8
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein US-09-025-7698-39
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      STRANDEDNESS
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476
472.5
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470.5
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   2005, 11:29:55 ; Search time 18.802 Seconds (without alignments) 480.403 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 39, Sequence 65, Sequence 65, Sequence 39, Sequence 39, Sequence 25, Sequence 25, Sequence 25, Sequence 25, Sequence 27, Sequence 41, Assequence 41
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Sequence 1
Sequence 1
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-025-769B-65

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US-09-490-153-65

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US-09-490-153-65

US-09-490-1324-39

US-09-490-1324-65

US-09-490-153-25

US-09-1018-148-79

US-09-1018-148-79

US-09-1018-148-11

US-09-111-116-110

US-09-111-116-111

US-09-111-116-111

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US-09-111-111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                      - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                          US-10-660-357A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length
                                                                                                                                                                                                                 November 9,
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540 540 540 540 540 540 541 541 531.5 531.

Result

2. 8999. 2. 8998. 2. 8998. 3. 8998. 3. 8998. 4. 8998. 4. 8988. 5. 8988. 6. 9988. 6. 998

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Gaps

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RESULT 4
US-09-490-070A-65
; Sequence 65, Application US/09490070A
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20006
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                    STATE: D.C.
COUNTRY: USA
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S 119
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                                                                 RESULT 3
US-09-490-070A-39
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                                                                             61 PSLKSRVTISVDTSKRQFSLKLSSVTAADTAVYYCARWGGGGFY--AMDYWGQGTLVTVS 118
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                                1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYN 60
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Pred. No. 7.3e-45;
5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   c/o Fish & Neave
                                                                                                                                                                                                                                                                                                                             APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
ARPLICANT: 11ag, Vic
APPLICANT: Ge, Liming
APPLICANT: Pluckthun, Andreas
APPLICANT: Pluckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: James F. Haley, Jr., Esq. STREET: 1251 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                  ; Sequence 65, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212)>>9->0.
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
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Best Local Similarity 86.8
Matches 105; Conservative
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US-09-025-769B-65
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61 PSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCARWGGDGFY--AMDYWGGGTLVTVS 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
                                                                                                                                                                                                             Moroney, Šimon
Plueckthun, Andreas
Flueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 83.2%; Score 540; DB 4; Length 119; Best Local Similarity 86.8%; Pred. No. 7.3e-45; Matches 105; Conservative 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-070A-39
Sequence 39, Application US/09490070A
Patent No. 656248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
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61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTWVTVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYN 60
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Squence 65, Application US/09490153
Fatent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Flueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)Peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE. 373
CORRESPONDENCE ADDRESSE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
                                                                                                                          CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
PRIDATION DATA: APPLICATION DATA:
APPLICATION DATA: APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION: TOTAL
                                                                                      c/o Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
83.2%; Score 540; DB 4; Length 11
Best Local Similarity 86.8%; Pred. No. 7.3e-45;
Matches 105; Conservative 5; Mismatches 9; Indels
               IITLE OF INVENTION: Protein/(Poly)peptide libraries
                                                                                    Haley, Jr., Esq. of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/STELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212)596-9090
                                 NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F.
                                                                                                           STREET: 1251 Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                         ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Indels
                                                                                                                          Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83.2%; Score 540; DB 4;
86.8%; Pred. No. 7.3e-45;
tive 5; Mismatches 9
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FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ge, Liming
Moroney, Simon
Plueckthun, Andreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 39, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
No. 6696240
SRAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 65
                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20006
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                        CITY: Washington
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Best Local Similarity 86.8
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                          STATE: D.C.
COUNTRY: USA
          Patent No. 6696248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 S 121
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61 PSLKSRVTISVDISKNOFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARWGGDGFY--AMDYWGQGTLVTVS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYN
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US-09-490-124-65
US-09-490-124-65

Sequence 65, Application US/09490324

Patent No. 6828422

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Pack, Peter

Ilag, Vic

Ge, Liming

Moroney, Simon

Pluckchun, Andreas

ITILE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

CITY: New York

CITY: New York

CORRESPONDENCE ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

CORRESPONDENCE ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 119;
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           CURRENT APPLICATION DATA:

APPLICATION DATA:
PLING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-198
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1955
ATTORNEY/AGENT INFORMATION:
NAME: Janaee F Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFRAX: (212)596-9000
TELEFRAX: (212)596-9000
TELEFRAX: (212)596-9000
TELEFRAX: (212)596-9000
TELEFRAX: (212)596-9000
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Pred. No. 7.3e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
83.2%; Score 540; DB
Best Local Similarity 86.8%; Pred. No. 7.3e
Matches 105; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: procein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-324-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10021
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 S 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSLKSRVTISVDŢSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTWVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORENTG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-REB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
US-09-0324-39
US-09-490-324-39
Sequence 39, Application US/09490324
Sequence 39, Application US/09490324
Settle No. 682842
Backer INFORMATION:
Hand, Vic Geber Ilag, Vic Geber Invention Norteney, Simon Plueckthun, Andreas
HITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
Halev. Jr., Esq. c/o Fish & Ne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 83.2%; Score 540; DB 4; Length 119; Best Local Similarity 86.8%; Pred. No. 7.3e-45; Matches 105; Conservative 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27, 794
REFERENCE DOCKET NUMBER: MORPHO/S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9000
SORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 65: US-09-490-153-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 119 amino acids
TYPE: amino acid
                                            ZIP: 10021
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10021
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Gaps

Indels

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61 PSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
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                                                                                                                                                                                                                                                                                                                                                     1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGEIYHSGSTNYN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 25, Application US/09490070A

Sequence 25, Application US/09490070A

Batent No. 6696248

GENERAL INFORMATION:
Raappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Pluckthun, Andreas

TITLE OF INVENTION: Procein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:
HAILE & MCAULIÉFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IRP FO Compatible
COBERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATORIT Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-ANG-1995
ATTORNEY AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTATION NUMBER: 31,298
REGISTATION NUMBER: 31,298
TELECOMMUTATION INFORMATION:
TELECOMMUTATION INFORMATION:
TELECOMMUTATION INFORMATION:
TELECOMMUTATION INFORMATION:
                                                                                                                                                                                                                                81.9%; Score 531.5; DB 3;
85.1%; Pred. No. 4.8e-44;
iive 7; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (202) 912-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                    LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                Query Match
Best Local Similarity 85.13
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington
                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                           MOLECULE TYPE: protein US-09-025-769B-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: D.C.
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTWVTVS 120
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Pred. No. 7.3e-45;
5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York COUNTRY: NSA YORK COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Knappik, Achim
APPLICANT: Fack, Peter
APPLICANT: 11ag, Vic
APPLICANT: G. Lining
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
CORRESPONDENCE ADDRESS:
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
                                                             ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/S
TELECOWNUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18 -AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REPERENCE/DOCKET NUMBER: MORPHO/5
TELECOMOUNICATION INFORMATION:
TELECHONE: (212) 596-9000
                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 25, Application US/09025769B Patent No. 6300064
GENERAL INFORMATION:
                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acidd
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                   83.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 86.8°
Matches 105; Conservative
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61 PSLKSRVTISVDTSKNOPSLKLSSVTAADTAVYYCARGRGG---GGVFDYWGQGTLVTVS 117
                                                                                                                PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
                                                      1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGEIYHSGSTNYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGEIYHSGSTNYN
                               1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 81.9%; Score 531.5; DB 4; Best Local Similarity 85.1%; Pred. No. 4.8e-44; Matches 103; Conservative 7; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-0an-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-PEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: James F. Haley, Jr., Esq. STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-324-25
                                                                                                                                                                                                                                                                                                                                                    Sequence 25, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212)596-9090
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SEQUENCE CHARACTERISTICS
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STATE: New York
                                                                                                                                                                                                                                          118 $ 118
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                                                                                                                                                                                                                                                                                                           RESULT 12
US-09-490-324-25
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                                                                   임
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                                                                                                                                                                                                                                        61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYXCARDQGQMLLPDAFDIWGQGTMVTVS 120
                                                                                                                                                                                                                                                                61 PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGRGG---GGVFDYWGQGTLVTVS 117
                                                                                                                                                           9
                                                                                                                                                                                 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGEIYHSGSTNYN 60
                                                                                                                                                      1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                   Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-490-153-25
; Sequence 25, Application US/09490153
; Sequence 25, Application US/09490153
; GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, vio
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                     DB 4;
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85.1%; Pred. No. 4.8e-44;
iive 7; Mismatches 8;
                                                                   Score 531.5; DB 4
Pred. No. 4.8e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
                                                                                                         7; Mismatches
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-070A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
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TYPE: amino acid
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INFORMATION FOR SEQ ID NO: 25:
                                                                   81.9%;
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                                                            Query Match
Best Local Similarity 85.18
Matches 103, Conservative
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Best Local Similarity 85.1
Matches 103; Conservative
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STATE: New York
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61 PSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCARDOGOWLLPDAFDIWGOGTWVTVS 120
                                                                                                                                                               63 PSLKSRVTISVDTSKSQFSLKLSSVTAADTAVYYCAR--GRY-----FDVWGRGTMVTVS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 BSLKSRVTISVDTSKSQFSLKLSSVTAADTAVYYCAR--GRY----FDVWGRGTMVTVS 115
                                                   1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN 60
                                                                              3 QVQLQQSGPGLVKPSETLSLTCTVSGDSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 81.6%; Score 529.5; DB 4; Length 244; Best Local Similarity 84.3%; Pred. No. 1.7e-43; Matches 102; Conservative 10; Mismatches 2; Indels 7;
           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: single chain antibody (scFv) fragments
US-09-138-091A-77
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Adams, Camellia W.
APPLICANT: Adams, Camellia W.
APPLICANT: Carter, Paul J.
APPLICANT: Carter, Paul J.
APPLICANT: Brandly, Barian M.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: 9491-013-27
CURRENT APPLICATION NUMBER: US/09/138,091A
CURRENT FILING DATE: 1999-08-21
PRIOR APPLICATION NUMBER: US 60/056,736
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 77
SOFTWARE: FastSEQ for Windows Version 4.0
           10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: November 9, 2005, 11:46:38 Job time : 18.802 secs
                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 77, Application US/09138091A; Patent No. 6737249; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
        Matches 102; Conservative
                                                                                                                                                                                                                                                                  116 $ 116
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US-09-138-091A-77
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LENGTH: 244
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1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN 60
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                                                                                                                                                                                                                                                                                               APPLICANT: ESCHER, ROBERT F. A.
TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
FILE REPERENCE: 100564-09049
CURRENT APPLICATION NUMBER: US/09/424,840B
CURRENT FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: DE 19820663.1
PRIOR APPLICATION NUMBER: DE 1975227.7
PRIOR APPLICATION NUMBER: DE 1975227.7
PRIOR APPLICATION NUMBER: DE 19723904.8
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 128
SOFTWARE PERCENT NOS: 128
SOFTWARE PERCENT NOS: 128
SOFTWARE PATENT NETALOR NOS: 128
SEQ ID NO 20
LENGTH: 120
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Pred. No. 4.9e-44;
6; Mismatches 10;
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Patent No. 6342220
GENERAL INFORMATION:
APPLICANT: Adams, Camellia
APPLICANT: W.
APPLICANT: Forter, Paul J.
APPLICANT: Fendly, Brian M.
APPLICANT: Fendly, Brian M.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
CURRENT APPLICATION NUMBER: US/08/918,148A
CURRENT FILING DATE: 1997-08-25
SEQ ID NO 79
                                                                                                                                                                                                                   ; Sequence 20, Application US/09424840B; Patent No. 6796398
; BENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
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84.4%;
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Best Local Similarity 84.4
Matches 103; Conservative
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; ORGANISM: artificial
US-08-918-148-79
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Best Local Similarity
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US-10-330-613-1
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Sequence 17,
Sequence 1, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1
Sequence 1
Sequence 1
Sequence 9
Sequence 9
Sequence 9
Sequence 3
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                                                                                                                                                                  1 QVQLQESGPGLVKPSETLSL.......WLLPDAFDIWGQGTMVTVSS
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(cgn2_6/ptodata1/pubpaa/BCT_NEW_PUB.pep:*

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(cgn2_6/ptodata1/pubpaa/USGB_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-330-633-1
US-10-330-530-1
US-10-660-357-1
US-10-660-357-1
US-10-330-613-9
US-10-330-530-9
US-10-330-530-9
US-10-330-530-9
US-10-330-530-37
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                                                                                                                                                                                                                                        1867879 segs, 418409474 residues
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                                                                                                                                                                                                                                                                                                                                                                                                   Published Applications AA:*
                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match
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Perfect score:
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Maximum DB
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US-10-660-357-37

US-10-292-088-142

US-10-292-088-142

US-10-994-60

US-10-994-60

US-10-994-60

US-10-309-762-24

US-10-309-762-23

US-10-309-762-23

US-10-309-762-23

US-10-309-762-29

US-10-309-762-29

US-10-309-762-102

US-10-309-762-102

US-10-309-762-102

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US-10-309-762-103

US-10-309-762-143

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US-10-173-551-24
US-10-844-424-20
US-10-805-177-56
US-10-067-800-68
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Publication No. US20030147809A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: ABGENIX.02A
CURRENT PAPLICATION NUMBER: US/10/330,613
CURRENT FILING DATE: 2001-12-26
PRIOR APPLICATION NUMBER: 60/346299
PRIOR APPLICATION NUMBER: 60/346299
PRIOR PILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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ORGANISM: Homo Sapiens
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Best Local Similarity
Matches 121; Conserv
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61 PSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTWVTVS 120
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                                                                                                                                           Sequence 17, Application US/10330530
Sequence 17, Application US/10330530
Publication No. US20030152514A1
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
FILE REFERENCE: ABGENIX.031A
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: US 60/346414
PRIOR PILING DATE: 2011-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FRAESEQ for Windows Version 4.0
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; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: BAT-Eli, Menashe
; APPLICANT: BAT-Eli, Menashe
; TITLE OF INVENTION: USFOR ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFREENCE: ABGRNIX: 030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; RIOR PALING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FRSESQ for Windows Version 4.0
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100.0%; Pred. No. 1.8e-50;
cive 0; Mismatches 0;
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Best Local Similarity 100.(
Matches 121; Conservative
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US-10-660-357-1
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| Publication No. US20030152514A1
| GENERAL INFORMATION:
| APPLICANT: Gudas, Jean
| TILLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
| FILE REPERENCE: ABGENIX.031A
| CURRENT APPLICATION NUMBER: US/10/330,530
| PRIOR APPLICATION NUMBER: US 60/346414
| PRIOR APPLICATION NUMBER: US 60/346414
| PRIOR FILING DATE: 2001-12-18
| NUMBER OF SEQ ID NOS: 40
| SEQ ID NO 1
| LENGTH: 121
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100.0%; Score 649; DB 14; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.8e-50;
Matches 121; Conservative 0; Mismatches 0; Indels 0.
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                                                                                                               Sequence 17, Application US/10330613
PUblication No. US20030147809A1
GENERAL INFORMATION:
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
FILE REPRENCE: ABGENIX.022A
CURRENT PILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: 60/346299
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo Sapiens
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LENGTH: 121
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US-10-330-530-1
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61 PSIKSRVTISVDTSKNQFSLRISSVTAADTALYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
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                            61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS
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                                                                                                                                                                                                                                           Sequence 9, Application US/10330530;
Publication No. US20030152514A1;
GENERAL INFORMATION:
APPLICANT: Glads, Jaan
TITLE OF INVENTION:
FILE REPERBENCE: ABGENIX. 031A;
CURRENT FILING DATE: 2002-12-26;
FRIOR APPLICATION NUMBER: US/10/330,530
CURRENT FILING DATE: 2002-12-26;
FRIOR APPLICATION NUMBER: US 60/346414;
PRIOR APPLICATION NUMBER: US 60/346414;
FRIOR FILING DATE: 2001-12-18;
NUMBER OF SEQ ID NOS: 40;
SEQ ID NO 9;
SEQ ID NO 9;
LENGTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.1%; Score 643; DB 14; Length 121; 98.3%; Pred. No. 6.1e-50; rive 2; Mismatches 0; Indels
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APPLICANT: Green, Larry L.
TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
TITLE OF INVENTION: ANTIGEN
FILE REFERENCE: ABGENIX.030C1
CURRENT APPLICATION NUMBER: US/10/660,357
CURRENT FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-12-26
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 121
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Matches 119; Conservative
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Matches 119; Conservative
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61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
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Pred. No. 6.1e-50;
2; Mismatches 0; Indels (
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i Sequence 9, Application US/10330613

i Publication No. US20030147809A1

i GENERAL INFORMATION:

APPLICANT: Gudas, Jean

ITLLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN

FILE REFERENCE: ABGENIX.022A

CURRENT APPLICATION NUMBER: US/10/330,613

CURRENT FILING DATE: 2002-12-26

PRIOR PILING DATE: 2001-12-18

NUMBER OF SEQ ID NOS: 40

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                          Sequence 17, Application US/10660357
Publication No. US20040115205A1
GENERAL INFORMATION:
APPLICANT: BAT-Eli, Menashe
APPLICANT: Green, Larry L.
TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
TITLE OF INVENTION: ANTIGEN
FILE REFERENCE: ABGENIX. 030C1
CURRENT FILING DATE: 2003-1030, 580
PRIOR APPLICATION NUMBER: 10/330,580
PRIOR APPLICATION NUMBER: 10/330,580
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FRASESEQ for Windows Version 4.0
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Pred. No. 1.8e-50;
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Best Local Similarity 100.(
Matches 121, Conservative
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Best Local Similarity 98.3
Matches 119, Conservative
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US-10-660-357-17
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LENGTH: 121
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                                                1 QVQLQESGPGLVKPSETLSLTCTVSGGSISTYYWSWIRQPPGKGLEWIGYIYYTGNTYYN 60
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Best Local Similarity 90.9%; Pred. No. 8e-46;
Matches 110; Conservative 7; Mismatches 4; Indels
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Sequence 37, Application US/10660357

Publication No. US20040115205A1

GENERAL INFORMATION:
APPLICANT: Bar-Eli, Menashe
TITLE OF INVENTION: USE OF NATIBODIES AGAINST THE MUC18
TITLE OF INVENTION: ANTIGEN
FILE REFERENCE: ABGENIX.030C1
CURRENT APPLICATION NUMBER: US/10/660,357
CURRENT FILING DATE: 2003-09-10
CURRENT FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-12-26
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; Publication No. US20030211100A1
; General INFORMATION:
    APPLICANT: BEDIAN, VAHE
; APPLICANT: GELADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: CIRNO.
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: AFF(3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT APPLICATION NUMBER: 60/348,980
; FILE REPERENCE: ASC.
; FILE REPERENCE: ASC.
; NUMBER: OF SEQ ID NOS: 147
; SEQ ID NO 142
; SEQ ID NO 142
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 37
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; ORGANISM: Homo Sapiens
US-10-660-357-37
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US-10-292-088-142
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                                                                                         PSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTWVTVS 120
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QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGY1YYTWTSNYN
                             1 QVQLQESGPGLVKPSETLSLICTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWITNYN
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TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
FILE REFERENCE: ABGENIX.031A
CURRENT APPLICATION NUMBER: US/10/330,530
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: US 60/346414
PRIOR APPLICATION NUMBER: US 60/346414
PRIOR PILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FASESEQ for Windows Version 4.0
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Publication No. US20030147809A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/330,613
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: 60/346299
FRIOR FILING DATE: 2001-12-18
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90.9%; Pred. No. 8e-46;
ive 7; Mismatches
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Pred. No. 8e-46;
7; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 90.9
Matches 110; Conservative
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Best Local Similarity 90.9
Matches 110; Conservative
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US-10-330-530-37
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US-10-330-530-37
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LENGTH: 121
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LENGTH: 121
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Search completed: November 9, 2005, 12:43:00 Job time : 68.2222 secs
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86.0%;
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Best Local Similarity 86.0
Matches 104; Conservative
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ORGANISM: Homo sapiens
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Publication No. US20030100058A1

GENERAL INFORMATION:
APPLICANT: Roschke, Viktor
APPLICANT: Rosch, Craig A.
APPLICANT: Ruben, Seeven, M.
ITLLE OF INVENTION: Human G protein Chemokine Receptor (CCR5) HDGNR10

FILE REFERENCE: 1488.1150001
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                                                                                    DB 15; Length 118;
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1.7e-41;
7; Indels
                                                                                  Query Match 85.3%; Score 553.5; DB 15; Length Best Local Similarity 87.6%; Pred. No. 6.2e-42; Matches 106; Conservative 7; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 109, Application US/10292088
| Publication No. US20030211100A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: BEDIAN, VAHE
| APPLICANT: CORVALAN, JOSE
| APPLICANT: CORVALAN, JOSE
| APPLICANT: TORVALAN, JOSE
| APPLICANT: FENG, XIAO-CHI
| APPLICANT: FENG, XIAO-CHI
| APPLICANT: FENG, XIAO-CHI
| APPLICANT: ANTIBODIES TO CD40
| FILE OF INVENTION: ANTIBODIES TO CD40
| FILE OF INVENTION: ANTIBODIES TO CD40
| FILE OF INVENTION NUMBER: US/10/292,088
| CURRENT APPLICATION NUMBER: 60/348,980
| PRIOR FILING DATE: 2001-11-09
| NUMBER OF SEO ID NOS: 147
| SOFTWARE: PATCHIN VET. 2.1
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Pred. No. 1.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 87.6%;
Matches 106; Conservative
                    ; ORGANISM: Homo sapiens
US-10-292-088-142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
US-10-292-088-109
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61 PSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCARDOGOWLLPDAFDIWGOGTMVTVS 120
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CURRENT FILING DATE: 2002-02-08

PRIOR APPLICATION NUMBER: PCT/USO1/04153

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 09/779,880

PRIOR PLILING DATE: 2001-02-09

PRIOR PLILING DATE: 2001-02-09

PRIOR PLILING DATE: 2001-06-12

PRIOR PLILING DATE: 2001-06-08

PRIOR PLILING DATE: 2001-08-08

PRIOR PLILING DATE: 2001-10-12

PRIOR PLILING DATE: 2001-12

PRIOR PLILING DATE: 2001-12

PRIOR PRILING DATE: 2001-12

PRIOR PRILING DATE: 2001-12

PRIOR PRILING DATE: 2001-12-21

NUMBER OF SEQ ID NOS: 70

SOFTWARE: PATENTING DATE: 2001-12-21

NUMBER OF SEQ ID NOS: 70

SOFTWARE: PATENTING DATE: 2001-12-21

NUMBER OF SEQ ID NOS: 70

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NUMBER OF SEQ ID NOS: 70

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1 QVQLQESGFGLVKPSETLSL......WLLPDAFDIWGQGTMVTVSS
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Copyright (c) 1993 - 2005 Compugen Ltd.
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|--------------------|------------|-------|------|-------|----------|
| | ALIGNMENTS | | | | |
| Ig heavy chain V-J | S57464 | 115 2 | 69.2 | 449 | 4.
S |
| Ig heavy chain V r | S31604 | 135 2 | 69.5 | 451 | 44 |
| Ig heavy chain V r | PH1673 | 109 2 | 69.5 | 451 | 43 |
| hypothetical hybri | A24770 | 140 2 | 9.69 | 452 | 42 |
| Ig V-D-J region (N | 869912 | 122 2 | 69.9 | 453.5 | 41 |
| Ig heavy chain V r | S12418 | 99 2 | 70.0 | 454 | 40 |
| Ig heavy chain pre | G1HUH2 | 146 1 | 70.0 | 454.5 | 39 |
| Ig heavy chain V-D | 844110 | 110 2 | 70.2 | 455.5 | 38 |
| Ig heavy chain V r | 809710 | 146 2 | 70.6 | 458 | 37 |
| Ig heavy chain V r | S54906 | 134 2 | 9.07 | 458 | 36 |
| Ig heavy chain V r | S26801 | 99 2 | 70.6 | 458 | 32 |
| Ig heavy chain V-I | D41287 | 122 2 | 70.8 | 459.5 | 34 |
| Ig heavy chain V r | S18557 | 116 2 | 70.9 | 460 | 33 |
| Ig heavy chain V r | S26804 | 97 2 | 70.9 | 460 | 32 |
| Ig heavy chain V-I | B49028 | 143 2 | 71.2 | 462 | 31 |
| Ig heavy chain V r | S12412 | 2 66 | 0.1/ | 465 | 2 |

| RESULT 1 137782 Ig variable region (VDJ) (clone T23-9) - human (fragment) C;Species: Homo sapiens (man) C;Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999 C;Accession: 137782; S25476 R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M. Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994 A;Ttle: Somatic diversification in the heavy chain variable region genes expressed A;Reference number: A36876; MUID:94119917; PMID:8290556 A;Accession: 137782 A;Status: preliminary A;Ancelliminary | A;Residues: 1-140 <res- 1-140="" <imm="" <res-="" a;cross-references:="" a;residues:="" c;superfamily:="" embl:x67906;="" homology="" immunoglobulin="" nid:g33582;="" pid:g33583="" pidn:caa48104.1;="" region;="" v=""> F;46-128/Domain: immunoglobulin homology <imm> Querry Match 83.7%; Score 543; DB 2; Length 140; Best Local Similarity 86.0%; Pred. No. 3.5e-41; Matches 104; Conservative 5; Mismatches 12; Indels 0; Gaps 0;</imm></res-> | Qy 1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN 60 | OY 61 PSLKGRUTISVDTSKNOFSLRLSSVTAADTÄVYYCARDQGQMLLPDAFDIWGQCTMVTVS 120 | Oy 121 S 121
Db 140 S 140 | RESULT 2 S31512 Ig heavy chain - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Accession: S31512 R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M. Submitted to the EMBL Data Library, December 1992 A;Reference number: S31509 A;Reference number: S31509 A;Status: proliminary A;Molecule type: mRNA A;Residues: 1-155 < CTHA> A;Accession: 1-155 < CTHA> A;Accession: Jibolaniary A;Molecule type: mRNA A;Residues: 1-155 < CHA> A;Accession: Jibolaniary A;Molecule type: mRNA A;Cross-references: EMBL:X69860; NID:g33082; PIDN:CAA49494.1; PID:g33083 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin |
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C,Accession: S31586
R,Culsinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: S31585
A;Accession: S31586
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                                                                                                                                                                                                                                                                                                          PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQG--QWLLPDAFDIWGQGTMVT 118
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C.Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
C.Accession: S30534
R.Mariette, X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
                                                                                                                                                                         OVOLOESGPGLVKPSETLSLTCTVSGGSISSYYWSWIROPPGKGLEWIGYIYYTWTSNYN
                                                                                                                                                                                                                                    33 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTGSATYN
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                                             DB 2; Length 155
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16-39;
---- 10; Indels
                                      Score 533; DB 2; Length 15
Pred. No. 3e-40;
5; Mismatches 13; Indels
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A;Acference number: S30520
A;Accession: S30534
A;Sterence
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81.1%; Score 526.5;
Best Local Similarity 86.0%; Pred. No. 1e-3
Matches 104; Conservative 6; Mismatches
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C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>
                                      Query Match
Best Local Similarity 83.7%;
Matches 103; Conservative
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A;Molecule type: mRNA
A;Residues: 1-130 <MAR>
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A;Molecule type: mRNA
A;Residues: 1-139 <CUI>
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VSS 155
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C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C; Accession: 81511
B; Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A; Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A; Reference number: 831509
A; Accession: 831511
A; Accession: 83151
A; Accession: S3151
A; Accession: Braininary
A; Residues: 1-155 ccHA>
A; Residues: 1-155 ccHA>
A; Residues: 1-155 ccHA>
A; Cross-references: EMBL: X68866; NID: 933094; PIDN: CAA49500.1; PID: 933095
C; Superfamily: immunoglobulin v region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin homology <IMM>
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R. Cuisnier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.

B. Cuisnier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.

B. Cuisnier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.

A. Description: Mechanisms that generate human immunoglobulin diversity operate from the A; Reference number: 831585

A. Accession: 831690

A. Accession: 841690

A. Accession
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                                                                                                                                                                                                                                                                                                                                                                            61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWL----LPDAFDIWGQGTM 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Homo sapiens (man)
| Species: Homo sapiens (man)
| Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                  1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
                                                                                                                                                                                                                                           QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTGSATYN
                                                                                                                                                                                                                                                                                                                                         PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQG--QWLLPDAFDIWGQGTMVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
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                                                                                                                                          Gaps
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                                                                     Length 155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Indels
                                                                                                                                   12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 533; DB 2;
Pred. No. 2.5e-40;
                                                                 Score 536; DB 2;
Pred. No. 1.6e-40;
7; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
F;47-129/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.1%; Score 533;
84.0%; Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain V region - human (fragment)
                                                                 82.6%;
ilarity 82.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 84.0 Matches 105; Conservative
                                                                                                 Best Local Similarity
Matches 102; Conserv
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Ig heavy chain - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSS 155
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A.Accession: Server mRNA A.Rolecule type: mRNA A.Rosidues: 1-140 <44R. A.Rosidues: 1-140 <44R. A.Rosidues: 1-140 <44R. A.Rosidues: EMBL:X54441; NID:g37815; PIDN:CAA38308.1; PID:g930118 R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkin R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkin R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkin R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkin R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkin R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkin R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkin R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkin R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkin R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkin R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkin R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkin R;Harindranath, R.L.; Notkin R;Harindranath, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.Species: Homo sapiens (man)
C.Date: 19-700-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C.Accession: S78052; S23717
R.Harindranath, N.
                                                                                                                             QVQLQESGPGLVKPSETLSLTCTVSVGSISGHYWSWIRQPPGKGLEWIAFIRYTGSTHYN
                                                                                            1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
                                                                                                                                                                                                             PSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS
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                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Cross-references: EMBL.X56158; NID:g37724; PIDN:CAA39626.1; PID:g37725 C. Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F;41-125/Domain: immunoglobulin homology < IMM>
                                    3,
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                                    9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.8%; Score 505; DB 2;
82.1%; Pred. No. 8.6e-38;
iive 7; Mismatches 11;
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A;Reference number: S78051
A;Accession: S78052
                                    Mismatches
                                    11;
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A,Residues: 15-111 <HAW>
A,Cross-references: EMBL:X54441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 82.1
Matches 101; Conservative
                                 Conservative
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                              98;
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                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31676
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
B;Date to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: S31585
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R;Mortari, F.; Wang, J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A;Description: Analysis of human cord blood Ig heavy chain IgA and IgG repertoire.
                                                                                                                                                                                                                                                                     59 YNPSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQ-WL-----LPDAFDIW 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCARDOGOWLLPDAFDIWGOGTWVTVS 120
                                                                                                                       58
                                                                                                                                                   1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGSYWSWIRQPAGKGLEWIGRIYTSGSTN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPAGKGLEWIGRIYTSGSTNYN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYLYYTWTSNYN 60
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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
                                                                                                                    1 QVQLQESGPGLVKPSETLSLTCTVSGGSIS--SYYWSWIRQPPGKGLEWIGYIYYTWTSN
                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PID:933894
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A; Residues: 1-118 <MOR>
A; Cross-references: EMBL: Z11958; NID: 933893; PIDN: CAA78015.1; P. C; Superfamily: immunoglobulin v region; immunoglobulin homology C; Keywords: heteroterramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
                                                             Indels
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Pred. No. 1.7e-38;
6; Mismatches 11;
Pred. No. 4.8e-39;
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81.0%; Pred. No. 2.7e-38;
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Best Local Similarity 83.5%;
Matches 101; Conservative 6
                           81.5%;
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                              Best Local Similarity 81.5
Matches 106; Conservative
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                                                                                                                                                                                                                                                                                                                                                           GOGTMVTVSS 121
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A; Residues: 1-137 <CUI>
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Best Local Similarity
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A, Status: preliminary
A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Status: preliminary
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A; Status: preliminal
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C'Speciés: Homo sapiens (man)
C'Speciés: Homo sapiens (man)
C'Date: 22-Nov-1993 #sequence revision 10-Nov-1995 #text_change 23-Jul-1999
C'Accession: 826906; 809421; 512415
R'Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
M. Mol. Biol. 227, 776-7798, 1992
A'Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A'Reference number: 826885; MUID:93021117; PMID:1404388
   C;Accession: S44125
R;HawKins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable
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A; Title: The smaller human V(H) gene families display remarkably little polymorphism. A; Reference number: S09421; MUID:90059975; PMID:2511001
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <TOM>
A;Cross-references: EMBL:Z12371; NID:g32962; PIDN:CAA78241.1; PID:g32963
A;Note: designated DP-71
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C;Species: Homo sapiens (man)
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                                                                                                                            A;Reference number: 544105
A;Accession: 544125
A;Accession: 544125
A;Actus: preliminary
A;Molecule type: DNA
A;Residues: 1-105 cHAW>
A;Cross-references: EMBL: 231383; NID:9472978; PIDN:CAA83258.1; D;Csymerfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heteroterramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
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A,Residues: 1-97 <SA2>
A,Residues: 1-97 <SA2>
A,Cross references: EMBL:X56359
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <!MM>
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Pred. No. 1.3e-36;
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Pred. No. 1.4e-36;
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A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-97 <SAN>
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l Similarity 94.8%;
92; Conservative
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A;Note: designated 4.11
A;Accession: S124A
A;Status: translation not shown
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Matches 92; Conserva
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Matches 92; Conserv
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A;Reference number: S78051
A;Accession: S78051
A;Molecule type: mRNA
A;Residues: 1-135 <4AR>
A;Coss-references: EMBL:X54437; NID:g37814; PIDN:CAA38306.1; PID:g930117
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
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C.Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C.Accession: S78051; S23716
R.Harindranath, N.
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
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                                                       F:1-14/Domain: signal sequence (fragment) #status predicted <SIG>F:15-140/Product: Ig heavy chain (fragment) #status predicted <MAT>F:29-111/Domain: immunoglobulin homology <IMM>
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Superfamily: immunoglobulin V region; immunoglobulin homology
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                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                             76.8%; Score 498.5; DB 2; 77.0%; Pred. No. 3.1e-37; tive 9; Mismatches 15;
                                                                                                                                                                        Query Match
Best Local Similarity 77.08
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Kodaira, M.; Kinashi, T.; Umemura, I.; Matsuda, F.; Noma, T.; Ono, Y.; Honjo, T.
J. Mol. Biol. 190, 529-541, 1986
A; Title: Organization and evolution of variable region genes of the human immunoglobulin
A; Reference number: A26340; MUID:87061007; PMID:3097326
                                                            Ig heavy chain V region - human (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: Homo 1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996 (Spacession: S0971) (Speciession: S0971)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain precursor V-II region (71-4) - human
C;Species: Homo sapiens (man)
C;Date: 05-Jun-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLQESGPGLVKPSETLSLTCTVSGGSISS -- YYWSWIRQPPGKGLEWIGYIYYTWTSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; · Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:X05711; NID:g33602; PIDN:CAA29183.1; PID:g296660 A;Note: the authors translated the codon GAG for residue 25 as Gln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ajintrons: 16/1
C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Keywords: heteroterramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-116/Product: Ig heavy chain V region 71-4 #status predicted <MAT>
F;34-116/Domain: immunoglobulin homology <INM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.3%; Score 489; DB 2; Length 146; 74.0%; Pred. No. 2.2e-36; live 11; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 75.2%; Score 488; DB 2; Length 116; Best Local Similarity 93.8%; Pred. No. 2.1e-36; Matches 91; Conservative 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-146 <HUG>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-118/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCAR 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 74.0*
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||:|| |||||
136 WGKGTTVTVSS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 WGQGTMVTVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-116 <KOD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: B26340
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9, 2005, 11:46:52 ; Search time 62.4712 Seconds (without alignments) 991.843 Million cell updates/sec
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1 QVQLQESGPGLVKPSETLSL.......MLLPDAFDIWGQGTMVTVSS 121
                                                                                                                                                                                                                                                                                                                                                                            1612378
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                   1612378 segs, 512079187 residues
                                                                         - protein search, using sw model
                                                                                                                                                                                                                                                                                            Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                            US-10-660-357A-17
                                                                                                                  November
                                                                                                                                                                                                                                                                         BLOSUM62
                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                  Perfect score:
                                                                           OM protein
                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                Run on:
                                                                                                                                                                                              Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: uniprot_sprot:*
2: uniprot_trembl:*

UniProt 03:*

Database

| | | di | | | SUMMARIES | | | |
|---------------|-------|----------------|----------------------------|----|-----------------|-------------|-------|---------|
| Result
No. | Score | Query
Match | å
Query
Match Length | DB | ΙD | Description | tion | |
| | 516 | 79.5 | 476 | 7 | Q6GMX1 | 06qmx1 | homo | sapien |
| 7 | 515 | 79.4 | 119 | 7 | Q9UL73 | 09u173 | homo | sapien |
| m | 508.5 | 78.4 | 465 | 7 | QGGMX6 | 9eqmx6 | homod | Bapien |
| 4 | 501.5 | 77.3 | 620 | 7 | Q96EY0 | Q96ey0 | homod | sapien |
| Ŋ | 498.5 | 76.8 | 477 | ~ | Q6GMX7 | 06qmx7 | | sapien |
| 9 | 495 | 76.3 | 139 | ~ | Q86SX2 | 086sx2 | homod | sapien |
| 7 | 493.5 | 76.0 | 478 | 7 | Q7Z379 | Q7z379 | рошо | sapien |
| 80 | 482.5 | 74.3 | 150 | ~ | 095973 | 095973 | homo | sapien |
| σ | 472.5 | 72.8 | 576 | N | Q6P4I8 | Q6p4i8 | homod | sapien |
| 10 | 472 | 72.7 | 492 | 7 | 072374 | 07z374 | homod | sapien |
| 11 | 460.5 | 71.0 | 496 | ~ | Q96KX8 | 096kx8 | homod | sapien |
| 12 | 454.5 | 70.0 | 146 | ٦ | HV2I HUMAN | P06331 | homod | sapien |
| 13 | 451 | 69.5 | 595 | ~ | Q8WUX4 | Q8wux4 | ношо | sapien |
| 14 | 451 | 69.5 | 597 | 7 | QGGMXS | Q6gmx5 | homod | sapien |
| 15 | 451 | 69.5 | 597 | ~ | O3B010 | 09bu10 | homod | sapien |
| 16 | 451 | 69.5 | 625 | ~ | Q96AA6 | Q96aa6 | рошо | sapien |
| 17 | 450 | 69.3 | 478 | ~ | Обичнз | Q6nyh3 | homod | sapien |
| 18 | 449 | 69.2 | 597 | ~ | Q9BQB8 | 09bqb8 | homo | sapien |
| 19 | 445 | 9.89 | 117 | Н | HV2G HUMAN | P01825 | homod | sapien |
| 20 | 444 | 68.4 | 129 | Н | HV2F HUMAN | P01824 | рошо | sapien |
| 21 | 435.5 | 67.1 | 130 | N | Q81Z <u>D</u> 7 | OBizd7 | homod | sapien |
| 22 | 416.5 | 64.2 | 116 | ~ | Q7Z3Y6 | Q7z3y6 | homod | sapien |
| 23 | 411.5 | 63.4 | 122 | 7 | Q9UL75 | Q9u175 | homod | sapien |
| | 407 | 62.7 | 479 | 7 | Q99M22 | Q99m22 | mus m | musculu |
| 25 | 398 | 61.3 | 476 | N | Q6MZX7 | Q6mzx7 | рошо | sapien |
| | 394.5 | 8.09 | 136 | 7 | Qelbqs | Q61bq5 | mus m | musculu |
| 27 | 394 | 60.7 | 137 | Н | HV46 MOUSE | P01822 | mus m | musculu |
| 28 | 390.5 | 60.2 | 473 | ~ | Q8TC63 | Q8tc63 | homo | sapien |
| 29 | 375 | 57.8 | 113 | ч | HV47 MOUSE | P01823 | mus m | musculu |
| 30 | 372 | 57.3 | 262 | 7 | 0652 <u>T</u> 1 | Q65zil | mus m | musculu |

Q91x92 mus musculu

Q91X92

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482

56.9

369.5

31

| | P18532 mus musculu
Q9ul74 homo sapien | | | | | | | | | |
|--------------------------|--|----------------------|--------|------------|--------|--------|--------|--------|--------|--------|
| HV60_MOUSE
HV62_MOUSE | HV61_MOUSE
Q9UL74 | HV43 MOUSE
081105 | Q99NG4 | HV02 XENLA | 09UL96 | Q6PJA4 | Q8WUK1 | Q9UL91 | Q6GMY2 | 622590 |
| | ч 2 | ~ 0 | ~ | H | N | N | N | N | ~ | N |
| 116 | 116 | 144 | 121 | 135 | 121 | 470 | 613 | 118 | 909 | 240 |
| 56.5 | 54.6 | 53.6 | 53.2 | 52.9 | 51.3 | 51.2 | 50.9 | 50.6 | 50.0 | 49.3 |
| 366.5 | 354.5
348 | 348 | 345.5 | 343.5 | 333 | 332 | 330.5 | 328.5 | 324.5 | 320 |
| 32
33 | 34
35 | 36 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

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MEDINE-2218825). PubMed=12477932; DOI=10.1073/pnas.242603899; MEDINE-2218825). PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Altschul S.F., Lordan H., Moore T., Max S.I., Wang J., Hsieh F., Stapleton M., Saress M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., McKerran K.J., Malek J.A., Gunacatne P.H., Massak S.A., McKerran K.J., Malek J.A., Gunacatne P.H., Nilalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C., Schultz J., Myers R.W., Butterfield Y.S., Achiguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S., Schmitz J., Marra M.A., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schein J.E., Schnerch A., Schein J.E., Schein J.E.
                                                                                                                                              Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Bukaryospiens (Human).
Hypothetical protein.
Hypothetical protein.
Hypothetial Hypotheman.
Hypothetial Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Straubberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073773; AAH7373.1; -.
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003596; Ig.
R InterPro; IPR003596; Ig.
R InterPro; IPR003596; Ig.
R Pfam; PP07654; Cl-set; 3.
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                                                                                                                                Last sequence update)
Last annotation update)
                                                    476 AA
                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
                                                    PRT;
                                                                                                  (TrEMBLrel. 27, C
(TrEMBLrel. 27, I
(TrEMBLrel. 27, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.
                                                    PRELIMINARY;
                                                                                                                                05-JUL-2004 (TrEMBLrel. 05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SM00409; IG; 2.
SM00407; IGc1; 3.
SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Spleen;
                                                                                                        05-JUL-2004
                                                    Q6GMX1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART;
RESULT 1
                              D6GMX1
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and mouse cDNA sequences.";
                       05-JUL-2004 (TrEMBLrel. 2. 05-JUL-2004 (TrEMBLrel. 2. 05-JUL-2004 (TrEMBLrel. 2. HYpothetical protein. Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Primary B-Cells;
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s 135
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Matches
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      ACTION OF THE PROPERTY OF THE 
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                                                                                                          3,
                                                                                                                                                                                                                         61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
                                                                                                                                             QVQLQESGPGLVKPSETLSLTCTVSGGSISS -- YYWSWIRQPPGKGLEWIGYIYYTWTSN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLQESGPGLVKPSETLSLTCTVSGGSICSYYWSWIRQPPGKGLEWIGYIYYSGSTNYT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                   20 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGDYYWSWIRQPPGKGLEWIGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
                                                                                                            Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                 Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.4%; Score 515; DB 2; Length 119; 82.6%; Pred. No. 1e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Indels
ll protein.
476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 119
119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;
                                                        Query Match 79.5%; Score 516; DB 2; L
Best Local Similarity 79.7%; Pred. No. 3.6e-43;
Matches 102; Conservative 10; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fetus.",
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, ARO33041, AAD56277.1;
PIR, PH0876, PH0876.
PIR, 512416, 512416.
HSSP, P01820, 1G70.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596, Ig-v.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       465 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9UL73;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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Best Local Similarity 82.6
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                        GTMVTVSS 146
                                                                                                                                                                                                                                                                                                                GTMVTVSS 121
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Hypothetical
SEQUENCE 47
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Q6GMX6
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TISSUE-Primary B-Cells;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

A Itschul S.P., Zeeberg B.B., Wagner L., Shemen C.M., Schuler G.D.,

A Itschul S.F., Zeeberg B.B., Barder T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,

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Radan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Morise P.M., Antra M.A.;

Jones S.J., Marra M.A.;

T "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 PSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCARGRFTY-----FDYWGQGTLVTVS 134
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                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases
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SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
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Pred. No. 2e-42;
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81.8%; Pred. No. 2c
8; Mismatches
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PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Created)
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EMBL; BC073766; AAH73766.1; --
InterPro; IPR00110; Ig-like.
InterPro; IPR003599; Ig-like.
InterPro; IPR0030596; Ig-MHC.
InterPro; IPR003596; Ig-W.
Pfam; PP07654; C1-set; 3.
Pfam; PP07654; C1-set; 3.
Pfam; SM00407; Ig; 4.
SMART; SM00407; IG21; 3.
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WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

METAGENER R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MISCHIL S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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Distribution D.F., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

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Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahesley J., Helton E., Ketreman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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Moriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,

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Jones S.J., Marra M.A.,

T. "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 620;
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INTERIOR; IPRO03597; 19.
INTERPO; IPRO03597; 19.
INTERPO; IPRO03597; 19.
INTERPO; IPRO03596; 19.
INTERPO; IPRO03596; 19.
INTERPO; IPRO03596; 19.
INTERPO; IPRO03596; 19.
INTERPO; IPRO0409; 16.
INTERPO; INTERPOSE 16.
INTERPOSE INTERPOSE 16.
INTERPOSE INTERPOSE 16.
INTERPOSE INTERPOSE 16.
INTERPOSE 16
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011857; AAH11857.2; -
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                                                                                          Last sequence update)
Last annotation update)
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Pred. No. 1.4e-41;
6; Mismatches 13
   620 AA.
                                                               Created)
   PRT;
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82.0%;
                                                         01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2004 (TrEMBLrel. 26,
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Best Local Similarity 82.0
Matches 100; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003599; Ig.
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                                                                                                                                                          IGHM protein.
Homo sapiens (Human).
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HSSP; P01820; 1G7J.
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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MEDINE-Primary B-Cells,

MEDINE-2188257; PubMed=12477932; DOI=10.1073/pnas.242603899;

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Kausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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477 AA; 51631 MW; 9FE59C09C50CFFB5 CRC64;
                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                            Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; BCC73765; AAH73765.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_W.
Fam; PP07654; C1-8et; 2.
Fam; PP07654; C1-8et; 2.
Fam; PR00407; ig; 3.
SWART; SW00407; IGC1; 3.
SWART; SW00407; IGC1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.8%;
                                                      05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Primary B-Cells;
                                                                                                                                               Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 S 121
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Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137
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PROSITE; PS00290; IG_MHC; UNKNOWN_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                        76.0%;
                                                                                                                                                 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                  Hypothetical protein
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
es 98; Conserv
                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                               136 VSS 138
                                                                                                                                                                                                                                                                                                                                                                      119 VSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSS 121
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                                                          SEQUENCE
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NON TER
SEQUENCE
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                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=IGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  095973;
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SIGNAL
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYSUE-Human rectum tumor;

C TISSUE-Human rectum tumor;

A Bloecker H., Beacher M., Mewes H.W., Weil B., Amid C., Osanger A.,

B Bloecker H., Wiemann S.;

C Lissue G., Han M., Wiemann S.;

E Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

R EMBL; BX38066; CAD97996.1; -.

R EMBL; BX38066; CAD97996.1; -.

R EMSP; PR003006; Ig-1ike.

R InterPro; IPR003597; Ig_cl.

R InterPro; IPR003597; Ig_cl.

R InterPro; IPR003596; Ig_WHC.

DR InterPro; IPR003596; Ig_WHC.

DR Ffam; PR0564; C1-8et; 2.

DR SMART; SM0406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                          01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Full-length cDNA clone CSODL004YM19 of B cells (Ramos cell line)
Homo sapiens (human) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 76.3%; Score 495; DB 2; Length 13
Local Similarity 94.9%; Pred. No. 1.2e-41;
les 93; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUEs calls;
Li W.B., Gruber C., Jessee J., Polayes D.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genoscope;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL: BX2483100; CAD62627.1; -.
HSSP; P01820; 1G7J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON TER 1 1 1 SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp686K04218 (Fragment).
Name=DKFZp686K04218;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCARD 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARD
                                      139 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               478 AA.
                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. TISSUE=B cells;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q7Z379
Q7Z379;
                                                             286SX2;
                                    Q86SX2
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                                                                                                                                                                                                                                                                                                                               59 YNPSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVŢ 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 YNPSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCAR----LGMGAFDFWGHGTMVT 134
                                                                                                                                                                                                            19 QVQLQESGPGLVKPSQTLSLTCTVSGGSIGSGDYFWSWIRQAPGRGLEWMGYIYYSGSTY 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 QLQLQESGPGLVKPSETLSLSCTVSGGSISSTNYYWGWIRQPPEKGLEWIGSLHNSGSDY 79
                                                                                                                                                                          1 QVQLQESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYTWTSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLQESGPGLVKPSETLSLTCTVSGGSISS -- YYWSWIRQPPGKGLEWIGYIYYTWTSN
                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                     5.
                                                          DB 2; Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.3%; Score 482.5; DB 2; Length 150; ilarity 79.7%; Pred. No. 2.3e-40; Conservative 6; Mismatches 12; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VH4 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SUN C.-H., SONG C.-H., Lee C.-H., Lee S.-K.;
Subnitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
BMBL; AF103795; AAC79084.1; -.
PIR; S31673; S31673.
PIR; S78056; S78056.
PIR; S78056; JGJU.
INTERPRO; IPRO07110; Ig-11ke.
INTERPRO; IPRO07110; Ig-11ke.
INTERPRO; IPRO07110; Ig-11ke.
INTERPRO; IPRO07110; Ig-11ke.
INTERPRO; IPRO0356; IGV: 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                     Indels
478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 19 Potential.
20 >150 WH4 heavy chain variable.
150 150 WW, 85664E04938AA7C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
VH4 heavy chain variable region precursor (Fragment)
                                  Score 493.5; DB 2;
Pred. No. 6.5e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        576 AA.
                                                                                                                  15; Mismatches
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SEQUENCE
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                                                07Z374;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                             STAK BORR REPRESENTATION OF THE PROPERTY OF TH
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                                                                                                                                                                                                                                                                                        TISSUE-Primary B-Cells;

XT TISSUE-Primary B-Cells;

XT TISSUE-Primary B-Cells;

XT STaubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XT Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B.B., Barcow K.H., Schaefer C.F., Bhat N.K.,

XT Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hasleh F.,

XT Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hasleh F.,

XT Sanderon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

XT Sapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

XT Sapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

XT Sands S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XT Soare S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

XI Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XT Norley K.C., Hale S., Garcia A.M., Gibbs R.A.,

XT Nadan A., Young A.C., Sherchenko Y., Bouffard G.G.,

XT Nadan A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

XT Nating M. Marra M.A.;

XT Scheetz T.E.,

XT Nesser M. Sandska U., Smailus D.E., Schnerch A., Schein J.E.,

XT Menster Norley R.M.;

XT Machine C.DNA serminares "...

XT Menster Norley R.M.;

XT Machine C.DNA serminares "...

XT And mouse C.DNA serminares "...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVQLQESGPGLVXPSETLSLTCTVSGGSI-SSYYWSWIRQPPGKGLEWIGYIYYTWTSNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Gaps
                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 472.5; DB 2; Length 576;
Pred. No. 1e-38;
9; Mismatches 10; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BC063184; AAH63384.1; -.
HSSP, P01820; 1A7N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00409, IG; 1.
SMART; SM00400; IGc1; 3.
SMART; SM00400; IGc1; 3.
SMART; SM00406; IGV; 1.
PROSITE; PSC00290; IG_LIKE; 4.
PROSITE; PSC00290; IG_MHC; UNKNOWN 2.
SEQUENCE 576 AA; 63363 MW; FBB97C949D720FIE CRC64;
                        27, Created)
27, Last sequence update)
27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL,

HSSP, P01820; 1A.W.

INCERPO; IPR003599; Ig.

INCERPO; IPR07110; Ig-like.

INCERPO; IPR003597; Ig_c1.

INCERPO; IPR003006; Ig_MHC.

Therpro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similaricy
nes 96; Conservative
                     05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF07654; C1-set;
Pfam; PF00047; iq; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TVTVSS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 MVTVSS 121
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                  IGHD protein.
Name=IGHD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   н
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 YNPSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARD-QGQ--WLLPDAFDIWGQGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUB-Human rectum tumor;
Bloecker H., Beecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
Pobo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX538077; CAD98001.1;
HSSP; P01820; 1G7J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGC27165 protein.
Homo sapions (Human).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 472; DB 2; Length 492;
Pred. No. 9.5e-39;
9; Mismatches 12; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;
                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                     01-0cT-2003 (TrEMBLrel. 25, Created)
01-0cT-2003 (TrEMBLrel. 25, Last sequence upda
01-MAR-2004 (TrEMBLrel. 26, Last annotation up
Hypothetical protein DKFZp686C02218 (Fragment)
Name-DKFZp686C02218;
  492 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                496 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN_2.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR007110; 19-11ke.
InterPro; IPR003597; 19_c1.
InterPro; IPR003065; 1g_MHC.
InterPro; IPR003596; 1g_MHC.
Pfam; PP07654; C1-set; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q96KX8;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00406; IGV;
                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 MVTVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVTVSS 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                      NCBI_TaxID=9606;
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NON TER
SEQUENCE
                                                                                                        DISULFID
                                                                                                                                                         Query Match
                                                                                                                                                                       Local
                                                    CHAIN
DOMAIN
DOMAIN
                                                                                            DOMAIN
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                                                                                                                                                                                 Matches
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    STITITES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 YNPSLKSRVTISVDTSKNQLSLKVRSVTAADTAVYFCARHGYSRSGR---TGAIDYWGQG 136
                                                                                                                                                                                                                                                                                                                                                                                                                               28
                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 ÓLÓLÓESGPGLVKSSETLSLTCTVSGGSISSSSÝÝWGWIRQPPGKGLEWIANTÝYSGITY 79
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S., Jones S.J., Marra M.A.; Greilus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; Greilus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; Greilus D.E., Grimman dinitial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                            QVQLQESGPGLVKPSETLSLTCTVSGGSI -- SSYYWSWIRQPPGKGLEWIGYIYYTWTSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 YNPSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCARD----OGOWLLPDAFDIWGOG
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-85205332; PubMed=3922855; DOI=10.1016/0378-1119(85)90092-7; Kudo A., Ishihara T., Nishimura Y., Watanabe T.; "A cloned human immunoglobulin heavy chain gene with a novel directrepeat sequence in 5' flanking region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                            Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                            Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO16599; AAH16369.1; -.
HSSP; P01876; 10W0.
                                                                                                                                                                                                                                                                                               Pfam; PF07654; C1-set; Z.
SWART; SW00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50290; IG_MHC; UNKNOWN 1.
SEQUENCE 496 AA; \(\bar{5}\)3331 MW; D346929849040D69 CRC64;
                                                                                                                                          roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                           Score 460.5; DB 2;
Pred. No. 1.4e-37;
8; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ign heavy chain V-II region ARH-77 precursor.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene 33:181-189(1985).
PIR; A02101; GHUHU2.
HSSP; POILSS; 7PAB.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; P:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR00714; Ig-like.
Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                            InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_Cl.
InterPro; IPR003065; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF07654; Cl-set, Z.
                                                                                                                                                                                                                                                                                                                                                                           71.0%;
74.0%;
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 74.0%,
--hes 94; Conservative
                                                                                                                              and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLVTVSS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TMVTVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                 TISSUE=Lung
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MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., TOshiyuki S., Carninoi P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
And Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
And Makan A., Young A.C., Shevchenko Y., Bouffard G.G.,
And Makan A., Young A.C., Shevchenko Y., Bouffard G.G.,
And Makan A., Young A.C., Shevchenko Y., Bouffard G.G.,
And Makan A., Young A.C., Shevchenko Y., Bouffard G.G.,
And Monses J.M. Maran M.A.,
And M. M.A., Rodrigues A.C., Grimwood J., Schmutz J., Myers R.M., Green B.D., Dickson M.C.,
And M. M.A., M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 QVQLQQWGAGLVKPSETLSLTCAVFGGSFSGYYWSWIRQPPGRGLEWIGEINHSGSTNYK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARD--QGQWLLPDAF---DIWGQGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                   Ig heavy chain V-II region ARH-77.. V segment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019235; AAH19235.2; -.
PIR; G34964; G34964.
HSSP; P01861; IADQ.
                                                                                                                                                                                                                                                                                                                                                                                      16228 MW; 8D7FD52BB218171F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.0%; Score 454.5; DB 1 72.2%; Pred. No. 1.4e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   595 AA
                                                                                                                                                                                                                                                                  J segment.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91; Conservative
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                                                                                                                                                                                                                                                                  146
115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 MVTVSS 121
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                                                                                                                                                                                                                                                                                                                                                                                  146 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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1118
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146
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NCBI_TaxID=9606;
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                                                                                                                                                                 Hypothetical
SEQUENCE 59
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XX MEDINE-2538825; PubMed=12477912; DOI=10.1073/pnas.242601899;

XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Calling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

XA Strausberg R.L., Feingold E.A., Shenmen C.M., Schuler G.D.,

XA Stachul S.F., Zeberg B. B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeberg B. B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Angeleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

""Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                       61 PSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCAR-----DQGQWLLPDAFDIWG 112
                                                                                                                                                                                                                                                                                                                              1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
                                                                                                                                                                                                                                                          Gaps
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                             Length 595;
                                                                                                                                                                                                                                                          17; Indels
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Straubberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; PRO03597; AAH73767.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.-11ke.
InterPro; IPR003597; Ig.-1.
InterPro; IPR003596; Ig.-1.
InterPro; IPR003596; Ig.-1.
                   SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS05035; IG_LKE; 5.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
Hypothetical protein.
SEQUENCE 595 AA; 65290 MW; 0D4B50776545714E CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                        69.5%; Score 451; DB 2;
69.8%; Pred. No. 1.5e-36;
iive 10; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                   90; Conservative
Pfam; PF07654; C1-set; 4.
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Best Local Similarity
Matches 90; Conservat
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MEDINE-2238825; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDINE-2238825; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K., A Diatchenko L., Marusina K., Farmer A.H., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A Hilaton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., A Hilaton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., A Hilaton M., Young A.C., Shevchenko Y., Bouffard G.G., A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., A Krzywinski M.I., Sakalaka U., Smailus D.E., Schnerch A., Schein J.E., Grimson D.M., Green E.D., Dickson M.C., Shell K.M., Gones S.J., Marra M.A., I., Shell K.M., Gones S.J., Marra M.A., Shell K.M., 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 PSLKSRVTISVDTSKKQLSLKLSSVNAADTAVYXCARVITRASPGTDGRY----GMDVWG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 QVQLQQWGAGILKPSETLSLTCGVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYLYYTWTSNYN
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 597;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
69.5%; Score 451; DB 2; Length 59;
Best Local Similarity 69.8%; Pred. No. 1.5e-36;
Matches 90; Conservative 10; Mismatches 17; Indels
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597 Aa; 65304 MW; 2AlE75F6AED85230 CRC64;
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Last annotation update)
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Pfam; PF00047; ig; 4.
SMART; SM00409; IG; 2.
SMART; SM004007; IGC1; 4.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS00299; IG_MHC; UNKNOWN_3.
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
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Submitted (FEB-2001) to the
EMBL; BC002963; AAH02963.1;
HSSP; P01861; 1ADQ.
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TISSUE=Lymph;
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us-10-660-357a-17.rup

Search completed: November 9, 2005, 13:05:48 Job time : 62.4712 secs

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9, 2005, 11:43:32; Search time 75.8346 Seconds (without alignments) 627.306 Million cell updates/sec
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653
1 QVQLVQSGAEVKKPGASVKV......GVHYYGMDVWGQGTTVTVSS 123
                                                                                                                                                                                                                                                                                                                                                                 2105692
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:*
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Mo. Score Match Length DB ID Description | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|--|---------------------|---|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|
| Auch Score Match Length DB ID 653 100.0 123 7 ADC99792 587.5 90.0 251 7 ADC9934 576 88.2 127 7 ADK18819 576 88.2 127 7 ADK18801 576 88.2 127 7 ADK18818 561 85.9 125 7 ADK1873 561 85.9 125 7 ADK1873 551 85.3 251 5 ABP45551 554 5 84.9 247 7 ADG96689 552 84.9 247 7 ADG96689 553 84.5 257 7 ADG96426 551 84.4 248 5 ABP4561 551 84.4 248 7 ADG96288 | pecription | 1 | | | _ | _ | _ | | | | | _ | | | - | | | | | Heavy | Human | Single | | | | | Single |
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57 | Length | | 123 | 123 | 123 | 125 | 251 | 251 | 127 | 127 | 127 | 127 | 121 | 125 | 125 | 125 | 126 | 251 | 251 | 123 | 247 | 247 | 257 | 257 | 249 | 248 | 248 |
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Match | | 100.0 | 100.0 | 100.0 | 90.8 | 90.0 | 90.0 | 88.2 | 88.2 | 88.2 | 88.2 | 86.5 | 85.9 | 85.9 | 85.9 | 85.5 | 85.3 | 85.3 | 85.1 | 84.9 | 84.9 | 84.5 | 84.5 | 84.5 | 84.4 | 84.4 |
| Result 100.1 | Score | | 653 | 653 | 653 | 593 | 587.5 | 587.5 | 576 | 576 | 576 | 576 | 565 | 561 | 561 | 561 | 558.5 | 557 | 557 | 556 | 554.5 | 554.5 | 552 | 552 | 551.5 | 551 | 551 |
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No. | | 7 | 2 | m | 4 | ស | 9 | 7 | 80 | 6 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 |

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|--------------------|--------------------|----------|--------------------|----------|--------------------|----------|-----------------|--------------------|--------------------|--------------------|----------|--------------------|----------|--------------------|----------|----------|--------------------|----------|----------|--|
| Abp45179 Human BLv | Adg96006 Single ch | | Adg96170 Single ch | _ | Adg96131 Single ch | <u>.</u> | 96262 Single ch | Add40567 4G11 heav | Abp45767 Human BLy | Adg96594 Single ch | | Adg96241 Single ch | | Adg96490 Single ch | | | Adg96402 Single ch | | | |
| Abp | Adg | dqv | Adg | Abp | Adg | App | Adg | Add | Abp | Adg | Abp | Adg | App | Adg | Abp | Abp | Adg | Adg | Abp | |
| | | | | | | | | | | | | | | | | | | | | |
| ABP45179 | ADG96006 | ABP45343 | ADG96170 | ABP45304 | ADG96131 | ABP45435 | ADG96262 | ADD40567 | ABP45767 | ADG96594 | ABP45414 | ADG96241 | ABP45663 | ADG96490 | ABP45861 | ABP45575 | ADG96402 | ADG96688 | ABP45568 | |
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| 255 | 255 | 257 | 257 | 251 | 251 | 248 | 248 | 132 | 248 | 248 | 249 | 249 | 252 | 252 | 251 | 251 | 251 | 251 | 257 | |
| 84.4 | 84.4 | 84.4 | 84.4 | 84.3 | 84.3 | 84.2 | 84.2 | 84.2 | 84.1 | 84.1 | 83.8 | 83.8 | 83.8 | 83.8 | 83.8 | 83.8 | 83.8 | 83.8 | 83.8 | |
| 551 | 551 | 551 | 551 | 550.5 | 550.5 | 550 | 550 | 549.5 | 549 | 549 | 547.5 | 547.5 | 547.5 | 547.5 | 547 | 547 | 547 | 547 | 547 | |
| 56 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | |

ALIGNMENTS

ADC99792 standard; protein; 123 AA.

RESULT 1 ADC99792

New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies. anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast; Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 21. 26-DEC-2002; 2002WO-US041581. 28-DEC-2001; 2001US-0346299P. (first entry) WPI; 2003-587113/55. (ABGE-) ABGENIX INC lung cancer; human. N-PSDB; ADC99794 WO2003057838-A2. Homo sapiens. 01-JAN-2004 17-JUL-2003. ADC99792; Gudas J;

Claim 1; SEQ ID NO 21; 78pp; English.

The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the pancreatic or condition uses to excite the expression of service call surface such as tumours, specifically melanoma, ossophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung canneer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody

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Gaps

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Indels

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Length 123;

Score 653; DB 7; Pred. No. 7.3e-53; Mismatches

100.0%; Sc 100.0%; Pr ive 0;

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61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETKVRGVHYYGMDVWGQGTTVT 120
                                                                                                                                                                              61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETKVRGVHYYGMDVWGQGTTVT 120
                                                                                                                     QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY
                                                                                                      1 QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY
                                                                      Matches 123; Conservative
                                                            Best Local Similarity
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                                                                                                                                                                                                                     VSS 123
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                  Sequence 123 AA;
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                                                                                                                                                                                                                                                                                                                                                 ADF09834;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has cytostatic and can be used in the production of a vaccine. The monoclonal antibodies against the MUC18 antigen are useful for diagnosing and treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or tumour metastasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-MUC18 antibody heavy chain, variable region, protein of the invention.
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                                                                                                                                                                                        AQKLQGRVTWTTDTSTSTAYMELRSLRSDDTAVYYCARETKVRGVHYYGMDVWGQGTTVT 120
                                                                                                                                                                         AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETKVRGVHYYGMDVWGQGTTVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
                                                                                                                  1 QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY
                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 21.
                                                                                                                                  1 QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY
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                                                            Length 123;
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                                                       100.0%; Score 653; DB 7;
100.0%; Pred. No. 7.3e-53;
iive 0; Mismatches 0;
heavy chain protein of the invention.
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                                                                                                                                                                                                                                                                                                                                 ADD05396 standard; protein; 123 AA.
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                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                     Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bar-Eli M;
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N-PSDB; ADD05398.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      metastatic tumor.
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                                                                                                                                                                                                                                                            VSS 123
                           Sequence 123 AA;
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                                                                                                                                                                                                                                                                                                 cell proliferation inhibition; MUC18 tumour antigen, anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour; carcinoma; cancer; malignancy; heavy chain; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibiting cell proliferation associated with expression of MUC18 antigen, involves incubating and inhibiting cell by administering MUC18 monoclonal antibody.
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                                                                                                                                                                                                                              Human anti-MUC18 monoclonal antibody heavy chain #6
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100.0%; Pred. No. 7.3e-53;
iive 0; Mismatches 0;
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ADF09834 standard; protein; 123 AA.
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                                                                                                                                                  (first entry)
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Matches 123; Conservative
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Sequence 125 AA;
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Best Local 8
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Matches
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ABP45910
ID ABP4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New specific binding agents (i.e. anti-Angiopoietin-2 antibodies), useful for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity, hemangioma, arteriosclerosis, atherosclerosis or endometriosis.
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                                                                                                                   AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETKVRGVHYYGMDVWGQGTTVT
                                                                                                                                                         61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETKVRGVHYYGMDVWGQGTTVT
                       QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY
                                                   QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ang-2; angiopoietin-2; anorectic; cytostatic; antiarteriosclerotic; gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;
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:e= "complementarity determining region (CDR)
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                                                                                                                                                                                                                                                                                                                                                                                      ABR55813 standard; protein; 125 AA.
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96. .11
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                                                                                                                                                                                                            61 AQKLOGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDRGIAARSAYYYGMDVWGQGTT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes novel antibodies that immunospecifically bind the Lymphocyte Stimulator (BLyS) polypeptides. BlyS is a member of the tumour necrosis factor (TNP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirineumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BuyS. The antibodies bind to BuyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression
                                                                                                      1 QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY
                                                                                                                          1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
                                                                                                                                                                           AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETKV--RGVHYYGMDVWGQGTT
                                                                      Gaps
                                                                      5
                                   Length 125;
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90.8%; Score 593; DB 6; Le
Pred. No. 2.7e-47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
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CAMBRIDGE ANTIBODY TECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                       ABP45910 standard; protein; 251 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-OCT-2000; 2000US-0240816P.
16-MAR-2001; 2001US-0276248P.
21-MAR-2001; 2001US-0277379P.
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                                                                    Conservative
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                                                al Similarity
113; Conserv
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90.0%;
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                                                                                                                                                                                                    Query Match
Best Local Similarity 88.3'
Matches 113, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jia X,
                                                                                                                                                                                                                                                                                                                                                    116 GTTVTVSS 123
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                                                                                                                                                                                                                                                                                                                                                                       GTTVTVSS
                                                                                                                                                                                 Sequence 251 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADK18819;
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ADK18819
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           diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                        115
                                                                                                                                                                                                                  61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARVTSLYSSSSGGYYYYGMDVWGR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  stimulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to novel antibodies that immunospecifically bind choose B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome 13d3 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The
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                                                                                                                                                                                                      AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETKV-----RGVHYYGMDVWGQ
                                                                                                                                                                               QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
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                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                             Single chain antibody that immunospecifically binds BLyS SeqID 1921.
                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody, B lymphocyte stimulator, BLyS; tumour necrosis factor, be cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.
and autoimmune disorders and
                                                                                                                                 2;
                                                                                                         5; Length 251;
                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaughan TJ, Hilbert D;
                                                                                                        Score 587.5; DB 5;
Pred. No. 1.9e-46;
4; Mismatches 6;
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19-DEC-2001; 2001US-0340817P.
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activity such as cancer,
                                                                                                        90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                     Query Match
Best Local Similarity 88.3
Matches 113; Conservative
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                                                                                                                                                                                                                                                                            GTTVTVS 128
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                                                                                  Sequence 251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003055979-A2
                                                          the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
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and
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present invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid archritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various activities such as antirheumatic, antiallergic and cytostatic. This polypeptide sequence is a single chain antibody that binds BLyS of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARVTSLYSSSSGGYYYGMDVWGR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 587.5; DB 7
Pred. No. 1.9e-46;
4; Mismatches 6
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Length 127;

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useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188 0.99 arising in the conditioned medium obtained when HEK233 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
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                                                                                                                               Indels
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                                                                                                    Score 576; DB 7;
Pred. No. 1.1e-45;
1; Mismatches 8;
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Best Local Similarity 87.4%;
Matches 111; Conservative
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                                                                               Sequence 127 AA;
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Sequence 127 AA

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                                          8; Indels
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  ; DB 7;
1.1e-45;
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Pred. No. 1.1e-45;
4; Mismatches 8
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                                          4; Mismatches
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Score 576;
Pred. No. 1
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88.2%;
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llarity 87.4%;
Conservative
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                       Similarity
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Best Local Similarity
Matches 111; Conserv
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                       Best Local Simi
Matches 111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ADK18607;
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                                                                                                                                                                                                                                                                                                                                                     RESULT 9
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Wed Nov

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AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
cinvention. The antibodies can be used in the treatment of obesity and
cinvention. The antibodies can be used to deliver drugs or
pro-drugs directly to the fat mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
detectable label such as radiolabel, fluorescent or chemical group and
used in methods of diagnosis in human subjects e.g. to determine the
cetermine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
cetermine the presence or level of adipocytes in a cell or tissue sample.
The antibodies of diagnosis can alternative means of treatment for obese
contact than undergoing surgery to remove excess fat. Antibodies
contact different types of fat deposits can also be produced e.g. intra-
abdominal fat associated with heart disease
                     61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDHYYDSSDYLYYYYGLDVWGQG 120
   61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETKVRG----VHYYGMDVWGQG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY
                                                                                                                                                                                                                                                                                                                                                      fat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 565; DB 4; Length 121; Pred. No. 1.1e-44;
                                                                                                                                                                                                                                                                                                                                                    Antibody, adipocyte; heavy chain; light chain; obesity; heart disease; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                 Anti-adipocyte monoclonal antibody heavy chain, FAT 36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                      AAU02549 standard; protein; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaughan TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 123; 182pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-OCT-2000; 2000WO-GB003900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0158812P
                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Edwards BM, Main SH,
                                                                          123
                                                                                                              127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-282031/29.
N-PSDB; AAS03449.
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                                                                        117 TTVTVSS
                                                                                                            121 TTVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200127279-A1
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                             29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-APR-2001.
                                                                                                                                                                                                                                         AAU02549;
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                                                                                                                                                                RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes an antibody or its binding fragment that binds platelet derived growth factor-DD (PDGF-DD), where the antibody is useful in preparing a medicament for treating nephritis. Also described: (1) a method of detecting nephritis; (2) a method of treating nephritis; (3) a method of inhibiting mesangial cell proliferation; and (4) a method of treating mesangial proliferative glomerulonephritis. The antibody has nephrotropic, antiinflammatory, dermatological, immunosuppressive and antidiabetic activities, and can be used in gene therapy. The antibody or its binding fragment, that binds PDGF-DD, can be used in preparing a medicament for treating nephritis and related disorders, e.g., mesangial proliferative glomerulonephritis. The present sequence represents a human monoclonal antibody (mab) variable region sequence, which is used in the exemplification of the present invention.
                      AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETKVRG----VHYYGMDVWGQG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                              antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD; nephritis; mesangial cell proliferation inhibition; mesangial proliferationsprintis; nephrotropic; antiinflammatory; dermatological; immunosuppressive; antiidiabetic; gene therapy; human; monoclonal antibody; mAb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            an antibody or its binding fragment that binds platelet derived factor-DD (PDGF-DD) for preparing a medicament for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Larochelle WJ, Lichenstein H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
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                                                                                                                                                                                                                                                                                                              Human mAb 1.33 heavy chain variable region protein SEQ ID NO:42.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.2%; Score 576; DB 8; 87.4%; Pred. No. 1.1e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 42; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Keyt B,
                                                                                                                                                                                                    ADL25432 standard; protein; 127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floege J, Gazit-Bornstein G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-SEP-2003; 2003WO-US029414.
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                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                     TTVTVS 127
                                                                        TTVTVSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-269881/25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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growth
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ADK18618 standard; protein; 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 125 AA;
                                                                                                                                                              WO2003057857-A2
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                                                                                                                                                                                                                                                                     Corvalan JRF,
                                                                                                                                          Homo sapiens
                                                                          06-MAY-2004
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                                                     ADK18618;
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            RESULT 13
ADK18618
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ADL25452
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            118
AQKLQGRVTWTTDTSTSTAYMELRSLRSDDTAVYYCARETKVRGV--HYYGMDVWGQGTT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AQKLQGRVTWTTDTSTSTAYMELRSLRSDDTAVYYCARDVEYYYDGSGYYYFDYWGQGTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modularing collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188 to 99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                         Weber R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
                                                                                                                                                                                                                                                                                                                                                                                                         New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.
                                                                                                                                                                                                    antiinflammatory; immunomodulator; cytostatic; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85.9%; Score 561; DB 7; Length 125; larity 87.2%; Pred. No. 2.6e-44; Conservative 3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                         Gazit G,
                                                                                                                                                                               Anti-human PDGF-D antibody protein related sequence #9.
                                                                                                                                                                                                                                                                                                                                                         Chen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 207; 255pp; English
                                                                                                                                                                                                                                                                                                                                                         Yang X,
                                                                                                                ADK18783 standard; protein; 125 AA.
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                                                                                                                                                                                                                                                                                                                                                        Feng X,
                                                                                                                                                                                                                                                                                          06-JAN-2003; 2003WO-US000398
                                                                                                                                                                                                                                                                                                              07-JAN-2002; 2002US-00041860
                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                       Jia X,
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-587119/55.
                                                                                                                                                                                                                                                                                                                                   (ABGE-) ABGENIX INC.
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Matches 109; Conserv
                                        VTVSS 123
                                                       117 VTVSS 121
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Bezabeh B;
                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                            06-MAY-2004
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                                                                                            RESULT 12
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AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETK--VRGVHYYGMDVWGQGTT 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.
                                                                                                                 antiinflammatory; immunomodulator; cytostatic; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 125;
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                                                      Anti-human PDGF-D antibody heavy chain protein sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 561; DB 7;
Pred. No. 2.6e-44;
3; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 42; 255pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yang X,
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Best Local Similarity 87.2%;
Matches 109; Conservative
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jia X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ABGE-) ABGENIX INC
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New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.
                                                                                     antiinflammatory; immunomodulator; cytostatic; gene therapy
                                          Anti-human PDGF-D antibody protein related sequence #156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 354; 255pp; English.
                                                                                                                                                                                                                                                           06-JAN-2003; 2003WO-US000398.
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    06-MAY-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-587119/55.
                                                                                                                                                                                                                                                                                                                                                (ABGE-) ABGENIX INC
                                                                                                                                                                        WO2003057857-A2
                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes an antibody or its binding fragment that binds platelet derived growth factor-DD (PDGF-DD), where the antibody is useful in preparing a medicament for treating nephritis. Also described: (1) a method of detecting nephritis; (2) a method of treating nephritis; (2) a method of treating nephritis; (3) a method of trough mesangial proliferative glomerulonephritis. The antibody has nephrotropic, antihoflammatory, dermatological, immunosuppressive and antidabetic activities, and can be used in gene therapy. The antibody or its binding fragment, that binds PDGF-DD, can be used in preparing a medicament for treating nephritis and related disorders, e.g., mesangial proliferative glomerulonephritis. The present sequence represents a human monoclonal antibody (mAb) variable region sequence, which is used in the
                                                                              antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD; nephritis; mesangial cell proliferation inhibition; mesangial proliferation undinities nephrotropic; antiinflammatory; dermatological; immunosuppressive; antiidiabetic; gene therapy; human; monoclonal antibody; mAb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of an antibody or its binding fragment that binds platelet derived growth factor-DD (PDGF-DD) for preparing a medicament for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Larochelle WJ, Lichenstein H;
                                          Human mAb 1.48.1 heavy chain variable region protein SEQ ID NO:62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 125;
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87.2%; Pred. No. 2.6e-44;
iive 3; Mismatches 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 62; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Keyt B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gazit-Bornstein G,
                                                                                                                                                                                                                                                                                                                                            16-SEP-2003; 2003WO-US029414.
                                                                                                                                                                                                                                                                                                                                                                                         16-SEP-2002; 2002US-0411137P
(first entry)
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Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 (ABGE-) ABGENIX INC. (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2004-269881/25
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                                                                                                                                                                                                                                                         WO2004024098-A2.
                                                                                                                                                                                                                Homo sapiens.
17-JUN-2004
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Weber R;

Gazit G,

Chen F,

Yang X,

Feng X,

growth

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The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modularing collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188. O 99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETKV----RGVHYYGMDVWGQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                   Length 126;
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                                                                                                                                                                                                                                                                                                                                                                                DB 7;
                                                                                                                                                                                                                                                                                                                                                                                Score 558.5; DB 7;
Pred. No. 4.4e-44;
4; Mismatches 9;
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                                                                                                                                                                                                                                                                                                                                                                                85.5%;
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Matches 109; Conservative
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ADK18930 standard, protein, 126 AA.

RESULT 15 ADK18930

ADK18930;

125 VTVSS 123

VTVSS

121

1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETK--VRGVHYYGMDVWGQGTT

QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY

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GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 9, 2005, 11:29:55; Search time 19.1128 Seconds

(without alignments)

480.403 Million cell updates/sec

Title: US-10-660-357A-21

Perfect score: 653
Sequence: 1 OVQLVQSCAEVKKPGASVKV.......GVHYYGMDVWGQGTTVTVSS 123

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Issued Patents AA:

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| ¢ | 22222222222222222222222222222222222222 | 28,
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| Sequence 41, Appl
Sequence 21, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 67, Appl
Sequence 65, Appl |
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| US-09-438-954-41
US-08-933-977C-19
US-08-453-877C-19
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US-08-450-809-14
US-08-561-521-12
PCT-US95-01219-12
US-09-513-999C-4112
US-09-513-999C-4112
US-09-213-99C-4112
US-09-313-65
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App RIGOR PRINCE 1991

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App RIGOR APPLICATION NUMBER 68 9022645.3

App RIGOR PRILING DATE: 1990-10-19

RIGOR PRILING DATE: 1990-11-12

RIGOR PRILING DATE: 1990-10-19

RIGOR PRILING DATE: 1990-11-12

RIGOR PRILING DATE: 1991-65-1

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Sequence 165, Application US/09726219A Patent No. 6806079 GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 272
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CORGANISM: Homo sapiens
US-09-726-219A-165
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LENGTH: 118
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AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETKVRGVHYYGMDVWGQGTTVT 120
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                                                                                                            1 OVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60
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                                                                                                                                                                                                              AQKLQGRVTWTTDTSTSTAYMELRSLRSDDTAVYYCAR--ETKVRGVHYYGMDVWGQGT 117
                                                                                                                                                                                                                                            61 AQKIQGRVTMITDTSTSTAYMELRSLRSDDTAVYYCVRLLPKRTATLHYY-IDVWGKGT 118
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                                                        3; Gaps
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Query Match
79.9%; Score 521.5; DB 4; Length 118;
Best Local Similarity 84.0%; Pred. No. 2.1e-43;
Matches 100; Conservative 6; Mismatches 10; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.2%; Score 517; DB 1; Length 121; 82.1%; Pred. No. 5.8e-43; Live 8; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMAN MONOCLONAL ANTIBODIES SPECIFIC 1
CELL CYCLE-INDEPENDENT GLIOMA SURFACE
ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage COMPUTER: IBM PC Compatible OPERATING SYSTEM: MS-DOS 6.00 SOFTWARE: ASCIT Editor CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No. 5639863 applicable
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FRIOR APPLICATION DATA: No. 5639863 applicable
ATTORNEY/AGENT INFORMATION:
NAWE: Lake, James R.
REGISTRATION NUMBER: 31081
REPERBENCE/DOCKET NUMBER: 31081
TELEPHONE: (416) 868-1482
TELEPHONE: (416) 868-1482
TELEPHONE: (416) 362-0823
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
STRANDEDNESS: not applicable
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08264093
; Patent No. 5639863
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBE
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: Ridout & Maybee
STREET: 2300 Richmond-Adelaide Centre
STREET: 101 Richmond Street West
CITY: Toronto
STREET: Ontario
STREET: Canada
ZIP: MSH 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 82.1<sup>1</sup>
Matches 101; Conservative
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20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY 79
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    Sequence 105, Application US/08545809A
Patent No. 6056878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
US-08-652-816A-19
i Sequence 19, Application US/08652816A
j Patent No. 5872215
j GENERAL INFORMATION:
j APPLICANT: Obtain JK
j APPLICANT: McCafferty, JG
j TITLE OF INVENTION: Specific binding members, materials and TITLE OF INVENTION: methods.
j NUMBER OF SEQUENCES: 53
c CORRESPONDRACE ADDRESS:
j ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
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                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
OSPTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNA AGENT THORNAMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 501; DB 3;
Pred. No. 2e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06501/004001
                                                                                                                                                                                                                     E: Fish & Richardson, P.C.
225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 200154
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 96.9<sup>3</sup>
Matches 95; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                        STATE: MA
COUNTRY: US
ZIP: 02110-2804
                                                                                                                                                                                                                                            STREET: 225 F
CITY: Boston
US-08-545-809A-105
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60 YAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETK-----VRGVHYYGMDV 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RECOMBINANT PEPTIDES DERIVED FROM THE MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND METHODS OF HUMANIZING ANTIBODY PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 75.2%; Score 491; DB 2; Length 129; Best Local Similarity 76.3%; Pred. No. 2.1e-40; Matches 100; Conservative 5; Mismatches 16; Indels
                                                               NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT SPLICATION DATA:

APPLICATION NUMBER: US/08/561,521

FLING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/186,269A

FILING DATE: 25-JAN-1994

ATTORNEY AGENT INFORMATION:

NAME: Smith, William L.

REFERENCE/DOCKET NUMBER: 15270-14

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-543-560

TELEPHONE: 415-543-5043

INFORMATION FOR SEQ ID NO: 45:

SEQUIRCE CHARACTERISTICS:
                                    Adhesion Molecule VLA-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 77, Application US/08525539A
Patent No. 6309636
GENERAL INPORMATION:
APPLICANT: DO COUTO, FERNANDO J.R.
APPLICANT: CERIANI, ROBERTO L.
APPLICANT: PETERSON, JERRY A.
TITLE OF INVENTION: MC3 ANTI-BA46 ANTITLE OF INVENTION: MC7HODS OF HUMANI
TITLE OF INVENTION: MC7HODS OF HUMANI
MUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: MORRISON & FOERSTER
755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 129 amino acids
amino acid
                                                                                                                                                        STREET: One Market Pl
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WGQGTTVTVSS 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-561-521-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-525-539A-77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 AQKFQGRVIMITIDISTSTAYMELRSLRSEDTAVYYCA--GRRGGFRFRPMDVWGQGIMVT 117
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Patent No. 584029
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
CORETING THEN PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-BC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 926372.6
FILING DATE: 23-SEP-1992
FILING DATE: 33-SEP-1992
FILING DATE: 07-BC-1995
FILING DATE: 01-UW-1994
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-UW-1994
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 36,107
RESERRENCE/DOCKET NUMBER: 28111/33308
FELING DATE: 01-UW-1994
ATTORNEY/AGENT INFORMATION:
NAME: DA-10 U-UW-1994
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
US-08-652-816A-19
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COMPUTER READABLE FORM:

WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FLING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FLING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, JT., ESQ.
REGISTRATION NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
     NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELEPHONE: 415-543-9600
TELEPHONE: 415-543-9600
TELEPHONE: 415-543-9600
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 36, Application US/09025769B; Patent No. 6300064; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (212) 596-9000
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                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                 PCT-US95-01219-45
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US-09-025-769B-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAISHVRQAPGQGLEWMGWINPYGNGDTN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAY-NGNTN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: An adhesion Molecule VLA-4
NUMBER OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREST: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.2%; Score 491; DB 3; Length 129; 76.3%; Pred. No. 2.1e-40;
       COMPUTER RELIGION TIER
MEDIUM TYPE: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,539A
FILING DATE: 14-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DYLAN, TYLER
REGISTRATION NUMBER: 27633-20001.21
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches
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FILING DATE: 25-JAN-1995
CLASSIFICATION: DATA:
PRIOR APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 45, Application PC/TUS9501219 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 706141
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 76.3
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 WGQGTTVTVSS 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
US-08-525-539A-77
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60 YAQKIQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETK-----VRGVHYYGMDV 112
                                                                                                                                  1 QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAY-NGNTN
                                                     10;
Ouery Match 75.2%; Score 491; DB 5; Length 129; Best Local Similarity 76.3%; Pred. No. 2.1e-40; Matches 100; Conservative 5; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5: James F. Haley, Jr., Esq. c/o Fish & Neave 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Knappik, Achim
APPLICANT: Knappik, Achim
APPLICANT: Back, Peter
APPLICANT: 11ag, Vic
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
CORRESPONDENCE ADDRESS:
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61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETKVRGVHYYGMDVWGQGTTVT 120
                                                                                                      61 AQKFQGRVIMIRDISISTAYMELSSLRSEDTAVYYCAR---WGGDGFYAMDYWGQGILVT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AQKLOGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETKVRGVHYYGMDVWGQGTTVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAVYYCAR---WGGDGFYAMDYWGQGTLVT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLVQSGAEVKKRGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGWINPNSGGTNY 60
                           1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGWINPNSGGTNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.1%; Score 490.5; DB 4; Length 120; 78.9%; Pred. No. 2.2e-40; ive 5; Mismatches 18; Indels 3
                                                                                                                                                                                                                                                                                                    Sequence 36, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
RAPPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Pluckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-490-070A-36
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 912-2020 INFORMATION FOR SEQ ID NO: 36: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 78.9'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: D.C.
COUNTRY: USA
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US-09-490-070A-36
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                                                                                                                       Length 120;
                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1251 Avenue of the Americas
STATE: New York
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CURRENT APPLICATION DATA:
APPLICATION NUBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Pack, Peter
APPLICANT: 1199, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Moroney, Simon
APPLICANT: Plucekthun, Andreas
ITILE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                                18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 75.1%; Score 490.5; DB 3; Best Local Similarity 78.9%; Pred. No. 2.2e-40; Matches 97; Conservative 5; Mismatches 18;
                                                                                                                   Score 490.5; DB 3
Pred. No. 2.2e-40;
5; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: MORPHO/S TELECOMMUNICATION INFORMATION: TELEPHONE: (212)596-9000
TELEFAX: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 59, Application US/09025769B Patent No. 6300064
                                                                                                                   75.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pacent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
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                                                                                                          Ouery Match
Best Local Similarity 78:99
Matches 97; Conservative
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            STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-36
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ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
amino acid
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Sequence 36, Application US/09490153
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ZIP: 20006

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRIN APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AuG-1995
ATTORNEY/AGENT INFORMATION:
NAME: COlin G. Sandercock, ESG.
RECISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 31,298
TELEFORMONICATION INFORMATION:
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TELEFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INF
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STREET: 1666 K Street, N.W., Suite 300
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                                                                                                                                                                                                                                                                            Sequence 59, Application US/09490070A
Patent No. 6695248
GENERAL INFORMATION:
APPLICANT Knappik, Achim
Hack, Peter
Ge, Liming
Moroney, Simon
TITLE OF INVENTION:
WUMBER OF SEQUENCES: 373
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MOLECULE TYPE: protein
US-09-490-070A-59
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RESULT 12 US-09-490-153-36

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61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETKVRGVHYYGMDVWGQGTTVT 120
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                                                                                                                                                                                                                                                            c/o Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
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                                                                   Pack, Peter
Ilag, Vic
Ge, Limin
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 75.1%; Score 490.5; DB 4; Best Local Similarity 78.9%; Pred. No. 2.2e-40; Matches 97; Conservative 5; Mismatches 18;
                                                                                                                                                                                                                                  STREET: 1251 Avenue of the Americas CITY: New York STATE: New York COUNTRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27, 794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
US-09-490-153-59
; Sequence 59, Application US/09490153
; Patent No. 6706494
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Ilag, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (212) 596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: <Unknown>TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
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61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETKVRGVHYYGMDVWGQGTTVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYM;HWPQAPQQGLEHMGWINPNSGGTNY 60
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                                                                                        COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,324

FILING DATE: 18-200

FILING DATE: 18-REB-1998

APPLICATION NUMBER: US/09/025,769

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

COMPUTER: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

COMPUTER: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

COMPUTER: 18-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 59, Application US/09490324

Patent No. 6828422

GENERAL INFORMATION:
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protain/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 490.5; DB 4
Pred. No. 2.2e-40;
5; Mismatches 18
    STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27, 794
REFERENCE/DOCKET NUMBER: MORPHO/5 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-490-324-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212)596-9000
TELEPRA: (212)596-9090
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 75.1%;
Best Local Similarity 78.9%;
Matches 97; Conservative
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COUNTRY: USA
                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARBTKVRGVHYYGMDVWGQGTTVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AQKFQGRVTMTRDTSISTAXMELSSLRSEDTAVYXCAR---WGGDGFYAMDYWGOGTLVT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEMMGWINPNSGGTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Gaps
                                                                                                                                                                                                                                                                                       COMPUTER: Floppy disk
COMPUTER: Eloppy disk
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
FRIDK APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
              Moroney, Simon
Plueckthun, Andreas
Plueckthun, Andreas
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.1%; Score 490.5; DB 4
78.9%; Pred. No. 2.2e-40;
tive 5; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27, 794
REFERENCE/DOCKET NUMBER: MORPHO/S TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear;

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-09-490-153-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 36, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 59
                                                                                                                                                                                                                                               ZIP: 10021
COMPUTER READABLE FORM:
Ge, Liming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 75.1°
Best Local Similarity 78.9°
Matches 97, Conservative
                                                                                                                                                                                 CITY: New York
STATE: New York
                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 VSS 120
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US-09-490-324-36
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Gaps

Sequence Sequence Sequence

207, Äpp 354, Appl 1562, App 1562, App 1562, App 133, Appl 1873, App 1610, App 1610, App 1610, App 1610, App 1190, App 1190, App 1190, App 1196, App 1315, Ap 1315, Ap 1315, Ap 1315, Ap 146, App 1472, App 1610, App 1610, App 1672, App 1672, App 1674, App 1778, App 1674, App 1778, App 1674, App 1674, App 1674, App 1674, App 1674, App

seduence sequence seq

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1 QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 653; DB 14; Length 123; 100.0%; Pred. No. 1e-54; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21, Application US/10330613
Publication No. US20030147809A1
GENERAL INFORMATION
APPLICATION NO. US20030147809A1
FILE REFERENCE: ABGENIX.02A
CURRENT APPLICATION NUMBER: US/10/330,613
CURRENT APPLICATION NUMBER: 0/346299
PRIOR APPLICATION NUMBER: 0/346299
PRIOR APPLICATION NUMBER: 0/346299
NUMBER OF SEQ ID NOS: 40 12-18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 123
US-11-031-485-42
US-11-031-485-42
US-10-041-860-207
US-10-645-838-62
US-10-645-838-62
US-10-29-880-748-1562
US-10-29-880-748-1562
US-10-29-880-748-1610
US-11-031-485-133
US-09-880-748-1610
US-11-031-485-133
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US-11-031-481-190
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US-10-293-418-1190
US-10-293-418-11354
US-10-293-418-1178
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US-10-293-418-1178
US-10-293-418-1178
US-10-293-418-1178
US-09-880-748-1178
US-09-880-748-1425
US-09-880-748-1425
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US-09-880-748-1586
US-09-880-748-1872
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    Best_Local Similarity 100.
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo Sapiens
US-10-330-613-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSS 123
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21, Appl
21, Appl
45, Appl
1921, Ap
1921, Ap
120, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243, App
325, App
42, Appl
                                                                                                                                   November 9, 2005, 11:40:37; Search time 68.3333 Seconds (without alignments) 753.137 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                             653
1 QVQLVQSGAEVKKPGASVKV......GVHYYGMDVWGQGTTVTVSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence Sequence
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14: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
                 GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-330-613-21
US-10-330-530-21
US-10-660-330-21
US-10-269-805-45
US-00-880-748-1921
US-11-031-485-120
US-11-031-485-120
US-10-041-860-31
US-10-041-860-325
US-10-665-383-42
                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                         1867879 segs, 418409474 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq length: 0
seq length: 200000000
                                                                                                                                                                                                                            US-10-660-357A-21
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Match 1
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90.8
90.0
90.0
89.5
88.2
88.2
88.2
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                                                                                                                                                                                                                                             Perfect score:
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653
587.5
587.5
584.5
576
576
576
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Minimum DB Maximum DB

Database

Searched:

Sequence:

Run on:

Sequence

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Gaps

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26459786011

Result No.

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61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETKV--RGVHYYGMDVWGQGTT 118
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PUBLICATION NO. US20030059937A1

GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/216,210

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR PLING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR PLING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR PLING DATE: 2001-05-25

NUMBER OF SQUING DATE: 2001-05-25
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                                                                                                                                                                                    US-10-269-805-45
; Sequence 45, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENDITON: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-72
CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR PILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 45
; LENGTH: 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 125;
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Pred. No. 5.8e-49;
4; Mismatches 6;
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CRGANISM: Homo sapiens
US-10-269-805-45
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ORGANISM: Homo sapiens
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Best Local Similarity
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Best Local Similarity
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                             VSS 123
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                                                                                                   US-10-330-230-21

Sequence 21, Application US/10330530

Publication No. US20030152514A1

GENERAL INFORMATION:
APPLICANT: Gudas, Jean

TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
FILE REFERENCE: ABGENIX.031A

CURRENT APPLICATION NUMBER: US/10/330,530

CURRENT APPLICATION NUMBER: US 60/346414

PRIOR FILING DATE: 2001-12-18

NUMBER OF SEQ ID NOS: 40

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 14; Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 653; DB 14; Length Best Local Similarity 100.0%; Pred. No. 1e-54; Matches 123; Conservative 0; Mismatches 0; Indels
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APPLICANT: Green, Larry L.
TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
TITLE OF INVENTION: ANTIGEN
FILE REFERENCE: ABGENIX.030C1
CURRENT APPLICATION NUMBER: US/10/660,357
CURRENT FILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PLING DATE: 2003-12-26
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21, Application US/10660357
Publication No. US20040115205A1
GENERAL INFORMATION:
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US-10-660-357-21
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US-10-330-530-21
121 VSS 123
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LENGTH: 123
TYPE: PRT
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LENGTH: 123
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61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETKVRGVHYYGMDVWGQGTTVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Grandly, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Feng, Xiao
APPLICANT: Feng, Xiao
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USE;
TITLE OF INVENTION: ANTIBODIES
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT APPLICATION NUMBER: 1002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 377
                                                                                                                                                                                                                                                                                                                                                                                             DB 20;
                                                                                                                                                                                                                                                                                                                                                                                     89.5%; Score 584.5; DB 20;
ilarity 91.1%; Pred. No. 3.6e-48;
Conservative 3; Mismatches 5;
                        APPLICANT: HAAK-FRENDSCHO, MARY
TITLE OF INVENTION: ANTIBODIES TO MAGCAM
FILE REFERENCE: ABX-PF6
CURRENT APPLICATION NUMBER: US/11/031,485
CURRENT FILING DATE: 2005-01-07
PRIOR FILING DATE: 2005-01-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin Ver. 3.3
SOFTWARE: Patentin Ver. 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 87.4
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
US-11-031-485-120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: homo sapiens
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Best Local Similarity
Matches 112; Conserv
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                                                                                                                                                                  61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETKV-----RGVHYYGMDVWGQ 115
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                                                                            1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
                                                                                                                                         61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETKV----RGVHYYGMDVWGQ
                                              QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY
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       5; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             JAPELICANT: Ruben et al.

JITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P2
CURRENT APPLICATION WHERE: US/10/293,418
CURRENT APPLICATION NUMBER: US/110/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/311,469
PRIOR PILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
PRIOR PPLICATION NUMBER: 60/295,499
PRIOR PLING DATE: 2001-03-25
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR PLING DATE: 2001-03-26
PRIOR PLING DATE: 2000-01-16
PRIOR PLING DATE: 2000-01-16
PRIOR PLING DATE: 2000-01-17
PRIOR PLING DATE: 2000-01-16
PRIOR PLING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247

**SEQ ID NO 1921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 587.5; DB 15; Length 251;
Pred. No. 4e-48;
4; Mismatches 6; Indels 5;
    6; Indels
    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1921, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
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Publication No. US20050232917A1
GENERAL INFORMATION:
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APPLICANT: MOLLOY, ELIZABETH
APPLICANT: KELLERMANN, SIRID-AIMEE
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Best Local Similarity 88.33
Matches 113; Conservative
  113; Conservative
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121 GTTVTVSS 128
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; ORGANISM: Homo sapiens
US-10-293-418-1921
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61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDHYYDSSDYLYYYYGLDVWGQG 120
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                                                                                                         1 QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60
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                                    4; Gaps
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Pred. No. 2.5e-47;
4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 42, Application US/10665383
Publication No. US2004014196941
GENERAL INFORMATION:
APPLICANT: Floege, Juergen
APPLICANT: Gazit, Gadi
APPLICANT: LaRochelle, William
APPLICANT: LaRochelle, William
TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
TITLE OF INVENTION: USING ANTI-PDGF-DD ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 42, Application US/11031485
Publication No. US20050232917A1
GENERAL INPORMATION:
APPLICANT: PULLEN, NICHOLAS
APPLICANT: MOLLOY, ELIZABETH
APPLICANT: RELLERMANN, SIRID-AIMEE
APPLICANT: RELERMANN, SIRID-AIMEE
APPLICANT: HAAK-FRENDSCHO, MARY
TITLE OF INVENTION: ANTIBODIES TO MACKAM
FILE REFERENCE: ABX-PF6
CURRENT APPLICATION NUMBER: US/11/031,485
CURRENT APPLICATION NUMBER: 60/535,490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: ABGENIX.052A
CURRENT APPLICATION NUMBER: US/10/665,383
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: 60/411,137
PRIOR FILING DATE: 2002-09-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 97
SOFTWARE: FastSEQ for Windows Version 4.0
Best Local Similarity 87.4%;
Matches 111; Conservative
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LENGTH: 127
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                                                                                                                                                     Sequence 243, Application US/10041860

Publication No. US2030157109A1

GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Tang, Xiao-Chi
APPLICANT: Feng, Xiao-Dong
APPLICANT: Feng, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: APPLICANT: Chen, Francine
APPLICANT: APPLICANT: And APPLICANT: Chen, Francine
APPLICANT: APPLICANT: Applicant APPLICANT: Corvalant
APPLICANT: APPLICANT: ADDITION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THERBOF
FILE REFERENCE: ABGENTX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT APPLICATION NUMBER: US/202-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FSELSEQ for Windows Version 4.0
SEQ ID NO 243
LENTH: 127
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Publication No. US20030157109A1

GENERAL INFORMATION:

APPLICANT: Corvain, Jose R.F.

APPLICANT: Feng, Xiao-Chi

APPLICANT: Feng, Xiao-Chi

APPLICANT: Teng, Xiao-Dong

APPLICANT: Reng, Xiao-Dong

APPLICANT: Reng, Xiao-Dong

APPLICANT: Reng, Xiao-Chi

APPLICANT: Washer, Richard

APPLICANT: Washer, Washe
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ORGANISM: homo sapiens
US-10-041-860-243
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|TTVTVSS 127
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121 TTVTVSS 127
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Query Match
Best Local Similarity 87.2%;
Matches 109; Conservative
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Best Local Similarity 87.2%;
Matches 109; Conservative
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                                           'ang, Xiao-Dong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-207
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                       APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                       Score 571.5; DB 2
Pred. No. 2.6e-46;
6; Mismatches 8
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Publication No. US2005022917A1
Publication No. US2005022917A1
APPLICANT: PULLEN, NICHOLAS
APPLICANT: PULLEN, NICHOLAS
APPLICANT: RELLERMANN, SIRID-AIMEE
APPLICANT: KELLERMANN, SIRID-AIMEE
APPLICANT: RELERMANN, SIRID-AIMEE
APPLICANT: HAAK-FRENDSCHO, MARY
TITLE OF INVENTION: ANTIBODIES TO MACKAM
FILE REFERENCE: ABX-PF6
CURRENT APPLICATION NUMBER: US/11/031,485
CURRENT FILING DATE: 2005-01-07
PRIOR PILING DATE: 2005-01-07
PRIOR FILING DATE: 2004-01-09
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Sequence 42. Application US/10041860

Publication No. US20030157109A1

GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
                                                                                                                                                                     Query Match
Best Local Similarity 87.9%;
Matches 109; Conservative 6
PRIOR FILING DATE: 2004-01-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 3.3
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SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 34
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Matches 108; Conservative
                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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US-11-031-485-34
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                                                       SEQ ID NO 42
LENGTH: 469
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Pred. No. 6.6e-46;
3; Mismatches 11; Indels
HAFLICANT: Gazit, Gaus,
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT AFPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4.2
LENGTH: 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine ...
APPLICANT: Grait, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
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Pred. No. 6.6e-46;
3; Mismatches 11;
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CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 207, Application US/10041860; Publication No. US20030157109A1; GENERAL INFORMATION:
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61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDVEYYYDGSGYYYFDYWGQGTL 120 qq

119 VTVSS 123 ||||| 121 VTVSS 125

ò qq

Search completed: November 9, 2005, 12:43:01 Job time : 69.3333 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

9, 2005, 12:25:58 ; Search time 13.2556 Seconds (without alignments) 892.802 Million cell updates/sec . November Run on:

US-10-660-357A-21 653 1 QVQLVQSGAEVKKPGASVKV......GVHYYGMDVWGQGTTVTVSS 123 score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:* Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | | de | | | SUMMARIES | |
|---------------|-------|----------------|--------|----|-----------|--------------------|
| Result
No. | Score | Query
Match | Length | DB | ΙD | Description |
| : | 559 | 85.6 | 129 | 2 | S36260 | Iq heavy chain V r |
| 7 | 549.5 | 84.2 | 124 | 7 | \$19665 | g heavy cha |
| ო | 533 | 81.6 | 122 | 7 | 836271 | chain V |
| 4 | 521 | 79.8 | 160 | ~ | PL0105 | nti-PR2 erythroc |
| S | 501 | 76.7 | 98 | ~ | S26919 | g heavy chain |
| 9 | 486.5 | 74.5 | 118 | 7 | PH1666 | g heavy |
| 7 | 483 | 74.0 | 127 | 7 | S34014 | g heavy chain V |
| 8 | 481 | 73.7 | 129 | ~ | S46393 | g heavy |
| σn | 480 | 73.5 | 119 | ~ | σ | g heavy |
| 10 | 477 | 73.0 | 131 | ~ | S21924 | g heavy chain V |
| 11 | 477 | 73.0 | 133 | ~ | Ŋ | g heavy |
| 12 | 477 | 73.0 | 627 | 7 | S14683 | g mu cha |
| 13 | 475.5 | 72.8 | 136 | ~ | 0960Н | g heavy |
| 14 | 474.5 | 72.7 | 132 | ~ | PH0954 | g heavy |
| 15 | 474 | 72.6 | 125 | ~ | S68170 | g heavy |
| 16 | 473 | 72.4 | 142 | ~ | A32483 | ь |
| 17 | 472.5 | 72.4 | | N | B32274 | g heavy |
| 18 | 7 | 72.1 | | 7 | PH0955 | g heavy chain |
| 19 | 469.5 | 71.9 | | ~ | 849530 | nti-Sm antibody |
| 20 | 68. | 71.7 | | 7 | S36265 | g heavy chain v |
| 21 | | 71.7 | 126 | 7 | B33548 | g heavy |
| 22 | 465 | 71.2 | 111 | ~ | S21925 | g heavy chain V |
| 23 | 464 | 71.1 | 123 | 7 | D33548 | g heavy chain V- |
| 24 | 61. | 70.7 | 122 | 7 | 095 | g heavy chain V |
| 25 | • | 7.07 | 136 | ~ | S31600 | g heavy chain V |
| 56 | 53. | 69.4 | 114 | ~ | PH1667 | g heavy chain V |
| 27 | 452.5 | 69.3 | 132 | ~ | 4639 | g heavy chain V |
| 28 | n | 69.1 | 131 | 7 | S26792 | g heavy cha |
| 29 | 449.5 | 68.8 | 120 | ~ | 3199 | g
be |

RESULT 2 S19665

Ig heavy chain V region (alpha-phOx15) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: \$19665; \$24442
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter A.Mol. Biol. 222, \$81-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on p A;Reference number: \$19663; MUID:92085276; PMID:1748994

A;Molecule type: mRNA A;Residues: 1-124 <MAR> A;Cross-references: EMBL:X61647 R;Jones, P.T. submitted to the EMBL Data Library, October 1991

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| chain | chain | chain | chain | chain | chain | chain | chain | chain | chain | chain | chain | chain | chain | chain | chain |
| heavy | heavy | heavy | heavy | heavy | heavy | heavy | heavy | heavy | heavy | heavy | heavy | heavy | heavy | heavy | heavy |
| Ig | Ig | I g | Ig | Ig | Ig | ΙĪ | Ig | Ig | PI | i BI | Ы | Ι | Iq | ы | Id |
| UNDH | 123623 | 0962 | 9257 | PH0952 | 0959 | 1957 | 3548 | 0783 | 1670 | 531596 | 1953 | B49590 | 526789 | 44151 | PH1665 |
| EI | 82 | PH | S2 | PH | PH | PH | A3 | \$2 | PH | 83 | H | B4 | 82 | 14 | H |
| - | 2 | 7 | 7 | 7 | ~ | 7 | | 7 | | ~ | 7 | ~ | ~ | 7 | 7 |
| 143 | 171 | 120 | 148 | 128 | 116 | 125 | 129 | 121 | 110 | 132 | 135 | 122 | 120 | 126 | 104 |
| 8. | 68.89 | 68.4 | 68.3 | 68.1 | 67.9 | 67.8 | 67.8 | 67.5 | 67.5 | 67.3 | 67.2 | 66.3 | 66.2 | 66.2 | 66.1 |
| 9 | | | 9 | 'n. | 5 | 143 | 443 | 441 | 0.5 | 9.5 | 439 | 433 | 2.5 | 432 | 31.5 |
| | 449.5 | 446.5 | 446 | 444 | 443 | 7 | • | | 44 | 43 | | | 43 | | 43 |

ALIGNMENTS

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S36260
Ig heavy chain V region (clone alpha-CEA4-8A) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36260 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36260 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36260
A;Fitle: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256, MUID:93178448; PMID:7679990
A;Reference number: S36256
A;Reseasion: S36260
A;Residue: pre-liminary; nucleic acid sequence not shown
A;Residues: 1-129 cGRIP.
A;Residues: 1-129 cGRIP.
A;Residues: 1-129 cGRIP.
A;Cross-references: EMBL:Z18851; NID:933124; PIDN:CAA79303.1; PID:9939903
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-96/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.6%;
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Matches 109, Conservative
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121 KGTTVTVSS 129
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RESULT 1
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Score 501;
Pred. No. 1
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F;132-144/Domain: J4 segment <JSG>
F;145-160/Domain: C region <CRG>
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Best Local Similarity 96.9%;
Matches 95; Conservative
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A;Residues: 1-98 <TOM>
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C;Species: Homo sapiens (man)
C;Date: 3: Amar-1990 #sequence_revision 31-Mar-1990 #text_change 26-Apr-1996
C;Accession: PLO105
R;Silberstein, L.E.; Litwin, S.; Carmack, C.E.
B;Silberstein, L.E.; Litwin, S.; Carmack, C.E.
A;Title: Relationship of variable region genes expressed by a human B cell lymphoma secr
A;Reference number: PLO106; MUID:89235583; PMID:2541221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: S36271

R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J EMBOJ. 12, 725-734, 1993

A;Title: Human anti-self antibodies with high specificity from phage display libraries. A;Reference number: S36256; MUID:93178448; PMID:7679990

A;Accession: S36271

A;Accession: S36271

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA
A,Accession: S2442
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Fesidues: 1-40, 'GLSGWOGSALTMVTQSILDK',61-118,'T',120-124 «JON»
A,Cross-references: EMBL:X61647, NID:g37667, PIDN:CA443828.1; PID:g1335368
A,Note: the difference for residues 41-60 results from misplacement of 10 bases in the C,Superfamily: immunoglobulin immunoglobulin homology
C,Superfamily: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V region (clone alpha-THY-29) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                   QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:218832; NID:933115; PIDN:CAA79284.1; PID:9939895 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F:15-98/Domain: immunoglobulin homology <IMM>
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81.6%; Score 533; DB 2; Length 122;
Best Local Similarity 85.2%; Pred. No. 2.7e-42;
Matches 104; Conservative 3; Mismatches 13; Indels
                                                                                                                                                                                                                                                                        Indels
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85.6%; Pred. No. 8.1e-44;
                                                                                                                                                                                                                                                                     5; Mismatches
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Matches 107; Conservative
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VT 122
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                                                                                                                                                                                                                           Query Match
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-160 <sILs.
A; Note: the authors translated the codon GAC for residues 108 and 109 as Glu
C; Comment: The antibody is one of the cold agglutinins that preferentially bind red blo
C; Superfamily: immunoglobulin v region; immunoglobulin homology
C; Superfamily: immunoglobulin bomology class
F; 1-19/Domain: signal sequence #status predicted <SIG>
F; 3-117/Domain: immunoglobulin homology class
F; 3-417/Domain: immunoglobulin homology class
F; 99-54/Region: complementarity-determining 2
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PHISES

To heavy chain V region (clone 6C9) - human (fragment)

C;Species: Homo sapiens (man)

C;Species: 14-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996

C;Accession: PHISES

R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.

J. Exp. Med. 178, 331-336, 1993

A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyl.
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: 826919
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: 826885; MUID:93021117; PMID:1404388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 AQNLQGRVTMTTDTSTSTAYMELRNLRSDDTAVYYCARAPGYCSGGGCYRGDDYWGQGTL 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 QVQLVASGAEVNKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISVYNGDTNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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1.9e-39;
ches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 521; DB 2;
Pred. No. 4.6e-41;
3; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
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61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETKVRGVHYYG------M 110
                                                                                                                                                                                                                                                                                                                                                       61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETKVRGVHYYGMDVWGQGTTVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGY----YYYYGMDVWGQGTTVT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gispecies: Homo sapiens (G6+ T-L33) - human (fragment)
Cispecies: Homo sapiens (man)
Cispecies: Homo Hosel
Rimartin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
Airlie: Evidence for somatic selection of natural autoantibodies.
Airlie: Evidence for somatic selection of natural autoantibodies.
Airlie: Podecession: PHO952; MUID:92202880; PMID:1552291
Airlie: Podecession: PHO961
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C.Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C.Accession: S21924; S21923
R.Friedman, D.F.
                                                                                                                                                                                                                  1 QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY
                                                                                                                                                                                                                                                  QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY
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                                                                                                                                                                 14;
                                                                                                          Length 129
C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
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C,Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
                                                                                                          73.7%; Score 481; DB 2; Length 12:
72.2%; Pred. No. 1.8e-37;
ive 7; Mismatches 16; Indels
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Pred. No. 2e-37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complementarity-determining
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F;51-67/Region: complementarity-determining
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                                                                                                                                                                                                                                                                                                                                                                                                                            111 DVWGOGTTVTVSS 123
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Best Local Similarity 78.09
                                                                                                       Query Match 73.7
Best Local Similarity 72.2
Matches 96; Conservative
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A, Accession: S21924
A, Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.Species: Homo sapiens (man)
C;Decies: Homo sapiens (man)
C;Decies: O2-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C;Accession: S34014; S30535
R;Mariette, X.; Tsapis, A.; Brouet, J.C.
Bur, J. Immunol. 23, 846-851, 1993
A.Title: Nucleotidic sequence analysis of the variable domains of four human monoclonal A;Reference number: S34001; MUID:93209281; PMID:7681398
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                                                                                                                                                                                                                                                                                                                                                                          1 QVQMVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEMMGMMNPSSGNTGY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 TMTTDTSTSTAYMELRSLRSDDTAVYYCARETKVRGV---HYYGMDVWGQGTTVTVSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RiFigini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A; Title: In vitro assembly of repertoires of antibody chains on the surface
A; Reference number: S46390; MUID:94254092; PMID:8196048
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C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
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A;Molecule type: DNA
A;Residues: 1-129 <FIG>
A;Cross-references: EMBL:231680; NID:9509786; PIDN:CAA83485.1; PID:91335146
                                                                                                                                                                                                                                                                                                                                          9 AEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNYAQKLQGRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY
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                                                                                                                                                                                                                                       Length 118;
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                                              A,Molecule type: mRNA
A;Residues: 1-118 <HIL>
A;Resrimental source: B cell
c;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-127 <MAR>
A;Cross-references: EMBL:Z18321
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                           Indels
A; Reference number: PH1642; MUID:93301610; PMID:8315388
                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                     Score 486.5; DB
Pred. No. 5e-38;
6; Mismatches 1
                                                                                                                                                                                                                                  ch 74.5%;
1 Similarity 79.7%;
94; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig heavy chain V region - human
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Best Local Similarity
                     PH1666
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C; Keywords: immunoglobulin; membrane protein
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Matches 9
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Fixibles, T.G.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.

Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1999

From the content of the
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                              A;Residues: 1-131 <FR1>
A;Cross-references: EMBL:X60505; NID:g33565; PIDN:CAA43025.1; PID:g33566; EMBL:X60504;
C;Genetics:
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C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C;Accession: C33548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OVOLVPSGAEVKKPGASVKVSCKASGYTFTSFGISWVROAPGOGLEWMGWISVYNGDTNY
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A;Residues: 1-627 <FRI>
A;Cross-references: EMBL:X17115; NID:g33450; PIDN:CAA34971.1; PID:g33451
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                            Length 131;
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                                                                                                                                                                                                                                                              C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;34-117/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text
C;Accession: S14683; S06047.
S;Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
Nucleic Acids Res. 18, 4278, 1990
A;Title: Complete nucleotide sequence of the membrane fo
A;Reference number: S14683; MUID:90332450; PMID:2115996
A;Accession: S14683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
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Pred. No. 4.3e-37;
                                                                                                                                                                                                                                                                                         Score 477; DB : Fred. No. 4.2e-3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Mismatches
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                                                                                                                                                                                                                                                                                            73.0%;
91.8%;
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                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 91.87
Matches 90, Conservative
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Best Local Similarity
Matches 97; Conserv
                                                                                                                             A; Introns: 16/1
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80 AQKFQGRVIITADESTSTAYMELSSLRSEDTAVYYCAK-TGILGPYSSGWYPNSDYYYYG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----VHYYG 109
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Dacession: PH0954
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Tills: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0960
                                                                                                                                                                                                                                                                                                                                                                            20 ÓVOLVÓSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYALSWVRQAPQQGLEWMGGIIPIFGTANY
                                                                                                                                                                                                                                                                                                          1 QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY
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                                                                                                                                                                                                                                12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R.Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
L. Exp. Med. 175, 983-991, 1992
A.Title: Evidence for somatic selection of natural autoantibodies.
A.Reference number: PH0952; MUID:92202880; PMID:1552291
A.Accession: PH0960
                                                                                                                                                   Length 627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-136 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                            18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETKVRG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region (G6+ T-L30) - human (fragment)
F:1-15/Domain: signal sequence #status predicted <SIG
F:16-627/Product: Ig mu chain #status predicted <WAT>
F:34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                   Score 477; DB 2;
Pred. No. 2.2e-36;
                                                                                                                                               Query Match
73.0%; Score 477; DB
Best Local Similarity 72.4%; Pred. No. 2.2e
Matches 97; Conservative 7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;31-35/Region: complementarity-determining 1 F;36-50/Region: framework 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;51-67/Region: complementarity-determining 2 F;68-98/Region: framework 3
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Ig heavy chain V region - human (fragment)
NyAlternate names: anti-cytomegalovirus glycoprotein B antibody
C;Species: Homo sapiens (man)
C;Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Jan-2000
C;Accession: 568170
R;Boeldicke, T.; Haase, B.; Boecher, M.; Lindenmaier, W.
R;Boeldicke, T.; Haase, B.; Boccher, M.; Lindenmaier, W.
A;Title: Human monoclonal antibodies to cytomegalovirus. Characterization and recombinan
A;Reference number: 568170; MUID:96128166; PMID:8536681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QYQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPQQGLEWMGGIIPIFGTANY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rosidues: 1-125 <BOE>
A;Cross-references: GB:S80750; NID:g1246061; PIDN:AAB35861.1; PID:g1246062
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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8
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72.6%; Score 474; DB 2; Length 125;
Best Local Similarity 74.2%; Pred. No. 7.6e-37;
Matches 95; Conservative 9; Mismatches 16; Indels
                                                                                                       Superfamily: immunoglobulin V region; immunoglobulin homology Keywords: heterotetramer; immunoglobulin 1-30/Region: framework 1
                    A Status: nucleic acid sequence not shown
A, Molecule type: DNA
A, Residues: 1-132 cMAR>
C, Superfamily: immunoglobulin V region; immunoglob
C, Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology < IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;58-98/Region: framework 3
F;99-120/Region: complementarity-determining 3
F;99-120/Region: complementarity-determining 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 WGGGTTVTVSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 VWGQGTTVTVSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTTVTVSS 123
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A; Accession: PH0954
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(C1903) 274A (C190A) 21117

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                                                          November 9, 2005, 11:46:52; Search time 63.5038 Seconds (without alignments) 991.843 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 QVQLVQSGAEVKKPGASVKV......GVHYYGMDVWGQGTTVFVSS 123
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065zc8
09brv0
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0901195
0901194
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0660030
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0690722
0901189
0600161
001743
062087
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P23083
Q924q6
Q6n095
Q8vcx7
Q9qxe9
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                                                                                                                                                                                                    1612378
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                              1612378 segs, 512079187 residues
                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
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Q6N030
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Q6ZPB7
Q6PJB2
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HV02_MOUSE
Q924P9
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HV1G HUMAN
Q924Q6
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Maximum Match 100%
Listing first 45 summaries
                                        - protein search, using sw model
                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
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0652C8
09BRV0
07Z7P5
09UL95
09UL94
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Q9GYZ2
Q9UL89
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O6PJF1
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2: uniprot_trembl:*
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seq length: 200000000
                                                                                                      US-10-660-357A-21
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Match Length DB
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                                                                                                                                              Scoring table: .
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Maximum DB
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                                                            Run on:
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| :4 mus musculu | Q9z1c4 | Q9Z1C4 | ~ | 118 | 58.9 | 384.5 | 42 |
|----------------|--------|------------|---|-----|------|-------|----|
| 10 mus musculu | P06330 | HV51_MOUSE | - | 118 | 59.0 | 385.5 | 44 |
| 12 mus musculu | Q92582 | 092552 | N | 170 | 59.1 | 386 | 43 |
| 7 mus musculu | P01757 | HV13_MOUSE | Н | 117 | 59.1 | 386 | 42 |
| :1 mus musculu | Q91wt1 | Q91WT1 | ~ | 481 | 59.3 | 387 | 41 |
| :1 mus musculu | Q7tmk1 | Q7TMK1 | N | 470 | 59.3 | 387 | 40 |
| of mus musculu | Q924p | Q924P7 | ~ | 145 | 59.3 | 387.5 | 39 |
| 75 mus musculu | 09j175 | Q9JL75 | 0 | 109 | 59.5 | 388.5 | 38 |
| 98 homo sapien | 09729 | Q9Y298 | ~ | 150 | 59.6 | 389 | 37 |
| | Q92583 | 092553 | ~ | 147 | 59.6 | 389 | 36 |
| 12 mus musculu | Q924Q2 | 092402 | ~ | 142 | 59.6 | 389 | 35 |
| 19 mus musculu | 092449 | 092409 | ~ | 145 | 59.6 | 389.5 | 34 |
| 24 mus musculu | Q991c4 | Q99LC4 | ~ | 463 | 59.8 | 390.5 | 33 |
| cl mus musculu | Q924r1 | Q924R1 | ~ | 145 | 59.8 | 390.5 | 32 |

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 AQNLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAKDQSYTTIPNDAFHIWGQGTMVT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 QVQLVQSGAEVKKPGASVKVSCKASGYTFSDHSITWLRQAPGQGLEWIGWISAYSGQTYY 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY
                                                                                                                                                                                                                                  TISSUE=Human rectum tumor;
TISSUE=Human rectum tumor;
The German Human cDNA Consortium;
The German Human cDNA Consortium;
A Wambutt R., Haubner D., Newes H.W., Weil B., Amid C., Osanger A.,
Fobo G., Han M., Wiemann S.,
L. Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBLSP: PO1751; Jac.
REMBL: BX640625; CAR45779.1; -.
RICEPTO: IPR003599; IG.
RICEPTO: IPR003109; IG.
RICEPTO: IPR003109; IG.
RICEPTO: IPR0031006; IG.
RICEPTO: IPR0031006; IG.
R. RICEPTO: IPR0031006; IG.
R. RICEPTO: IPR0031006; IG.
R. RICEPTO: IPR0031006; IG.
R. SMART; SM00409; IG.; 4.
SMART; SM00406; IG.; 4.
SMART; SM00406; IG. II.KE; 4.
R. SMART; EMS00310; IG. II.KE; 4.
R. PROSITE; PSS0835; IG.—MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 501; DB 2; Length 500;
Pred. No. 5.6e-45;
9; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         500 AA; 54160 MW; 3C423A17D65A41E4 CRC64;
                                                                05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
Hypothetical protein DKFZp686C02220 (Fragment).
Name=DKFZp686C02220;
                               500 AA
                                                             (TrEMBLrel. 27, Created)
                               PRT;
                                                           05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 76.7%;
1 Similarity 77.2%;
95; Conservative
                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
NON TER 1
SEQUENCE 500 AA; 5
                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                      NCBI_TaxID=9606;
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                                              Q6N091;
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0924q1 0921a6 0652r6

Q921A6 Q65ZR6

Gaps

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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Morer T., Max S.I., Wang J., Heiseh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casrainci P., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Weckernan K.J., Malke J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rachards S., Worley K.C., Hale S., Garcia A.M., Robrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mitting M., Andan A., Young A.C., Shevchenko Y., Bouffard G.G.,
M. Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.;

""Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                     61 AQRFQGRVTMTRDTSISAAYMEVSRLRSDDTAVYYCAREG--TGSAIYGMDVWGQGTLVT 118
                                                                                                                                                                      61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETKVRGVHYYGMDVWGQGTTVT 120
                                                                        1 QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60
                                                                                                     1 QVQLVQSGAEVKKRGDSVKXVSCKASGYTFSDHYMHWYRQAPGQGLEWMGWIDPNNGDTRF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Prostate;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.4%; Score 472.5; DB 2; Length 500; 71.1%; Pred. No. 6.3e-42; ive 10; Mismatches 22; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
REL; BC005551; AAH05951.1; -.
RHSSP; P01876; 10W0.
R InterPro; IPR003100; Ig_1ike.
R InterPro; IPR003100; Ig_MHC.
R InterPro; IPR003306; Ig_MHC.
R InterPro; IPR003306; Ig_MHC.
R InterPro; IPR003596; Ig_WHC.
R Pfam; PF07654; C1-set; Z.
R Pfam; PF07654; C1-set; Z.
R Pfam; PF07654; C1-set; Z.
Pred. No. 2e-42;
6; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     500 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
75.6%;
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Best Local Similarity 71.1
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.
                          93; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGC27165 protein.
Homo sapiens (Human)
Best Local Similarity
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                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETKV------RGVHYYGMDVW 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYYMMVRQAPGQGPEMMGVINPSGGSARY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.1%; Score 490.5; DB 2; Length 159; 72.3%; Pred. No. 2.1e-44; ive 13; Mismatches 16; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 244;
                                                                                                                                                                                                                                                                                                                                          Tilson M.D.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; AY039025; AAK82649.1; -.
HSRP; P01869; 1AE6.
InterPro; IPR007110; Ig-like.
InterPro; IPR007586; Ig-v.
SMART; SM004406; IGv; I.
PROSITE; PS0835; IG LIKE; 1.
SEQUENCE 159 AA; I7497 MM; 5D29537E881FAF02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26127 MW; 4B1F17868338F2BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97362799; PubMed=9219263;
Kontermann R.B., Wing M.G., Winter G.;
"Complement recruitment using bispecific diabodies.";
M.B. Biotechnol. 15:629-631(1997).
EMBL; Y13057; CAA73500.1; -.
InterPro; IPR00110; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Single-chain Fv (Fragment).
                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.6%; Score 474; DB 2;
                                                 159 AA
                                                                                                                                                                      Putative matrix cell adhesion molecule-3.
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                                                 PRT;
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SWART; SM00409; IG; 2.
SWART; SM00406; IGv; 2.
PROSITE; PS50835; IG LIKE; 2.
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 72.3%
nes 94; Conservative
                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GQGTTVTVSS 123
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                                                                                                                                                                                                   Homo sapiens (Human)
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SEQUENCE
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                                                                   096080
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RESULT 2
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20 QVHLVQSGAEVKKPGASVKLSCKTSGYNFSSYDLIWVRQAPGQGLEWMGWISAHNGDTKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                        137 VSS 139
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01-MAY-2000
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SEQUENCE
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Best Local
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A Klausner R. D., Collins F. S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Bordrehnko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKennan R.J., McKernan K.J., Maalek J.A., Gunzardne P.H.,
Richards S., Worley K.C., Hale S., Garria A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rabey J., Helton E., Ketterman M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Jones S.J., Marra M.A.,
Jones S.J., Marra M.J.,
Jones S.J., Marra M.J.,
Jones S.J., Marra M.J.,
Jones S.J., Marr
                                                                                                                                                                                                                                     AQKLQGRVTWTTDTSTSTAYMELRSLRSDDTAVYYCAR----ETKVRGVHYYGMDVWGQ 115
                                                                       QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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EMBL; BC051328; AAH51328.1; -.
HSSP; P01857; 1HZH.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             469 AA.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
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Interpro: IPR003597; Ig_cl.
Interpro: IPR003065; Ig_MIC.
Interpro: IPR003065; Ig_V.
Pfam; PP07654; Cl-set; J.
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                                                                                                                                                                                                                                                                                                                                    GTTVTVSS 123
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140 GTTVTVSS 147
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Best Local Similarity
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1;
                                 61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETKVRGVHYYGMDVWGQGTTVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AQKVQGRVTMTRDTTISTAYMELSRLRSDDTAVYYCARSQGGRIAAAGDAFDIWGQGTM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVOLVESGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 464; DB 2; Length 125;
Pred. No. 1.1e-41;
9; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clin. Immunol. Immunopathol. 87:184-192 (1998).
EMBL, AF035019; AAD56255.1; -.
HSSP; P01751; INQB.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                  125 AA
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61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETKVRGVHY-----YGMDVWGQ 115
                       61 AQKFQGRVTWIRDISTSTVYWELSSLRSEDTAVYYCA-----RGLYVVVPAAFSRFDYWG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 APRFQGRVTWTRDASFSTAYMDLRSLRSDDSAVFYCAKSDPFWSDYYNFDYSYTLDVWGQ 139
  61 AQKLQGRVTMTIDTSTSTAYMELRSLRSDDTAVYYCARETKVRGVH-----YYGMDVWG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 QTQLVQSGAEVRKPGASVRVSCKASGYTFIDSYIHWIRQAPGHGLEWVGWINPNSGGTNY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 20-147.

Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;

(In) Bach M.K. (eds.);

Immediate horsersensitivity: modern concepts and developments, pp.1-36, marcel Dekker, New York (1978).

-I- MISCELLANEOUS: This epsilon chain was isolated from a myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=83065234; bubMed=6815656;
MEDLINE=83065234; bubMed=6815656;
MEDLINE=83043 and H.V., Houghton M., Derbyshire R.B., Viney J., Bell L.O., Gould H.J.;
"Cloning and sequence determination of the gene for the human "mumoglobulin epsilon chain expressed in a myeloma cell line.";
Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
6-OCT-2001 (Rel. 40, Last sequence update)
65-JUL-2004 (Rel. 44, Last annotation update)
1g heavy chain V-I region ND precursor (Fragments).
1d heavy pains (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68.8%; Score 449.5; DB 1; Length 147; 67.2%; Pred. No. 4.8e-40; ive 13; Mismatches 24; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain V-I region ND.
Ig-like.
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16491 MW; 948F9F72A5366C20 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein.
SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin V region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T -> V (in Ref. 2).
IH -> HI (in Ref. 2).
VG -> GV (in Ref. 2).
Missing (in Ref. 2).
                                                                                                                                                                                                                                                 147 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP, P01751, INOB.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SMO0406; IGv; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct protein sequencing; Immunogle
Pyrrolidone carboxylic acid; Signal.
SIGNAL
                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86; Conservative
                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131
20
21
21
21
54
68
125
                                                                                         115 OGTTVTVSS 123
                                                                                                                     116 QGTLVTVSS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 GTTVTVSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                 HV1C HUMAN P01744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
DOMAIN
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DISULFID
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CONFLICT
NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 69.0%; Score 450.5; DB 2; Length 124; Best Local Similarity 70.5%; Pred. No. 3.1e-40; Matches 91; Conservative 10; Mismatches 17; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; MEDLINE=98277139; Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.; "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                      "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
SEQUENCE FROM N.A. MEDINE=98177139; PubMed=9614934; DOI=10.1006/clin.1998.4531; MEDINE=98277139; Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                  69.4%; Score 453; DB 2; Length 119; 74.0%; Pred. No. 1.6e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                               20; Indels
                                                                                                                                                                                                                                                                                                                                        119 AA; 13205 MW; 13E64F5345F4A16E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;
                                                                                                    fetus...;

Clin. Immunol. Immunopathol. 87:184-192(1998).

EMBL; APO35020; AA556256.1;

HSSP; P01751; INQB.

InterPro; IPR007110; Ig-like.

InterPro; IPR003565; Ig-v.

SMART; SM00406; IGV; I.

PROSITE; P850835; IG_LIKE; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ciin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035022; AAD56258.1; -.
HSSP; P01751; INQB.
InterPro; IPR007110; Ig-like.
SMART; SM00406; IGV; I.
PROSTIE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                               8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                               91; Conservative
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                                                                                                                                                                                                                                                                                                                     119
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Gaps

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95 AQRFQGRVSMTRDTSTSTIYMELSSLRSEDTAMFFCARAGPGYGTSASYY-FDYWGQGTL 153
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                      TISSUE-Human rectum tumor;
The German Human cDNA Consortium;
Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
Submitted (Aug-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX640710; CAE45829-1;
HSSP; P01751; 1A6W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Monoclonal anti-idiotypic antibody NP30 heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 66.8%; Score 436; DB 2; Length 119; Best Local Similarity 69.9%; Pred. No. 1.1e-38; Matches 86; Conservative 12; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                            67.2%; Score 438.5; DB 2; Length 70.4%; Pred. No. 2.8e-38; Live 12; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECUENCE FROM N.A.
SONG X.T., Feng Z.Q., Guan X.H.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF282622; AAG01452.1; --
HSSP; P01751; 1A6W.
InterPro; IPR007110; 1g-11ke.
InterPro; IRR003596; Ig_v.
SMART; SM00406; IGv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              498 AA; 54125 MW; 40B3208A84E03B46 CRC64;
                                                                                                                                                                                                                                                                                            PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                     InterPro; IPR007159; IG.
InterPro; IPR007110; Ig-like.
InterPro; IPR0073597; Ig_C1.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
SMART; SM00409; IG; 4.
SMART; SM00407; IGC1; 3.
SMART; SM004007; IGC1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 70.4
88; Conservative
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                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
NON TER 1
SEQUENCE 498 AA; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 VTVSS 158
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        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119
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                                                                                                                                                                                                                                                                                             RY [1]

SEQUENCE FROM N.A.

RC TISSUE-Human rectum tumor;

RG The German Human cDNA Consortium;

R Poustka A., Albert R., Moosmayer F., Schupp I., Wellenreuther R.,

R Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;

RIBL, Bx640724, CAE45841.1; -.

RBBL, Bx640724, CAE45841.1; -.

RRSP; P01864; AAO.

RICEPTO; IPR001359; Ig.

RICEPTO; IPR001406; Ig.

REART; SM00409; IG; 3.

REART; SM00406; IGv; 1.

REART; RS00241; HTH ARAC_FAMILY 1; UNKNOWN 1.

REART; PS002815; IG. LIKE; 4.

REART; REART; RICEPTO; IRROWN 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                Eukaryora, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.5%; Score 440.5; DB 2; Length 518; 69.9%; Pred. No. 1.8e-38; ive 13; Mismatches 23; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 518 AA; 57019 MW; 93B5F98613BF6382 CRC64;
                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686016217 (Fragment).
Name=DKFZp686016217;
                                                                                                       Ą
                                                                                                                                                                                    Hypothetical protein DKFzp686I15212 Name=DKFzp686I15212;
                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86; Conservative
                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
140 GTTVTVSS 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
                                                                                                                                                                                                                         Homo sapiens (Human)
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Q6N041;
                                                                                                     O6N030
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Matches
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SEQUENCE FROM N.A.
TISSUE=Lung;
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05-JUL-2004
                                                                                                                                                                                         and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QGRVTMITIDISTSTAYMELRSLRSDDIAVYYCARETKVRGVHYYGMDVWGQGTTVTVSS 123
QVQLVESGAEVRKPGASVRVSCKASGYTFTGYYMNWVRQAPGHGLEWIGYINPSRGYTNY
                               5 VQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWLGWISAYNGNTNYAQKL
                   AQXLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETKVRGVHYYGMDVWGQGTTVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                    "Myošin-reactive autoantibodies in rheumatic carditis and normal fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035025; AAD56261.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUB=Glandular pool- thyroid;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDINE-98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; WHO X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 116;
                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 419.5; DB 2; Length
Pred. No. 6e-37;
8; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              12605 MW; C8F9131DE13EA898 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                          Created)
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INTEXPRO; 1PR007110; 1g-like.
INTEXPRO; 1PR001596; 1g_v.
SMART; SW00406; 1Gv; 1.
PROSITE; PS50815; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 72.3%;
Matches 86; Conservative 8
                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2004 (TrEMBLrel. 26,
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                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein. Homo sapiens (Human).
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PIR; PH1671; PH1671.
                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                    116 AA;
                                                             VSS 123
                                                                                VSS 119
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SEOUENCE
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                                                                                                                  RESULT 13
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A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Alachar R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Antschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

R. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

R. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R. Brownstein M.J., WcKernan K.J., Mallek J.A., Gunarane P.H.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R. Richards S., Worley W. Green E.D., Dickson M.C.,

R. Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R. Richards S.L., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Tophersation and initial analysis of more than 15,000 full-length human
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypotherical protein. SEQUENCE 480 AA; 51997 MW; 2E286C57E4F0ED65 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Pred. No. 5.3e-36;
9; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    480 AA.
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INTERPRO 1 PR003199, 19.
INTERPRO 1 PR003199, 19.
INTERPRO 1 PR003597, 19.
INTERPRO 1 PR003596, 19.
FAM. PF07654, CI-SEL; 2.
SWART; SW00409, 1G; 4.
SWART; SW00407, 1Gcl; 3.
SWART; SW00407, 1Gcl; 3.
PROSITE; PS083599; 1G LIKE; 4.
PROSITE; PS08299; 1G LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BC065733; AAH65733.1;
HSSP; P01751; 1A6W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA sequences."
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Attausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Attausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A histchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A stapleton M., Soares M.B., Bonaldo M.F., Carahnoi P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunstane P.H.,
A Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
A Hakton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Jones S.J., Marra M.A.,
A nones S.J., Marra M.A.,
A marra M.A.,
A nones S.J., Marra M.A.,
A marra M.A.,
A nones S.J., Marra M.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Gaps
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.9%; Score 417; DB 2; Length 480; 66.4%; Pred. No. 5.3e-36; ive 10; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO16381; AAH16381.1; -.
HSSP; P01881; IADO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 480 AA; 52586 MW; 64DC641AE47CD6C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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InterPro; IPR003599; IG.
InterPro; IPR003597; IG_CI.
InterPro; IPR003597; IG_MIC.
InterPro; IPR003596; IG_WIC.
InterPro; IPR003596; IG_WIC.
InterPro; IPR003596; IG_WIC.
SWART; SW00409; IG; Z.
SWART; SW00400; IG; J.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 66.48
Matches 87; Conservative
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TISSUE=Lung;
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Corres Mande Lands Course

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9, 2005, 11:43:32 ; Search time 73.3684 Seconds (without alignments) 627.306 Million cell updates/sec
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1 QVQLQESGPGLVKPSQTLSL......DRETAGFDYWGQGTLVTVSS 119
GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                Copyright
                                                                                                    November
                                                                                                                                                                                                                                               Scoring table:
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2105692 Total number of hits satisfying chosen parameters:

2105692 seqs, 386760381 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries A Geneseq 16Dec04:* Database :

geneseqp20028:* geneseqp2003as:* geneseqp2003bs:* geneseqp20048:* geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Description | Adc99796 Anti-huma | Add05400 Anti-MUC1 | Adf09838 Human ant | Adc99784 Anti-huma | Add05388 Anti-MUC1 | Adf09826 Human ant | Aab62765 Human HIV | Aab62745 Human HIV | Adp03968 Murine-ex | Adp03870 Murine-ex | Adp03970 Murine-ex | Adp03879 Murine-ex | Adp03878 Murine-ex | Aab62775 Human HIV | | | Adk52356 Human ant | Adp03974 Murine-ex | Adp03873 Murine-ex | Abp45983 Human BLy | 0 | ~ | Abp98691 Human GAH | Abp98683 Human GAH | 9 Human |
|-----|-----------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|----------|--------------------|--------------------|--------------------|--------------------|----------|----------|--------------------|--------------------|----------|
| | ID | ADC99796 | ADD05400 | ADF09838 | ADC99784 | ADD05388 | ADF09826 | AAB62765 | AAB62745 | ADP03968 | ADP03870 | ADP03970 | ADP03879 | ADP03878 | AAB62775 | ADJ80377 | ADP03961 | ADK52356 | ADP03974 | ADP03873 | ABP45983 | ADG96810 | AAR30143 | ABP98691 | ABP98683 | ADG43869 |
| | ength DB | 119 7 | 119 7 | 119 7 | 117 7 | 117 7 | 117 7 | 122 4 | 123 4 | 118 7 | 123 7 | 119 7 | 123 7 | 123 7 | 120 4 | 121 7 | 119 7 | 446 8 | 120 7 | 120 7 | 252 5 | 252 7 | 119 2 | 119 6 | 119 6 | 119 7 |
| ٠., | Query
Match Length | 100.0 | 100.0 | 100.0 | 88.2 | 88.2 | .88.2 | 87.7 | 87.2 | 87.0 | 86.8 | 9.98 | 86.3 | 86.3 | 86.2 | 86.1 | 86.0 | 96.0 | 85.9 | 85.9 | 85.8 | .85.8 | 85.7 | 85.7 | 85.7 | 85.7 |
| | Score | 636 | 636 | 636 | 561 | 561 | 561 | 558 | 54 | 553.5 | 552 | 551 | 549 | 549 | 548 | 547.5 | 547 | 547 | 4 | 546.5 | 4 | 545.5 | 545 | 545 | 545 | 545 |
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| Adg28266 Method of Adg03874 Murine-ex Adg03874 Murine-ex Adw78433 Antibody Abb97976 Heavy cha Adg88414 anti-Ob-R Adg0876 Anti-huma Add05380 Anti-huma Add05380 Anti-mUCI Adf09818 Human ant Adg03877 Murine-ex Adg03871 Murine-ex Adg03981 Murine-ex Adg03982 Murine-ex Adg03982 Murine-ex Adg03982 Murine-ex Adg03982 Murine-ex Adg039876 Murine-ex Adg03976 Murine-ex Adg03976 Murine-ex | Aau81276 Human trk
Ab119829 Human VEG
Adh13871 Human vas
Adp03969 Murine-ex |
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ALIGNMENTS

anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast; Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 25. ADC99796 standard; protein; 119 AA (first entry) lung cancer; human. 01-JAN-2004 ADC99796; RESULT 1 ADC99796

26-DEC-2002; 2002WO-US041581. 28-DEC-2001; 2001US-0346299P. WO2003057838-A2. sapiens. 17-JUL-2003. Ношо

WPI; 2003-587113/55. (ABGE-) ABGENIX INC N-PSDB; ADC99798 Gudas J;

New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.

Claim 1; SEQ ID NO 25; 78pp; English.

The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the pancreatic or colorectal tumours, specifically melanoma, oesophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung cancers as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody

Pred. No. 1.1e-48;

100.0%;

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Best Local Similarity
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                                                                                                                                                            61 YNPSEKSRITLSVDTSKNOPSEKLNSMTAADTAVYYCARDRETAGFDYWGQGTLVTVSS 119
                                                                                                                                                                            YNPSLKSRITLSVDTSKNQFSLKLNSMTAADTAVYYCARDRETAGFDYWGQGTLVTVSS 119
                                                                                                                                                                                                                                                                                                                                                                monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
                                                                                                                          QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY
                                                                                                                                                                                                                                                                                                                                       Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 25.
                                                                                                        1 QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY
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                                                  Length 119;
                                                     100.0%; Score 636; DB 7; 100.0%; Pred. No. 1.1e-48;
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Mismatches
heavy chain protein of the invention
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                                                                              Conservative
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N-PSDB; ADD05402.
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Best Local Similarity
Matches 119; Conserv
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                          Sequence 119 AA;
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DB 7; Length 119;

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Query Match

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                                                                                                                                                                                                                           61 YNPSLKSRITLSVDTSKNQFSLKLNSMTAADTAVYYCARDRETAGFDYWGQGTLVTVSS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell proliferation inhibition; MUC18 tumour antigen; anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour; carcinoma; cancer; malignancy; heavy chain; human.
Gaps
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100.0%; Pred. No. 1.1e-48;
ive 0; Mismatches 0;
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   119; Conservative
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01-JAN-2004 (first entry)
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                                                                                                                                                                                                                                                                     anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the cell surface such as tumnours, specifically melanoma, oscophageal, pancreatic or colorectal tumnours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody heavy chain protein of the invention.
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Pred. No. 4.9e-42;
9; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 13; 78pp; English.
                                                                                      ADC99784 standard; protein; 117 AA.
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Matches 105; Conservative
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                                                                                                                                                                                                                                                                                                                                             lung cancer; human.
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                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                 ADC99784;
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The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds WUC18, and contacting the tumour with the antibody resulting inhibited proliferation of the cells. The monoclonal antibody has cytostatic and can be used in the production of a vaccine. The monoclonal antibodies against the WUC18 antigen are useful for diagnosing and treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or tumour metastasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-WUC18 antibody heavy chain, variable region,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 13.
                                                                                   monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccin
antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY
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88.2%; Pred. No. 4.9e-42;
iive 9; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell proliferation inhibition; MUC18 tumour antigen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 13; 87pp; English.
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Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gudas J, Bar-Eli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-577496/54.
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                                                                                                                                                                                                                                                                                    WO2003057006-A2.
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                                                                                                                                                                                                         Homo sapiens.
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The present invention provides the protein and coding sequences for the variable regions of human monoclonal antibodies which are immunoreactive with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120. These can be used in diagnosis and therapy of HIV-1 infection
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                                                                                                                                                                         Novel human monoclonal antibody immunoreactive with human immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1 in biological sample and providing passive immunotherapy to HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus-1; HIV-1; human monoclonal antibody; envelope glycoprotein; gp120; diagnosis.
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Pred. No. 9.5e-42;
9; Mismatches 5; Indels
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                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                      English.
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     99US-0141701P
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Best Local Similarity 86.8%;
Matches 105; Conservative
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                                                                                                                                                                                                                                                                      Claim 1; Page 63; 81pp;
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                                                                               Reitz MS
                                                                                                                  WPI; 2001-112438/12.
N-PSDB; AAF29066.
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 122 AA;
                                                                                                                                                                                                                                 infected mammal.
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     30-JUN-1999;
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                                                                               Watkins BA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid sequence represents a heavy chain from an MUC18 tumour antigen-specific
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "NOINCIONAL ANTIDODY; tumour metastasis inhibition; tumour; cancer; malignancy; heavy chain; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus-1; HIV-1; human monoclonal antibody; envelope glycoprotein; gpl20; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human HIV-1 monoclonal antibody SEQ ID NO: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 13; 83pp; English
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     anti-MUC18 monoclonal antibody;
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                                                                                                                                                                                                              28-DEC-2001; 2001US-0346414P
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                                                                                                                                                                         26-DEC-2002; 2002WO-US041580
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Matches 105; Conservative
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N-PSDB; ADF09828.
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                                                                                                                                                                                                                                                   (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 117 AA;
                                                                                                 WO2003057837-A2
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                                                              Homo sapiens
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                         carcinoma;
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AAB62765 RESULT

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Gaps

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29-JUL-2004
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                                                                                                                                           Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen; cytostatic; colorectal neoplasm; renal cell carcinoma; cervical intraepithelial squamous neoplasia; cervical intraepithelial glandilar neoplasia; oesophageal; breast cancer; gene therapy; murine; mouse; human; heavy chain variable domain.
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                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel isolated monoclonal antibody (mAb) comprising a heavy chain polypeptide and light chain polypeptide having a sequence chosen from one of 53 fully defined amino acid sequences given in the specification, where the antibody specifically binds carbonic anhydrase IX (CA IX) tumour antigen. The antibody of the invention demonstrates cytostatic activity and may be useful for treating a tumour, such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
                                                           The present invention provides the protein and coding sequences for the variable regions of human monoclonal antibodies which are immunoreactive with human immunodeficiency virus-1 (HTV-1) envelope glycoprotein gp120. These can be used in diagnosis and therapy of HIV-1 infection
                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 138.
                                                                                                                                                                                                                                                                                                         QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY
                                                                                                                                                                                                                                               New anti-CA IX monoclonal antibody, useful for treating a tumor e.g., colorectal neoplasms, colorectal tumors, cervical arcinoma, cervical intraepithelial squamous and glandular neoplasia or esophageal tumors.
                                                                                                                                                                                                    Gaps
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                                                                                                                                                                    DB 4; Length 123;
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                                                                                                                                                                 Score 554.5; DB
Pred. No. 2e-41;
9; Mismatches
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                              81pp; English
                                                                                                                                                                  87.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JUL-2004 (first entry)
                                                                                                                                                                                 Best Local Similarity 85.2
Matches 104; Conservative
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                              Page 50;
                                                                                                                                      Sequence 123 AA;
infected mammal
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                              Claim 1;
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                                                                                                                                                                                                                                                                                                                                                       118
                                                                                                                                                                  Query Match
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cervical intraepithelial squamous and glandular neoplasia, oesophageal tumnour or breast cancer, possibly via gene therapy. The current sequence is that of a murine-expressed anti-human CA IX monoclonal antibody VH (heavy chain variable domain) protein of the invention. The protein was generated via the introduction of the human CA IX protein into a transgenic mouse strain.
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                                                                                                                                                                                                                                                                                                                             Length 118;
                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                             Score 553.5; DB 7
Pred. No. 2.3e-41;
6; Mismatches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 10; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP03870 standard; protein; 123 AA
                                                                                                                                                                                                                                                                                                                                87.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-DEC-2002; 2002WO-US038550.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Handa M,
                                                                                                                                                                                                                                                                                                                                                                 89.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-523295/49.
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                                                                                                                                                                                                                                                                                                                                                             1 Similarity
106; Conserv
                                                                                                                                                                                                                                                            Sequence 118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003048328-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-DEC-2001;
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Length 119;

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Query Match
Best Local Similarity 87.4%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                            29-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                       12-JUN-2003
                                                                                                                                                                                                                  ADP03879;
                                                                                                                                                                 RESULT 12
                                                                                                                                                                               ADP03879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel isolated monoclonal antibody (mAb) comprising a heavy chain polypeptide and light chain polypeptide having a sequence chosen from one of 53 fully defined amino acid sequences given in the specification, where the antibody specifically binds carbonic anhydrase IX (CA IX) tumour antigen. The antibody of the invention demonstrates cytostatic activity and may be useful for treating a tumour, such as colorectal neoplasm, renal cell carcinoma, cervical arreaphinelial squamous and glandular neoplasia, oseophageal tumour or breast cancer, possibly via gene therapy. The current sequence is that of a murine-expressed anti-human CA IX monoclonal antibody WH (heavy chain variable domain) protein of the invention. The protein was generated via the introduction of the human CA IX protein into
                                                                                                                            61 YNPSLKSRITLSVDTSKNQFSLKLNSMTAADTAVYYCARDRETAG----FDYWGQGTLVT 116
                                                                                                                                        monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen; cytostatic; colorectal neoplasm; renal cell carcinoma; cervical intraepithelial squamous neoplasia; cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
                                                                           9
                                                                                                   9
                                                                                                                                                                                                                                                                                                                                              Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 140.
                                                                                           QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New anti-CA IX monoclonal antibody, useful for treating a tumor e.g., colorectal neoplasms, colorectal tumors, cervical arcinoma, cervical intraepithelial squamous and glandular neoplasia or esophageal tumors.
                                                                           QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy; murine; mouse; human; heavy chain variable domain.
                                                   4,
                         Length 123;
                         Score 3.2c. 1.

Pred. No. 3.3e-41;

Pred. Then 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; SEQ ID NO 140; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallo M;
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                                                                                                                                                                                                                                                                    ADP03970 standard, protein, 119
                                                  9
                       86.8%;
86.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-DEC-2001; 2001US-0337275P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Handa M,
                                                                                                                                                                                                                                                                                                                     (first entry)
                                               Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transgenic mouse strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-523295/49.
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                                     Local Similarity
                                                                                                                                                                            VSS 119
Sequence 123 AA;
                                                                                                                                                                                                     VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003048328-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified,
                                                                                                                                                                                                                                                                                                                     29-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-JUN-2003
                                                                                                                                                                             117
                                                                                                                                                                                                                                                                                             ADP03970;
                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gudas J,
                                                                                                                                                                                                                                                      ADP03970
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Sequence 119 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen; cytostatic; colorectal neoplasm; renal call carcinoma; cervical intraepithelial squamous neoplasia; cervical intraepithelial glandiar neoplasia; oesophageal; breast cancer; gene therapy; murine; mouse; human; heavy chain variable domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel isolated monoclonal antibody (mAb) comprising a heavy chain polypeptide and light chain polypeptide having a sequence chosen from one of 53 fully defined amino acid sequences given in the specification, where the antibody specifically binds carbonic anhydrase IX (CA IX) tumour antigen. The antibody of the invention demonstrates cytostatic activity and may be useful for treating a tumour, such as colorectal neoplasm, renal cell carcinoma, cervical intraepithelial squamous and glandular neoplasia, ossophageal tumour or breast cancer, possibly via gene therapy. The current sequence is that of a murine-expressed anti-human CA IX monoclonal antibody VH (heavy chain variable domain) protein of the invention. The protein was generated via the introduction of the human CA IX protein into a
                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                            Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New anti-CA IX monoclonal antibody, useful for treating a tumor e.g., colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical intraepithelial squamous and glandular neoplasia or esophageal tumors.
                                                                                                                                             QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY
                                                                                                                                                                                                             QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTY
                                                                          Gaps
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Score 551; DB 7; Length 11
Pred. No. 3.9e-41;
5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Indels
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Pred. No. 6e-41;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallo M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 19; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADP03879 standard; protein; 123 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-DEC-2002; 2002WO-US038550.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-DEC-2001; 2001US-0337275P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Handa M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 85.4
Matches 105, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transgenic mouse strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gudas J, Foltz I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-523295/49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003048328-A2.
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61 YNPSLKSRVIISVDTSENQFSLKLSSVTAADTAVYYCARERVTDYYYYGLDVWGQGTTVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel isolated monoclonal antibody (mAb) comprising a heavy chain polypeptide and light chain polypeptide having a sequence chosen from one of 53 fully defined amino acid sequences given in the specification, where the antibody specifically binds carbonic anhydrase IX (CA IX) tumour antigen. The antibody of the invention demonstrates cytostatic activity and may be useful for treating a tumour, such as colorectal neoplasm, renal cell carcinoma, cervical intraeptibelial squamous and glandular neoplasia, oesophagaal tumour or breast cancer, possibly via gene therapy. The current sequence is that of a murine-expressed anti-human CA IX monoclonal antibody VH (heavy chain variable domain) protein of the invention. The protein was generated via the introduction of the human CA IX protein into a
                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer;
                        9
                                                                                                                                                                                                                                                                                                                                                             Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 18.
YNPSLKSRITLSVDTSKNQFSLKLNSMTAADTAVYYCARDRET----AGFDYWGQGTLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New anti-CA IX monoclonal antibody, useful for treating a tumor e.g., colorectal neoplasms, colorectal tumors, cervical intraepithelial squamous and glandular neoplasia or esophageal tumors.
                                                                                                                                                                                                                                                                                                                                                                                                   monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen; cytostatic; colorectal neoplasm; renal cell carcinoma; cervical intraepithelial squamous neoplasia; cervical intraepithelial glandular neoplasia; oesophageal; breast gene therapy; murine; mouse; human; heavy chain variable domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallo M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 18; 89pp; English.
                                                                                                                                                                                                                                                       ADP03878 standard; protein; 123 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-DEC-2002; 2002WO-US038550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-DEC-2001; 2001US-0337275P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Handa M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transgenic mouse strain.
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                                                                                                                           VSS 119
                                                                                                                                                               VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003048328-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                              29-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-JUN-2003.
                                                                                                                           117
                                                                                                                                                                                                                                                                                          ADP03878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gudas J,
                                                                                                                                                                                                                   RESULT 13
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             61 YNPSLKSRVIISVDTSENQFSLKLSSVTAADTAVYYCARERVTDYYYYGLDVWGQGTTVT 120
 YNPSLKSRITLSVDTSKNOFSLKLNSMTAADTAVYYCARDRET----AGFDYWGQGTLVT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides the protein and coding sequences for the variable regions of human monoclonal antibodies which are immunoreactive with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120. These can be used in diagnosis and therapy of HIV-1 infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human monoclonal antibody immunoreactive with human immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1 in biological sample and providing passive immunotherapy to HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YNPSLKSRITLSVDTSKNOFSLKLNSMTAADTAVYYCARDRETAGFDYWGQGTLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                  Human immunodeficiency virus-1; HIV-1; human monoclonal antibody; envelope glycoprotein; gp120; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 548; DB 4;
Pred. No. 7.2e-41;
                                                                                                                                                                                                                        Human HIV-1 monoclonal antibody SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                            AAB62775 standard; protein; 120 AA.
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                                                                                                                                                                                                                                                                                                                                                                     23-JUN-2000; 2000WO-US017327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 86.2%;
Best Local Similarity 87.4%;
Matches 104; Conservative
                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Reitz MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-112438/12.
                                                  117 VSS 119
                                                                            123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infected mammal.
                                                                                                                                                                                                                                                                                                                 WO200100678-A1.
                                                                          121 VSS
                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Watkins BA,
                                                                                                                                                                                                                                                                                                                                           04-JAN-2001.
                                                                                                                                                                                               03-APR-2001
 19
                                                                                                                                                                     AAB62775;
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ADJ80377
ID ADJ80
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AC ADJ80
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Conservative

Local Similarity

Best Local Sim Matches 105;

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Query Match

Length 123;

Score 549; DB 7 Pred. No. 6e-41; Mismatches

86.3%;

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QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGYYWSWIRQHPGKGLEWIGYIYYSGSTY QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY

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Antibody variable heavy chain with homology to mouse anti-human antibody.
                                                                                                                                                                 Producing a hybrid antibody or hybrid antibody fragment by operatively linking the selected framework sequences to one or more complementarity determining regions of the initial antibody.
                             hybrid antibody; antibody; framework region; homology; immunogenicity.
                                                                                                                                                                                               Example 1; SEQ ID NO 137; 77pp; English.
                                                                                        03-DEC-2002; 2002WO-US038450.
                                                                                                      03-DEC-2001; 2001US-0336591P.
06-MAY-2004 (first entry)
                                                                                                                     (ALEX-) ALEXION PHARM INC
                                                                                                                                                  WPI; 2003-513753/48.
                                                                                                                                    Wu D;
                                                          WO2003048321-A2
                                            Unidentified
                                                                         12-JUN-2003
                                                                                                                                    Rother R,
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The invention relates to a method of producing a hybrid antibody or hybrid antibody fragment by: (i) providing an initial antibody having specificity for a target; (ii) determining the sequence of a variable region of the initial antibody; (iii) selecting a first component of the variable region consisting of RRI, FR2, FR3 and FR4; (iv) comparing the sequence of the first component to sequences contained in a reference database of antibody sequences or antibody fragment sequences from a target species; (v) selecting a sequence from an antibody in the database which demonstrates a high degree of homology to the first component; (vi) selecting a second component selected from the group consisting of FR1, FR2, FR3 and FR4; (vi) comparing the sequence of the second component to sequences contained in a reference database of antibody sequences or antibody fragment sequences from the target species; (vii) selecting a sequence from the database which demonstrates a high capture of the second component and which is from a different antibody than the selected antibody; and (ix) operatively linking the selected framework sequences to one or more complementarity determining captured antibody fragment (lained). The antibody and antibody fragment. The method is useful for produce a hybrid antibody cor hybrid antibody fragment (lained). The antibody and antibody rangener. This produces antibodies that charable light chain to receive the CDRs. This produces antibodies that the entities and exhibit reduced imminogenicity while maintaining an optimum binding profile. This sequence represents an antibody variable heavy chain which has good homology to an initial murine anti-human mannose binding lectin antibody (ADJ80371). The sequence was used to generate a hybrid antibody of the invention.

1 VQLQBSGPGLVKPSQTLSLTCTVSGGSISSGGYYWNWIRQHPGKGLEWIGYIYYSGSTYY 60 2 VQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTYY 86.1%; Score 547.5; DB 7; Length 121; larity 86.0%; Pred. No. 8e-41; Conservative 7; Mismatches 7; Indels 3. 7; Indels Similarity Sequence 121 AA; Local Simi hes 104; Query Match Best Loca Matches

Gaps

3;

61 NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGLKWGSNHYFDYWGQGTLVTVS 120

119 S 119

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NPSLKSRITLSVDTSKNOFSLKLNSMTAADTAVYYCARDRETAG---FDYWGQGTLVTVS

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s 121 121 g 9, 2005, 12:55:29 Search completed: November Job time : 74.3684 secs

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TELEX:
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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Sequence 5, Appli
Sequence 5, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 25, Appli
Sequence 25, Appli
Sequence 25, Appli
Sequence 25, Appli
Sequence 26, Appli
Sequence 37, Appli
Sequence 37, Appli
Sequence 39, Appli
Sequence 65, Appli
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480.403 Million cell updates/sec
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                                                                                                                   November 9, 2005, 11:29:55 ; Search time 18.4912 Seconds
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636
1 QVQLQESGPGLVKPSQTLSL......DRETAGFDYWGQGTLVTVSS 119
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-017-628-5

US-09-017-628-5

US-09-017-628-5

US-09-467-903-5

US-09-467-903-5

US-09-490-729-145

US-09-490-153-25

US-09-490-153-25

US-09-490-153-25

US-09-490-153-25

US-09-490-153-39

US-09-490-070A-65

US-09-490-153-39

US-09-490-153-39

US-09-490-153-39

US-09-490-153-39

US-09-490-153-39

US-09-490-153-65

US-09-490-153-65
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US-09-017-628-11
US-09-014-880-11
                                                                                                                                                                                                                                                                                                                                         513545 segs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                             - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB peq length: 200000000
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Match Length
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                                                                                                                                                                                                   Title:
Perfect score:
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Sequence 839, App
Sequence 13, Appl
Sequence 14, Appl
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Saiko HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Yoko HIRAAWA
APPLICANT: No. 5767246iniko ITO
APPLICANT: Kazuhiro NAGAIKE
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
TITLE OF INVENTION: Cell Membrane
MUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                     Sequence
Sequence
Sequence
                                                                       Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
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US-08-450-363-11

US-09-467-903-11

US-08-485-8093-116

US-08-488-127-48-2

US-08-918-148-79

US-09-138-0918-77

US-09-424-8408-20

US-08-484-850-12

US-09-383-916-12

US-09-383-916-12

US-09-424-8408-20

US-09-46-837

US-09-260-527-3

US-09-203-76-839

US-09-203-76-839

US-09-203-76-839

US-09-582-816A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: CONTY: Washington STATE: D. C. COUNTRY: U.S.A. COUNTRY: U.S.A. ZIP: 20005 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IBM Compatible
                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OCTUBEN 1 THE COMPOSITION OF THE CONTRIBUTION OF THE CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,125
FILING DATE:
CLASSIPRICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                      US-08-360-125-5; Sequence 5, Application US/08360125; Patent No. 5767246; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REPRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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85.7%; Score 545; DB 2; Length 119; 84.9%; Pred. No. 5e-47;
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: Ind Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,578
FILING DATE: May 25, 1995
CLASSIFICATION NUMBER: 08/360,125
RICHARD APPLICATION DATA:
APPLICATION NUMBER: 09/360,125
RILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER: 33,367
RELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUB TYPE:
CELL TYPE: Hybridoma producing human
CELL TYPE: antibody GAH
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DATE:

DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

RELEYANT RESIDUES IN SEQ ID NO:

US-08-450-578-5
                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 119 amino acide
TYPE: amino acide
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
LOCATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acid
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PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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JOURNAL:
VOLUME:
ISSUE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY 60
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                                                                                      INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL TYPE: antibody GAH
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-5
                                                                                                                                                                                                                                                                                                                                                                                          IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                      ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
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      ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                        UNITS:
FEATURE:
NAME/KEY:
LOCATION:
                                                        ORGANISM:
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VOLUME:
                                                                          STRAIN:
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US-09-014-880-5
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US-08-450-363-5
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                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: HOSOKAWA, Saiko
APPLICANT: TAGAWA, Toshiaki
APPLICANT: HOSOKAWA, Yoko
APPLICANT: HIRAZAWA, Yoko
APPLICANT: HIRAZAWA, Yoko
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
TITLE OF INVENTION: SUFFACE ANTIGEN OF CANCER CELL MEMBRANE
FILE REFERENCE: 177/527361K4
CURRENT APPLICATION NUMBER: US/09/017,628
CURRENT APPLICATION NUMBER: 08/360,125
EARLIER PELLING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-014-880-5
; Sequence 5, Application US/09014880
; Patent No. 599029.
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
     0; Gaps
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  9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Hybridoma producing human antibody GAH
US-09-017-628-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSE: Wenderoth, Lind & Ponack, L.L.P. STRET: 2033 K Street, N.W., #800 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
  9; Mismatches
                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/09017628
Patent No. 5990287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 119
Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20006
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1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSCGFYWNWIRQHPGKGLEWIGYIYYSGSTY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Yoko HIRAXAWA
APPLICANT: Yoko HIRAXAWA
APPLICANT: No. 6436434ihiko ITO
APPLICANT: Kazuhiro NGAJIKE
ITILE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
TITLE OF INVENTION: Call Membrane
TITLE OF INVENTION: 42
CORRESPONDENCE: 42
CORRESPONDENCE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY
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Pred. No. 5e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/450,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Wenderoth, Lind & Ponack
805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein ORIGINAL SOURCE: CELL TYPE: Hybridoma producing human CELL TYPE: antibody GAH
          CLASSIFICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/450,578
FILING DATE: MAY 25, 1995
PRIOR APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION NUMBER: 07/905,534
PRIOR APPLICATION NUMBER: 07/905,534
PTILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: WARTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08450363
Patent No. 6436434
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: TOSHIAKI TAGAWA
January 28, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington
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TITLE OF INVENTION: Human Monoclonal Antibody
Specifically Binding to Surface Antigen of Cancer
Cell Membrane
61 YNPSLKSRVTISLDTSKSQFSLKLSSLTAADTAVYYCARSTRLRGADYWGQGTMVTVSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: Hybridoma producing human antibody GAH
CELL LINE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Warren M.Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: «Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEPK: «Unknown>
TELEFX: «Unknown>
TELEFX: «Unknown>
TELEFX: «Unknown>
TELEFX: «Unknown>
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/467,903
FILING DATE: 21-Dec-1999
CLASSIFICATION NUMBER: 08/450,363
APPLICATION NUMBER: 08/450,363
APPLICATION NUMBER: 08/360,125
APPLICATION NUMBER: 07/995
APPLICATION NUMBER: 07/905,534
FILING DATE: December 20, 1994
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1991
APPLICATION NUMBER: JP158859/1991
FILING DATE: June 28, 1991
APPLICATION NUMBER: JP158860/1991
FILING DATE: June 28, 1991
APPLICATION NUMBER: JP158860/1991
FILING DATE: June 28, 1991
APPLICATION NUMBER: JP158861/1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 2033 K Street, N.W., #800
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DEVELOPMENTAL STAGE: <Unknown>
                                                                                                                                                                                                                                                                         No. 6787153ihiko ITO
Kazuhiro NAGAIKE
                                                                                                                       Sequence 5, Application US/09467903
Patent No. 6787153
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 119 amino acids
                                                                                                                                                                                                                        Toshiaki TAGAWA
Yoko HIRAKAWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: <Unknown>
STRAIN: <Unknown>
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ANTI-SENSE: «Unknown»
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                      US-09-467-903-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL TYPE: antibody GAH
CELL LINE:
CELL LINE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                         PILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: WATTEN NUMBER: 33,367
REGISTRATION NUMBER: 33,367
TELEPHONICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-363-5
                         CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
     FILING DATE: May 25, 1995
                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
LOCATION DENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
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POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN:
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us-10-660-357a-25.rai

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80 YNPSLKSRVTISVDTSQNQFSLRLSSVTAADTAVYYCAKDHRATRDGYQLEYRGFDYWGQ 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 QVQLQESGPGLVKPSETLSLTCAVSGGSITSGGYYWSWIRQPPGKGLEWIGYIYYSGSTL 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 473;
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 523.5; DB 3 Pred. No. 3.6e-44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Incyte Pharmaceuticals, Inc
                                                                                                                                                                 Sequence 4, Application US/09049672A
Patent No. 6135941
GENERAL INFORMATION:
                                                                                                                                                                                                                           Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNIES 21P: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
TOTAL TREE
MEDIUM TYPE: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                  Au-Young, Janice
Corley, Neil C.
Guegler, Karl J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 473 amino acide TYPE: amino acid
                                                                                                                                                                                                                                          Lal, Preeti
Tang, Y. Tom
Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                      112 GTLVTVSS 119
                                                                         140 GILVTVSS 147
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TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                   US-09-049-672A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY:
STATE:
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Best Local S:
Matches 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSCGFYWNWIRQHPGKGLEWIGYIYYSGSTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 YNPSLKSRVTISLDTSKSQFSLKLSSLTAADTAVYYCARSTRLRGADYWGQGTWVTVSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 YNPSLKSRITLSVDTSKNOFSLKLNSMTAADTAVYYCARDRETAGFDYWGQGTLVTVSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 545; DB 4; Length 119;
Pred. No. 5e-47;
9; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INPORMATION:
APPLICANT: Ni et al.
ITLE OF INVENTION: 32 Human secreted proteins
ITLE OF INVENTION: 32 Human secreted proteins
CURRENT PELLING DATE: 2001-03-08
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: PCT/US00/26013
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR APPLICATION NUMBER: 1999-09-24
NUMBER OF FILING DATE: 1999-09-24
NUMBER: PALENTIN OF 2.0
                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                     POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 145, Application US/09800729 Patent No. 6605592
                                                                                                                                                                                    LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
ORGANELLE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.7%;
               IMMEDIATE SOURCE:
   LIBRARY: <Unknown>
   CLONE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 78.9%
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 84.9°
Matches 101; Conservative
                                                                                                                            UNITS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                        DOCUMENT NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
CORGANISM: Homo sapiens
US-09-800-729-145
                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                JOURNAL:
                                                                                                                                                                                                                                                                                                               VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-800-729-145
                                                                                                                                                FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-467-903-5
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US-09-490-153-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 YNPSLKSRITLSVDTSKNQFSLKLNSMTAADTAVYYCARDRETAG-FDYWGQGTLVTVSS 119
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Pred. No. 6.8e-44;
6; Mismatches 9; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CALP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
PILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENTCE/DOCKET NUMBER: AORPHO/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                               STREET: 1251 Avenue of the Americas
CITY: New York
COUNTRY: New York
COUNTRY: New York
COUNTRY: New York
COUNTRY: New York
CITY: New York
COUNTRY: New York
CITY: New York
CITY: New York
CITY: New York
CITY: New York
                                                                                                                   Sequence 25, Application US/09025769B

Patent No. 6300064

GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: 11ag, Vic
APPLICANT: Ge, Liming
APPLICANT: Plueckthun, Andreas
TITUE OF INVENTION:
TITUE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25, Application US/09490070A
Patent No. 656248
GENERAL INFORMATION:
APPLICANT Knappik, Achim
Pack, Peter
Plack, Peter
Plack, Peter
Plack, Peter
Ge, Liming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 25:
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85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212/2)
TELEPHONE: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 85.0°
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein
US-09-025-769B-25
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140 TVSS 143
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US-09-490-070A-25
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61 YNPSLKSRITLSVDTSKNOFSLKLNSMTAADTAVYYCARDRETAG-FDYWGQGTLVTVSS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGEIYHSGSTN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                Esq. c/o Heller Ehrman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York STATE: New York ZUNNTRY: New York ZIP: 10021
                                                                                                                                                                                                                                                         ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 80.7%; Score 513.5; DB 4; Length Best Local Similarity 85.0%; Pred. No. 6.8e-44; Matches 102; Conservative 6; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
G, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                      ADDRESSEE: Colin G. Sandercock, Esq. c, White & McAuliffe STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-070A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25, Application US/09490153 Patent No. 6706484 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                              CITY: Washington
STATE: D.C.
COUNTRY: USA
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61 YNPSLKSRITLSVDTSKNQFSLKLNSMTAADTAVYYCARDRETAG-FDYWGQGTLVTVSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLQESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGEIYHSGSTN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGY1YSSGSTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 513.5; DB 4; Length 118;
Pred. No. 6.8e-44;
6; Mismatches 9; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MUSLIC, MINES, ELLEN E.
APPLICANT: MUSLIC, MINES, DEFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABA.-PF1
CURRENT APPLICATION NUMBER: U5/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR PILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Indels
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Pred. No. 5.3e-43;
                            APPLICATION NUMBER: EP 95 11 3021.0 FILING DATE: 18-AUG-1995 ATTORNEY/AGENT INFORMATION:
                                                                                         NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/S
TELECOMMUNICATION INFORMATION:
TELEPAR. (212) 596-9000
TELEFAR. (212) 596-9000
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Mismatches
                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 25: US-09-490-324-25
                                                                                                                                                                                                                                                                               LENGTH: 118 amino acids
                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/09472087 Patent No. 6682736
                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 85.0°
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLQESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGEIYHSGSTN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York STATE: New York
                                        COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IDM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25, Application US/09490324

Patent No. 6828422

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Indg, Vic

GG, Liming

Moroney, Simon

Pluckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                             APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
TELECOMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 80.7%; Score 513.5; DB 4 Best Local Similarity 85.0%; Pred. No. 6.8e-44; Matches 102; Conservative 6; Mismatches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-153-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10021
COMPUTER READABLE FORM:
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Gaps

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1 SGPGLVKPSQILSLTCTVSGGSISSGGHYWSWIRQHPGKGLEWIGYIYYIGNTYYNPSLK 60
                                     Gaps
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Length 172;
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RESULT 14

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7 SGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTYYNPSLK 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79.6%; Score 506.5; DB 4; Length 172; 84.2%; Pred. No. 5.3e-43; Live 7; Mismatches 10; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 79.1%; Score 503; DB 4; Length 117; Best Local Similarity 83.2%; Pred. No. 7.5e-43; Matches 99; Conservative 8; Mismatches 10; Indels
                                                                                                                  APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NUNEU, MARK J.
APPLICANT: NUSEU, MARK J.
APPLICANT: MUSILER, SILLER E.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: CORVALAN, JOSE R.
ITILE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PP1
CURRENT APPLICATION WUMBER: US/09/472,087
CURRENT APPLICATION WUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 147
SOUTWARE: PALENTIN UNCS: 147
SQUID NO 86
ILENGTH: 172
TYPE: PRT
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; Patent No. 6827925
; GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Williams, Andrew J
APPLICANT: Tempest, Philip R
APPLICANT: Tempest, Philip R
APPLICANT: Holter, Thor L
APPLICANT: Ackson, Helen
APPLICANT: Main, Sarah H
APP
Sequence 86, Application US/09472087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 84.2
Matches 96; Conservative
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, ORGANISM: Homo sapiens
US-09-720-493-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-09-472-087-86
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1 QVQLQESGRGLVKPSQTLSL.....DRETAGFDYWGQGTLVTVSS
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US-10-984-960A-20
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Gapop 10.0 , Gapext 0.5
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100.0%; Pred. No. 1.9e-48;
Live 0; Mismatches 0;
US-10-309-762-10

US-10-309-762-140

US-10-308-360-8

US-10-309-762-18

US-10-308-81-37

US-10-308-81-37

US-10-308-81-37

US-10-984-960A-56

US-10-984-960A-56

US-10-984-960A-56

US-10-984-960A-56

US-10-984-960A-56

US-10-984-960A-56

US-10-988-36-14

US-10-983-762-14

US-10-483-994-7

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US-10-309-762-14

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US-10-988-360-40

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Publication No. US20030147809A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC
FILE REPERENCE: ABGENIX.022A
CURRENT APPLICATION NUMBER: US/10/330,613
CURRENT FILING DATE: 2002-12-26
PRIOR PAPLICATION NUMBER: 0/346299
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 119
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US-10-330-613-25
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Matches 119; Conserv
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LENGTH: 117
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Sequence 25, Application US/10330530
Publication No. US20030152514A1
GENERAL INFORMATION:
APPLICANT: GUAGE, Jean
TITLE OF INVENITON: METHODS FOR USING ANTI-MUC18 ANTIBODIES
FILE REFERENCE: ABGENIX.031A
CURRENT APPLICATION NUMBER: US/10/330,530
CURRENT FILING DATE: 2002-12-26
PRIOR PELING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 119
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Publication No. US20040115205A1
GENERAL INFORMATION:
TUTLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
CURRENT PEPLICATION NUMBER: US/10/660,357
CURRENT FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
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SOFTWARE: FastSEQ for Windows Version 4.0
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; Sequence 13, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 119; Conservative
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Best Local Similarity 100.
Matches 119; Conservative
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US-10-660-357-25
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US-10-330-530-25
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; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean

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1 QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY 60
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| Publication No. US20030152514A1
| GENERAL INFORMATION:
| APPLICANT: Gudas, Jean
| TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
| PILE REFERENCE: ABGENIX.031A
| CURRENT APPLICATION NUMBER: US/10/330,530
| CURRENT FILING DATE: 2002-12-26
| PRIOR FILING DATE: 2001-12-18
| NUMBER OF SEQ ID NOS: 40
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 13
| LENGTH: 117
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Pred. No. 7.5e-42;
9; Mismatches 3; Indels
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Publication No. US20040115205A1
GENERAL INFORMATION:
APPLICANT: Bar-Eli, Menashe
APPLICANT: Green, Larry L.
TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
TITLE OF INVENTION: ANTIGEN
FILE REFERENCE: ABGENIX.030C1
CURRENT APPLICATION NUMBER: US/10/660,357
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 10/330,580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 561; DB 14;
Pred. No. 7.5e-42;
9; Mismatches 3;
FILE REFERENCE: ABGENIX.022A
CURRENT APPLICATION NUMBER: US/10/330,613
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: 60/346299
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                88.2%;
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ORGANISM: Homo Sapiens
US-10-330-530-13
                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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APPLICANT: Morrison, Robert Kendall
APPLICANT: Morrison, Raren Jane Meyrick
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
ITILE OF INVENTION: ANTIHODIES AND RELATED MOLECULES THAT BIND TO PSCA PROTEINS
FILE REFERENCE: 51158-20088.20
CURRENT APPLICATION NUMBER: US/11/131,648
CURRENT APPLICATION NUMBER: 60/616,381
PRIOR PILING DATE: 2004-10-05
PRIOR PILING DATE: 2004-10-12
PRIOR APPLICATION NUMBER: 60/617,881
PRIOR PILING DATE: 2004-10-21
PRIOR PILING DATE: 2004-10-21
PRIOR PILING DATE: 2004-10-21
PRIOR PILING DATE: 2004-10-22
PRIOR PILING DATE: 2004-10-22
PRIOR PILING DATE: 2004-10-32
PRIOR PILING DATE: 2004-05-28
PRIOR PILING DATE: 2004-05-28
PRIOR PILING DATE: 2003-05-30
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                    APPLICANT: Zhong, Halhong
APPLICANT: Zhong, Halhong
APPLICANT: Larochelle, William J.
TITLE OF INVENTION: ANTIBODIES AGAINST SECRETORYLEUKOCYTE PROTEASE INHIBITOR
FILE REFERENCE: Cura 970
CURRENT APPLICATION NUMBER: US/10/984,960A
CURRENT FILING DATE: 2004-11-08
PRIOR APPLICATION NUMBER: 60/518,275
PRIOR PILING DATE: 2003-11-07
NUMBER OF SEQ ID NOS: 112
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLQESGPGLVKPSQTLSLTCTVSGVSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 87.5%; Score 556.5; DB 18; Length 122; Best Local Similarity 86.9%; Pred. No. 1.9e-41; Matches 106; Conservative 7; Mismatches 6; Indels 3;
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Morrison, Robert Kendall
Morrison, Karen Jane Meyrick
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Sequence 15, Application US/11131648

Publication No. US20050221400A1

GENERAL INFORMATION:
APPLICANT: Gudas, Jean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jakobovits, Aya
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
US-11-131-648-15
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US-10-984-960A-20
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LENGTH: 136
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APPLICANT: Foltz, Ian
APPLICANT: Foltz, Ian
APPLICANT: Tes, Kam Fai
APPLICANT: Jeffers, Michael
APPLICANT: Jeffers, Michael
APPLICANT: Starling, Gary
APPLICANT: Masses, Peter
APPLICANT: Khramtsov, Nikolia
TITLE OF INVENTION: DOWAIN AND MUCIN DOMAIN 1 (TIM-1) ANTIGEN AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YNPSLKSRITLSVDTSKNOFSLKLNSMTAADTAVYYCARDRETA-----GFDYWGQGTLV 115
                                                                                                                                                                                                                                                                                                                                       1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY 60
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Pred. No. 8.8e-42;
7; Mismatches 6; Indels 5;
                                                                                                                                                                                                                      Length 117;
                                                                                                                                                                                                                                                               3; Indels
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CURRENT APPLICATION NUMBER: US/10/805,177
CURRENT FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: 60/456,652
PRIOR FILING DATE: 2003-03-19
NUMBER OF SEQ ID NOS: 141
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 53
LENGTH: 125
PRIOR FILING DATE: 2002-12-26
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 53, Application US/10805177 Publication No. US20050084449A1 GENERAL INFORMATION:
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US-10-660-357-13
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Best Local Similarity
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US-10-984-960A-20
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US-10-805-177-53
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                                                                                             LENGTH: 117
                                                                                                                      TYPE: PRT
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ORGANISM: Homo sapiens
US-10-309-762-10
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US-10-309-762-138
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Matches 106; Conserv
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US-10-309-762-10
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                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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APPLICANT: Shao, Hui
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
TITLE OF INVENTION: ANTHEODIES AND RELATED MOLECULES THAT BIND TO PSCA PROTEINS
FILE REFERENCE: 51158-20088.20
CURRENT APPLICATION NUMBER: US/11/131,648
CURRENT PILLO DATE: 2004-10-05
PRIOR APPLICATION NUMBER: 60/616,381
PRIOR PLING DATE: 2004-10-12
PRIOR APPLICATION NUMBER: 60/617,881
PRIOR PLING DATE: 2004-10-21
PRIOR APPLICATION NUMBER: 60/633,077
PRIOR FILING DATE: 2004-10-21
PRIOR APPLICATION NUMBER: 60/633,077
PRIOR FILING DATE: 2004-05-28
PRIOR PLING DATE: 2004-05-28
PRIOR FILING DATE: 2003-05-30
NUMBER OF SEQ ID NOS: 78
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                                                                                                                     12 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTY
                                                                                                                                                                                      61 YNPSLKSRITLSVDTSKNQFSLKLNSMTAADTAVYYCARDRET------AGFDYWGQGT
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                                                                                             QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY
                                                Gaps
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87.2%; Score 554.5; DB 20; Length 136;
Best Local Similarity 84.8%; Pred. No. 3.2e-41;
Matches 106; Conservative 6; Mismatches 6; Indels 7;
Score 554.5; DB 20; Length 136;
Pred. No. 3.2e-41;
6; Mismatches 6; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Xiao-Chi, Jia
APPLICANT: Morrison, Robert Kendall
APPLICANT: Morrison, Karen Jane Meyrick
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 39, Application US/11131648
Publication No. US20050221400A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Jakobovits, Aya
Query Match
Best Local Similarity 84.8%;
Matches 106; Conservative
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APPLICANT:
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RESULT 11

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61 YNPSLKSRITLSVDTSKNQFSLKLNSMTAADTAVYYCARDRETAG----FDYWGQGTLVT 116
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SEMERAL INFORMATION:
APPLICANT: Galds, Jean
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANYIBODIES AGAINST CARBOXIC ANHYDRASE IX
TITLE OF INVENTION: ANYIBODIES AGAINST CARBOXIC ANHYDRASE IX
TITLE OF INVENTION: AUVIBODIES AGAINST CARBOXIC ANHYDRASE IX
CURRENT APPLICATION UNBER: 105/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 87.0%; Score 553.5; DB 15; Length 118; Best Local Similarity 89.1%; Pred. No. 3.5e-41; Matches 106; Conservative 6; Mismatches 6; Indels 1;
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                                                                                                                           APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
PRIOR FILING DATE: 2001-12-03
                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSEQ for Windows Version 4.0
; Sequence 138, Application US/10309762; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
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                                                                                               Sequence 140, Application US/10309762
| Publication No US20040018198A1
| GENERAL INPORMATION:
| APPLICANT: Gudas, Jean
| APPLICANT: Handa, Masahisa
| APPLICANT: Gallo, Michael
| TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
| FILE REFERENCE: ABGRINX: 0.27A
| CURRENT APPLICATION NUMBER: 105/10/309,762
| CURRENT FILING DATE: 2002-12-02
| PRIOR PELING DATE: 2001-12-03
| NUMBER OF SEQ ID NOS: 246
| SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 86.6%; Score 551; DB 15; Length 119; Best Local Similarity 87.4%; Pred. No. 5.8e-41; Matches 104; Conservative 5; Mismatches 10; Indels
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86.0%; Pred. No. 5.9e-41;
iive 9; Mismatches 6;
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APPLICANT: Chayur, Tariq
APPLICANT: Chayur, Tariq
APPLICANT: Uabkoveky, Boris
APPLICANT: Ores, Jarry
APPLICANT: Green, Larry
APPLICANT: Habcook, John
APPLICANT: Wieler, James
APPLICANT: Wieler, James
APPLICANT: Wieler, James
APPLICANT: Hagberg, Brad
TITLE OF INVENTION: 1L-18 Binding Proteins
FILE REFERENCE: BEC-085
CURRENT APPLICATION NUMBER: US/10/706,689
CURRENT APPLICATION NUMBER: 2003-11-12
NUMBER OF SEQ ID NOS: 47
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Publication No. US20050100965A1
GENERAL INFORMATION:
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Best Local Similarity 86.0
Matches 104; Conservative
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ORGANISM: Homo sapiens
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US-10-706-689-8
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61 YNPSLKSRITLSVDTSKNQFSLKLNSMTAADTAVYYCARDRETAG--FDYWGQGTLVTVS 118
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                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ghayur, Tariq
APPLICANT: Labkovsky, Boris
APPLICANT: Labkovsky, Boris
APPLICANT: Voss, Jeffrey
APPLICANT: Green, Larry
APPLICANT: Green, Larry
APPLICANT: Jia, Xiao-chi
APPLICANT: Jia, Xiao-chi
APPLICANT: Wieler, James
APPLICANT: Hegberg, Brad
TITLE OF INVENTION: IL-18 Binding Proteins
FILE REFERENCE: BEC. OSSUS
CURRENT APPLICATION NUMBER: US/10/988,360
CURRENT FILING DATE: 2004-11-12
NUMBER OF SEQ ID NOS: 47
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ORGANISM: Homo sapiens
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1 QVQLQESGPGLVKPSQTLSL.....DRETAGFDYWGQGTLVTVSS 119
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Listing first 45 summaries
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| N. MOTEST N. MOTEST N. TIELS N | Kimortari, F.; Ocns, H.D.; wedgwood, K.U.F. Nucleic Acids Res. 19, 673, 1991 Nucleic Acids Res. 19, 673, 1991 Alfille: Immunoglobulin variable heavy chai A;Reference number: \$13519; MUD:91187691; A;Recession: \$13519 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-147 < MOR> A;Cross-references: EMBL:X56158; NID:g37724 C;Superfamily: immunoglobulin V region; imm C;Keywords: heterotetramer; immunoglobulin | h.D.; r
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19 V-D-J region (ND) - human
C;Species: Homo sapiens (man)
C;Date: 14-Reb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: S6912
R;Sahota, S.; Hamblin, T.; Oscier, D.G.; Stevenson, F.K.
Leukemia 8, 1285-1289, 1994
A;Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of mult.)
A;Reterence number: S69909, MUID: 94335315; PMID: 8057663
A;Accession: S6912
A;Acce
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A; Reference number: S78051
A; Accession: S78051
A; Accession: S78051
A; Residues: 1-135 cHAR>
A; Residues: 1-135 cHAR>
A; Cross-references: EMBL: X54437; NID: g37814; PIDN: CAA38306.1; PID: g930117
B; Harindranth, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkin. Int. Immunol. 3, 865-875, 1991
A; Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and b
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                                                                                                                                                                                                                                                                                                                       64 YNPSLKSRVTISVDTSKNQPSLKLSSVTAADTAVYYCARGSSVLLWFGELLYYFDYWGGG 123
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                                                                                                                                                                                   QVQLQESGPGLVKPSETLSLTCTVSGGSISS--YYWSWSRQPPGKGLEWIGYIYYSGSTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RVQLQESGPGLVKPSQTLSLTCSVSGGSISSDGHFWNWIRQHPGKGLEWIGNIYFSGSSY
                                                                                                                                                                                                                                                                                  YNPSLKSRITLSVDTSKNQFSLKLNSMTAADTAVYYCARDRETA-----GFDYWGQG
                                                                                                                                       1 OVOLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY
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       Length 130;
                                                                     Indels
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A;Reference number: S23716; MUID:92031262; PMID:1718404
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78.6%; Score 500; DB 2; L. 78.7%; Pred. No. 7e-38; ive 6; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 499.5; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
78.5%; Score 499.5;
Best Local Similarity 78.7%; Pred. No. 7.3e
Matches 96; Conservative 12; Mismatches
Query Match 78.6
Best Local Similarity 78.7
Matches 100; Conservative
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A; Molecule type: mRNA
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Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
Accession: 137782; S25476
                                                                                                                                                                                                                                                     QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY
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                                                                         Length 147;
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                                                                     Score 515; DB 2; Length 14
Pred. No. 3.6e-39;
7; Mismatches 12; Indels
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F;41-125/Domain: immunoglobulin homology <IMM>
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                                                                     Query Match
Best Local Similarity 82.6%;
Matches 100; Conservative
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Best Local Similarity 82.1
Matches 101; Conservative
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C;Accession: 837456
R;McIntosh, R.S.; Tandon, N.; Weetman, A.P.
submitted to the EMBL Data Library, September 1993
A;Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from A;Reference number: 837453
  A, Residues: 1-99 < wEN>
A, Residues: 1-99 < wEN>
A, Cross-references: EMBL:Z14237; NID:g37706; PIDN:CAA78606.1; PID:g1335372
A, Cross-references: EMBL:Z14237; NID:g37706; PIDN:CAA78606.1; PID:g135372
B, Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A, Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A, Reference number: S26885; MUID:93021117; PMID:1404388
A, Accession: S26900
A, Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain V region - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44113
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K. submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable A;Reference number: S44105
A;Accession: S44113
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig mu chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Cross-references: EMBL:X75024; NID:g404313; PIDN:CAA52932.1; PID:g758095 C; Superfamily: immunoglobulin V region; immunoglobulin homology F;6-90/Domain: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 GLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTYYNPSLKSRI
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                                                                                                                                                                                                       A;Cross-references: EMBL:Z12365; NID:g32948; PIDN:CAA78235.1; PID:g32949 (S.Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: hererotetramer; immunoglobulin F;15-99/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                             Length 99;
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Pred. No. 2.6e-37;
8; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                           Score 494; DB 2; Length 99
Pred. No. 1.8e-37;
5; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                         77.7%;
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                                                                                                                                                                                                                                                                                                                                Local Similarity
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Best Local Similarity
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A;Molecule type: mRNA
A;Residues: 1-116 <MCI>
                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-99 <TOM>
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                                                                                                                                                                                                                        QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY
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ن
                                                       F:1-13/Domain: signal sequence (fragment) #status predicted <SIG>F:14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>F:27-111/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 128;
                                                                                                                                              Length 135;
;Cross-references: EMBL:X54437
;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                    14; Indels
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                                                                                                                                            Score 498; DB 2;
Pred. No. 1.1e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 496; DB 2;
Pred. No. 1.6e-37;
8; Mismatches 15;
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                                                                                                                                                                                9; Mismatches
                                                                                                                                         78.3%;
78.0%;
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79.3%;
                                                                                                                                                                                    Conservative
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                                        C; Keywords: immunoglobulin
                                                                                                                                       Query Match
Best Local Similarity
Matches 96; Conserv
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Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain - human
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Gaps

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C;Accession: S31586
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
Submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: S31585
                                                                                                                                                                                                                                                                   80 YNPSLRSRVTISVDTSKNOPSLKLGSVTAADTAVYYCARVLVSRTSISQYSYYMDVWGKG 139
                                                                                                                                                                                                                                        61 YNPSLKSRITLSVDTSKNOFSLKLNSMTAADTAVYYCAR------DRETAGFDYWGQG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 YNPSIKSRVTMSVDTSKNQPSIKLSSVTAADTAVYYCARGGLGIRRGAFDIWGQGTMVTV 137
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C.Date: 03.Mar-1994 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C.Accession: S30530
R.Mariette, X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
                                                                                                                                                                                20 QVQLQESGPGLVKPSETLSVTCTVSGGSVSSSGLYWSWIRQPPGKGPEWIGYIYYSGSTN
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                                                                                                                               1 QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: EMBL:Z14196; NID:g30978; PIDN:CAA78565.1; PID:g30979 (S.Uperfemilty: immunoglobulin V region; immunoglobulin homology C,Keywords: heterotetramer; immunoglobulin P;34-VIG/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 139;
                        Length 146;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 486.5; DB 2; Length
Pred. No. 1.2e-36;
8; Mismatches 12; Indels
                                                                          14; Indels
                   ; Score 487; DB 2;
; Pred. No. 1.2e-36;
11; Mismatches 14
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C;Species: Homo sapiens (man)
                        76.6%;
74.0%;
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Best Local Similarity 79.5%;
Matches 97; Conservative
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119
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A;Molecule type: mRNA
A;Residues: 1-123 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-139 <CUI>
                                                                                                                                                                                                                                                                                                                                              113 TLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S31586
A; Status: preliminary
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C. Accession: S31676

C. Submitted to the EMBL Data Library, June 1992

A. Description: Mechanisms that generate human immunoglobulin diversity operate from the A. Beerance number: S31585

A. Accession: S31676

A. Accession: S31676

A. Molecule type: mRNA

A. Molecule type: mRNA

A. Molecule type: mRNA

A. Molecule type: mRNA

A. Cross-references: EMBL: Z14182; NID:g31031; PIDN: CAA78551.1; PID:g31032

C. Superfamily: immunoglobulin V region; immunoglobulin homology

C. Keywords: heterotetramer; immunoglobulin

F; 34-116/Domain: immunoglobulin homology < IMM>
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C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
R;Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990
A;Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains A;Reference number: S09710; MUID:90262535; PMID:2111699
A;Accession: S09711
A;Accession: S09711
A;Accession: RNAA
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Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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                                                                                                                                                                                                                                                                                         1 QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY
                                            A;Cross-references: EMBL:Z31389; NID:g472967; PIDN:CAA83264.1; PID:g940524 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: hererotetramer; immunoglobulin F;15-99/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
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                                                                                                                                                                                   Score 493; DB 2;
Pred. No. 2.8e-37;
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C;Keywords: heterotetramer; immunoglobulin
F;34-118/Domain: immunoglobulin homology <IMM>
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C;Species: Homo sapiens (man)
                                                                                                                                                                                   77.5%;
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Matches 96; Conservative
                      1-121 <HAW>
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                      A;Residues:
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S31676
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77

Gaps

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Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 2.0-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: 820780
R;Mortari, F; Wang, J; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A;Description: Analysis of human cord blood Ig heavy chain IgA and IgG repertoire.
A;Reference number: 820764
A;Reference number: 820764
A;Statuus: preliminary
A;Molacule type: DNA
A;Residues: 1-118 <MOR>
A;Cross-references: EMBL:211958; NID:g33893; PIDN:CAA78015.1; PID:g33894
C;Superfamily: Immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
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                                                                                                  1 QVQLQESGPGLVKPSETLSLTCTVSGYSISS-GYYWGWIRQPPGKGLEWIGSMFHSGSSY 59
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                             6; Gaps
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Best Local Similarity 77.4%; Pred. No. 1.8e-36;
Matches 96; Conservative 10; Mismatches 12; Indels
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9, 2005, 11:46:52; Search time 61.4386 Seconds (without alignments) 991.843 Million cell updates/sec
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1 QVQLQESGPGLVKPSQTLSL.....DRETAGFDYWGQGTLVTVSS 119
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt 03:*

Database

1: uniprot_sprot:*
2: uniprot_trembl:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | sapien | sapien | sapien | sapien | sapien | sapien | sapien | sapien | sapien | sapien | musculu | musculu | musculu | musculu | musculu | sapien | sapien | sapien | musculu | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | tion | homo | homo | homo | рошо | рошо | ношо | homo | homo | homo | рошо | ношо | homo | homo | homo | homo | homo | homo | ношо | homo | homo | homo | homo | พนธ ก | mus n | mus n | mus n | mus n | рошо | рошо | рошо | บ ธกพ |
| | Description | Q6gmx1 | Q6gmx6 | 07z379 | Q6gmx7 | 096ey0 | 09u173 | 095973 | Q96kx8 | Q6p4i8 | Q72374 | Q8izd7 | Q86sx2 | P01824 | Q9u175 | Q6nyh3 | Q8wux4 | Q6gmx5 | 09bu10 | Q96aa6 | 09bqb8 | P06331 | Q8tc63 | Q99m22 | Q61bq5 | P01822 | Q65zil | P01823 | P01825 | Q6mzx7 | Q7z3y6 | 091x92 |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | 1 | | | | | | | | | | | | | A. | | | | | | | | N. | | | | SE | | SE | A.N | | | |
| | QI | Q6GMX1 | Q6GMX6 | Q7Z379 | Q6GMX7 | Q96EY0 | Q9UL73 | 095973 | Q96KX8 | Q6P4I8 | 972374 | Q81ZD7 | Q86SX2 | HV2F HUMAN | Q9UL75 | Q6NYH3 | Q8WUX4 | Q6GMX5 | Q9BU10 | Q96AA6 | о во во | HV2I_HUMAN | Q8TC63 | Q99M22 | QGLBQS | HV46_MOUSE | Q65ZI1 | HV47 MOUSE | HV2G HUMAN | Q6MZX7 | Q7Z3Y6 | Q91X92 |
| | BB | 8 | ~ | ~ | 7 | 7 | ~ | ~ | 7 | 7 | ~ | 7 | N | - | 0 | ~ | ~ | 7 | 7 | ~ | ~ | - | ~ | ~ | ~ | - | 7 | - | - | ~ | ~ | 7 |
| | Match Length DB | 476 | 465 | 478 | 477 | 620 | 119 | 150 | 496 | 576 | 492 | 130 | 139 | 129 | | | | 597 | 597 | 625 | 597 | 146 | 473 | 479 | 136 | 137 | 262 | 113 | 117 | 476 | 116 | 482 |
| *
Ouery | Match | 82.1 | 79.8 | 79.2 | 77.1 | 77.0 | 76.4 | 74.9 | 74.8 | 73.3 | | 71.9 | 71.5 | 69.8 | 68.0 | 67.5 | 8.99 | 66.8 | 66.8 | 8.99 | 65.9 | 65.6 | 65.2 | 64.3 | 64.1 | ٠ | ٠ | 63.8 | 63.7 | 60.8 | 60.5 | 58.1 |
| | Score | 522 | 507.5 | 503.5 | 490.5 | 489.5 | | 476.5 | 475.5 | 466.5 | 461 | 457.5 | 455 | 444 | 432.5 | 429 | 425 | 425 | 425 | 425 | 419 | 417.5 | 414.5 | 409 | 407.5 | 407 | 407 | 406 | 405 | 387 | œ | 369.5 |
| Result | No. | 7 | 7 | m | 4 | ហ | 9 | 7 | ω | σ | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 52 | 56 | 27 | 28 | 29 | 30 | 31 |

| P18533 mus musculu P18531 mus musculu P01819 mus musculu P18532 mus musculu O95794 mus musculu Q91196 homo sapien Q81117 homo sapien P01816 homo sapien Q6177 homo sapien Q6177 homo sapien Q6177 homo sapien | |
|---|------------|
| HV62 MOUSE
HV60_MOUSE
HV61_MOUSE
HV61_MOUSE
Q99NG4
Q91U.96
Q811U5
HV02 XENLA
Q9UL72
HV2C HUMAN
Q61D78
Q6EQA4
Q9EQA4 | HV2D_HUMAN |
| | - |
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1117
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1108 | 125 |
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3 61.5
3 61.5
3 61.5
3 10.5
3 | 323 |
| W W W W W W W W A A A A A A A A A A A A | 4.
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ALIGNMENTS

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**X Subasepteen; **X MEDLINE=2288257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Distribute, D., Marushia K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., A Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKertan K.J., Malek J.A., Gunaratne P.H., Millaho D.K., Marzh D.M., Sodergran R.J., Lu X., Gibbs R.A., Villaton D.K., Marzh D.M., Sodergran B.J., Lu X., Gibbs R.A., A whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Breabey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Nordmutz J., Myers R.M., Touchman J.W., Gromutz J., Myers R.M., Butterfield Y.S., Jones S.J., Marrae M.A., Jones S.J., Marrae M.A., Jones S.J., Marrae M.A., Sone S.J., Marrae M.A., Sone S.J., Marrae M.A., Sone S.J., Marrae M.A., Sone M. C., Schoret Chan IS,000 full-length human and mouse CDNA sequences.";
                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Straubberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
BMBL; BC073773, AH73773.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig. c1.
InterPro; IPR003596; Ig. MHC.
InterPro; IPR003596; Ig. WHC.
InterPro; IPR003596; Ig. V.
Pfam; PP07654; C1-set; 3.
                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                     476 AA
                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 3.
SMART; SM00406; IGC1; 3.
PROSITE; PSS0835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                   PRT;
                                                                         05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                     PRELIMINARY;
                                                                                                                                  Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                     Q6GMX1
RESULT 1
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Gaps

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61 YNPSLKSRITLSVDTSKNQFSLKLNSMTAADŢAVYYCARDRET-AGFDYWGQGTLVTVSS 119
                                                                                                                                                                                                                                                                                                                  20 QVQLQESGPGLVXPSETLSLTCTVSGGSIS--GYYWSWIRQPAGKGLEWIGRIYTSGSTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 QVQLQESGPGLVKPSQTLSLTCTVSGGSIGSGDYFWSWIRQAPGRGLEWMGYIYYSGSTY
                                                                                                                                                                                                                    1 QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TSUBSHHamman rectum tumor;
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
Fobo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX538066; CAD97996.1;
HSSP; P01820; 1G7J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                      79.8%; Score 507.5; DB 2; Length 465; 84.9%; Pred. No. 3.3e-44; ive 7; Mismatches 8; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.2%; Score 503.5; DB 2; Length 478; 79.2%; Pred. No. 8.9e-44; ive 12; Mismatches 12; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;
                              Hypothetical protein.
SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2004 (TrEMBLrel. 25, Last sequence update)
Hypothetical protein DKF2p686K04218 (Fragment)
Hyme-EKFZp686K04218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INCEPPO I PRO0710; IG-like.
INCEPPO I PR003597; IG C1.
INCEPPO I PR003597; IG C1.
INCEPPO I PR003596; IG MHC.
INCEPPO I PR00554; IG V.
PFam; PF07654; C1-set; Z.
PR081TE; PS06045; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN Z.
     PS00290; IG MHC; UNKNOWN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 25, (TrEMBLrel. 25,
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                                                                                                                                                                Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQÜENCE
        PROSITE;
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                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YNPSLKSRITLSVDTSKNQFSLKINSMTAADTAVYYCARD-----RETA--GFDYWGQG 112
                                                                                                                                                                                           9
                                                                                                                                                                                                                                             79
                                                                                                                                                                                                                    QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGDYYWSWIRQPPGKGLEWIGYIYYSGSTY
                                                                                                                                                                                         1 QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY
                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                          8;
                                                                                Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                              52286 MW; 622AABA5C62DDE9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sci. U.S.A. 99:16899-16903(2002)
                                                                                82.1%; Score 522; DB 2; Lv 80.3%; Pred. No. 1.1e-45; ive 9; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              465 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; BC073766; AAH73766.1; -. InterPro; IPR003599; Ig. InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003597; Ig_c1.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF0044; C1.set; 3.
Pfam; PF0047; ig; 4.
SMART; SM0040; IG; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL_2004 (TrEMBLrel. 27, 05-JUL_2004 (TrEMBLrel. 27, 05-JUL_2004 (TrEMBLrel. 27, Hypothetical protein. Home sapiens (Human).
                                                                                                      Best Local Similarity 80.3%;
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
Hypothetical protein. SEQUENCE 476 AA; 5
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TMVTVSS 146
                                                                                                                                                                                                                                                                                                                                                                                                     TLVTVSS 119
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                                                                                Query Match
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RESULT 2 Q6GMX6

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(Fragment)
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Q9UL73;
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                                                  MEDINE-2218825; PubMed=11477932; DOI=10.1073/pnas 242603899;
XX MEDINE-2218825; PubMed=11477932; DOI=10.1073/pnas 242603899;
X Grausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
X Alachul S.F., Zeeberg B.S., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Alschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
A Diatchenko L., Marusina K., Farmer A.H., Rubin G.M., Hong L.,
Diatchenko L., Marusina K., Farmer A.H., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Villalon D.K., Marny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Nilalon D.K., Marny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Nilalon D.K., Marny D.M., Sodergren B.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 77.1%; Score 490.5; DB 2; Length 477; Local Similarity 81.7%; Pred. No. 2e-42; nes 98; Conservative 6; Mismatches 13; Indels 3.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 2e-42;
6; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; BC073765, AAH73765.1; -...
EMBL; BC073765, AAH73765.1; -...
InterPro; IPR003599; Ig. cl.
InterPro; IPR003599; Ig. cl.
InterPro; IPR003597; Ig. cl.
InterPro; IPR003597; Ig. cl.
InterPro; IPR003596; Ig. MHC.
InterPro; IPR003596; Ig. WHC.
InterPro; IPR003596; Ig. W.
PE07654; Cl-set; Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 477 AA; 51631 MW; 9FES9C09C50CFF85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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PROSITE; PS00290; IG MHC; UNKNOWN 2.
                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF07654; C1-set, 2. Pfam; PF00047; ig; 3. SMART; SM00409; IG; 4. SMART; SM00407; IGC1; 3. SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Primary B-Cells;
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Homo sapiens (Human)
                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
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MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;
X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
X Alausner R.D. Collins F.S., Wagner L.S., Shenmen C.M., Schuler G.D.,
A Alausner R.D., Collins F.S., Wagner L.S., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Latchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mitting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Coriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Jones S.J., Marra M.A.;
T Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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2
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011857; AAH11857.2; -.
PIR; S15590; S15590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Indels
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PROSITE; PS00290; IG MHC; UNKNOWN 3.
SEQUENCE 620 AA, 68125 MW; 990AlA4A6E8FF27B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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8; Mismatches 11
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InterPro; IPR007110; Ig-like.
InterPro; IPR0013597; Ig cl.
InterPro; IPR001006; Ig MHC.
InterPro; IPR003596; Ig v.
Pfam; PF07654; Cl-set; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 4
SMART; SM00406; IGv; 1.
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RA Strausberg R.L., Feingold E.A., Crouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Alteshul S.F., Zeeberg B., Buercow K.H., Schaefer C.F., Bhar N.K.,
RA Alteshul S.F., Zeeberg B., Buercow K.H., Schaefer C.F., Bhar N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
R. Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
R. Bosak S.A., McEwan D.J., McKernan K.J., Malak J.A., Gunaratne P.H.,
R. A. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
R. Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
R. Helton E., Ketteman M., Madan A., Gubes R.A.,
R. Raha J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
R. Rozywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YNPSLKSRITLSVDTSKNQFSLKLNSMTAADTAVYYCA----RDRETAGFDYWGQGTLV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 YNPSLKSRVTISVDTSKNQLSLKVRSVTAADTAVYFCARHGYSRSGRTGAIDYWGQGTLV 139
                                                                                61 YNPSLKSRITLSVDTSKNQFSLKLNSMTAADTAVYYCARDRETAGFDYWGQGTLVTVSS 119
                                                                                                   80 YNPSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCAR-LGMGAFDFWGHGTMVTVSS 137
                   20 QLQLQESGPGLVKPSETLSLSCTVSGGSISSTNYYWGWIRQPPEKGLEWIGSLHNSGSDY
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QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY
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                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO16369; AAH16369.1; -.
HSSP; P01876; 10W0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IRR007110; Ig-like.
InterPro; IRR003597; Ig_c1.
InterPro; IRR003506; Ig_rMc.
InterPro; IRR003506; Ig_v.
Pfam; PF07654; C1-set; Z.
SMART; SM00406; IGv; 1.
PROSITE; PS500835; IG_LIKE,
PROSITE; PS00290; IG_MC; UNKNOWN 1.
SRQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;
                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                 496 AA
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                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.
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TISSUE=Lung;
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TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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Q96KX8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLQESGPGLVKPSETLSLTCTVSGGSICS--YYWSWIRQPPGKGLEWIGYIYYSGSTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YNPSLKSRITLSVDTSKNOFSLKLNSMTAADTAVYYCARDRETAG--FDYWGOGTLVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                         "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
                                                        MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74.9%; Score 476.5; DB 2; Length 150; 75.6%; Pred. No. 1.6e-41; Live 14; Mismatches 14; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potential.
VH4 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                      'Match 76.4%; Score 486; DB 2; Length 11 Local Similarity 81.0%; Pred. No. 1.2e-42; les 98; Conservative 5; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
Submitted (CCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AP103795; AAC79084.1; -.
PIR; S31673; S31673.
PIR; S78056; S78056.
HSSP; P01820; 1G77.
                                                                                                                                                                                                                                                                                                                                                                                               119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150 AA; 16315 MW; 85664E04938AA7C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAX-2004 (TrEMBLrel. 26, Last annotation update)
VH4 heavy chain variable region precursor (Fragment)
                                                                                                                                                              Cin. Immunol. Immunopathol. 87:184-192 (1998).
EMBL; AF035041; AAD56277.1; -.
PIR; PH0876; PH0876.
PIR; S12416; S12416.
HSSP; P01820; 1G7J.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SWART; SM00406; IGV.
PROSTIE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR007110; Ig-like.
InterPro; IPR001596; Ig_v.
SMART; SM00406; IGv; 1.
PROSITE; PS50815; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 75.68
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19
>150
150
                                                                                                                                                                                                                                                                                                                                                                              119
                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S 119
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                                                                                                                                                                                                                                                                                                                                                      NON TER
NON TER
SEQUENCE
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Best Local S
Matches 98
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                                                                                                                                                 fetus.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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SIGNAL
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YNPSLKSRITLSVDTSKNOFSLKLNSMTAADTAVYYCARDRE--TAGFDYWGQGTLVTVS 118
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                                                                                                                                                                                         01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2004 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hyporhetical protein DKFZp686C0218 (Fragment).
Name=DKFZp686C0218;
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Anti-thyroglobulin heavy chain variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 72.5%; Score 461; DB 2; Length 49 Local Similarity 73.6%; Pred. No. 2.4e-39; Lonservative 12; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Human rectum tumor;
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Og
Fobo G., Han M., Wiemann S.;
Submitted (JUV. Wiemann S.;
Submitted (JUV. CAD98001.1; -.
EMBL, BX538077; CAD98001.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;
                                                                                                                                                                492 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR007110; Ig-like.
InterPro; IPR003106; Ig_C1.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003596; Ig_WHC.
InterPro; IPR003596; Ig_V.
Pfam; PF07654; C1-set; Z.
PR00406; IGV.
PR0SITE; PS06290; IG_LIKE; 4.
PROSITE; PS06290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8IZD7;
01-WAR-2003 (TrEMBLrel, 23, Created)
01-WAR-2003 (TrEMBLrel, 23, Last seq
01-WAR-2004 (TrEMBLrel, 26, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
Jang Y.-J., Chung J., Park J.-Y.,
                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                 S 119
                                                                                S 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s 152
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                                                 119
                                                                                146
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                                                                                                                                                                Q7Z374
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10 2812D7
AC Q812DD AC Q81ZDD DT 01-MA DT 01-MA DT 01-MA DE Anti-OS Homo OC Mamma OC Mamma OC NX NCBI-RP SEQUE
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                                                                                                                                                                                                                                                                                                                                   SCHENE FIGURE 18, TEACHS, MEDINE-21388257; PubMed=12477932; DOI=10.1073/pnas.242603899; ACTAUSBERG R.L., Feingold E.A., Grouse L.H., Derge J.G., Altausherg R.L., Feingold E.A., Grouse L.H., Derge J.G., Altausher R.D., Collins F.S., Wangner I., Schaefer C.F., Bhat N.K., A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A Diatchenko L., Marusina K.P., Farmer A.A., Rubin G.M., Hong L., Branderon M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Staplecon M., Josáres M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Altakebley R.W., Touchman J.W., Green E.D., Dickson M.C., Altakebley R.W., Touchman J.W., Green B.D., Dickson M.C., Altakebley R.W., Touchman J.W., Green E.D., Dickson M.C., Shaking M., Marinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., "Grouse Chantz J., Myers R.M., Tourden and initial analysis of more than 15,000 full-length human T. M. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC063384; AAH63384.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWART; SW00409; IG; I.
SWART; SW00407; IGc1; 3.
SWART; SW00407; IGc1; 3.
SWART; SW00406; IGV; I.
PROSITE; PS00290; IG_MRC; UNKNOWN 2.
SEQUENCE 576 AA; 63363 MW; FBB97C949D720F1E CRC64;
                                                                                                                                                         27, Created)
27, Last sequence update)
27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.3%; Score 466.5; DB 2
77.7%; Pred. No. 7.8e-40;
ive 7; Mismatches 17
                                                                                                                              576 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig-cl.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003596; Ig-v.
Pfam; PF07654; Cl-set; Z.
Pfam; PF07647; ig; 1.
                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 77.7
ses 94; Conservative
                                                                                                                                                         05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                           Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P01820; 1A7N
               119
                                             TVSS 143
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
             TVSS
                                                                                                                                                                                                         IGHD protein.
Name=IGHD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
                                            140
             116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                          Q6P418
Q6P418;
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Matches
                                                                                             RESULT 9
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Gaps

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61 YNPSLKSRITLSVDISKNOFSLKINSMIAADIAVYYCARDR-----ETAGFDYWG 110
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                                                                                                                                        Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                   MEDLINE-82222235; PubMed-6806818; Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.; Complete amino acid sequence of the delta heavy chain of human immunoglobulin D.";
                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
-!- MISCELLANEOUS: This chain was isolated from an IgD myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDINE-9814914; DOI=10.1006/clin.1998.4531; MEDLINE-98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Wux X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69.8%; Score 444; DB 1; Length 129; 65.9%; Pred. No. 3.2e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ol-MAR-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
(Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 AA; 14117 MW; D5D53D47ABE51319 CRC64;
                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SWART; SM00406; IGv; 1.
Direct protein sequencing; Immunoglobulin V region.
DOMAIN 1 113 Ig-like.
                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Ig heavy chain V-II region WAH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        PIR; A02099; DEHUWA.
HSSP; P01820; 1G7J.
GlycoSuiteDB; P01824; --
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR07110; Ig-11ke.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 65.99
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 QGTLVTVSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 OGTTVHVSS 129
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                                                                                                                                                                                                NCBI_TaxID=9606;
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                                     HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON TER
SEQUENCE
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                                     셤
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                                                                                                                                                                                                                                                                                                                                                               61 SGSPYYAPSLRSRVIISVDTSKNQLSLRLSSVTAADTAVYYCASPTHCSGGGCYAFFQHW 120
                                                                                                                                                                                                                                                                                                                                             ----YYNPSLKSRITLSVDTSKNOFSLKLNSMTAADTAVYYCARDRETAG-----FDYW 109
                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                            1 QVQLQQSGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQSPGKGLEWIGSLYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGST-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human) (Fragment).

Homo sapiens (Human).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Full-length cDNA clone CSODLO04YM19 of B cells (Ramos cell line)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                            / Match 71.9%; Score 457.5; DB 2; Length 130; Local Similarity 69.2%; Pred. No. 1.3e-39; Los 90; Conservative 12; Mismatches 17; Indels 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Match 71.5%; Score 455; DB 2; Length 139;
Local Similarity 88.0%; Pred. No. 2.5e-39;
les 88; Conservative 6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genoscope;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX248300; CA662627.1; -.
HSSP; PD1820; IG7J.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGV; 1.
PROSTIE; PS50835; IG_LIKE; 1.
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
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TISSUBER cells;
Li W.B., Gruber C., Jessee J., Polayes D.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                        130 AA; 13901 MW; 036131FC6EC1551E CRC64;
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              EMBL; AY145445; AAN64329.1; -... HSSP; PO1820; 1G7J. InterPro; IPR007110; Ig-like. InterPro; IPR003596; Ig-v. SMART; SM0406; IGv; 1... PROSITE; PSS0835; IG_LIKE; 1... NON TOTA
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 NDYRVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCARDLELLGQFDYWGQGTLVTV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLQOSGPGLVKPSQTLSLTCAISGDSVSSNSAAWNWIRQSPSRGLEWLGRTYYRSKWY
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"Myosin-reactive autoantibodies in rheumatic carditis and normal
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122 AA; 13719 MW; 56CB0612586A6529 CRC64;
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Last annotation update)
                                                                           Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035039; AAD56275.1; -.
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InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
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Best Local Similarity 68.9$
Matches 84; Conservative
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PS0089.
PS0090.
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PS0089; 1
PS0090; 1
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S24700;
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YNPSLKSRITLSVDTSKNOFSLKLNSMTAADTAVYYCAR--DRETAGFDYWGQGTLVTVS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 YNPSLESRVTMSVDTSKDOFSMKLTSVTAADTAIYYCARGYGGKSRYFDLWGRGVPVTVS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 QVDLQESGPGLVKPSETLSLTCSVSGDSIAS--YYWSWIRKSPQGGMEWIGYIFHSGTTL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYIYSSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Indels
                                                                                                                                              the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 478 AA; 51856 MW; 5F8B98F60F077256 CRC64;
and mouse cDNA sequences.";
Proc. Natl, Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.5%; Score 429; DB 2;
69.4%; Pred. No. 5e-36;
iive 16; Mismatches 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                              InterPro; IPR003599; Ig.
InterPro; IPR003100; Ig-like.
InterPro; IPR003509; Ig cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig v.
Pfam; PF07654; Cl-set; Z.
                                                                                                                       Strausberg R.;
Submitted (FEB-2004) to the
EMBL; BC066594; AAH66594.1;
HSSP; P01820; 1A7N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84; Conservative
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SMART; SM00407; IGC1; :
SMART; SM00406; IGV; 1
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Best Local Similarity
                                                                    SEQUENCE FROM N.A.
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                                                                                                rissum=Blood;
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(CMO) MATTE FIRM CHAI

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

9, 2005, 11:43:32; Search time 73.985 Seconds (without alignments) 627.306 Million cell updates/sec November Run on:

US-10-660-357A-29 629

1 QVQLVESGGGVVQPGRSLRL.....FGVVIDYGMDVWGQGTTVTV 120 Title: Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* Database

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Description | Adc99800 Anti-huma | | | Ads84372 Human ant | Adr68514 Anti-EPO- | Ads84396 Human ant | Adr68538 Anti-EPO- | Ads84376 Human ant | Ads84368 Human ant | Adr68518 Anti-EPO- | Adr68510 Anti-EPO- | Aam51167 Human DP- | Aae37209 Human AB- | Adp22128 Human ant | Adk18593 Anti-huma | Adk18785 Anti-huma | Adk18858 Anti-huma | Adl25404 Human mAb | Adp03979 Murine-ex | Adp03962 Murine-ex | Adp03963 Murine-ex | Aay93734 The heavy | Aae35889 Human 11. | Adp22316 Human ant | Adp47227 Human pho |
|-------------------------------|--------------------|----------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| ID | ADC99800 | ADD05404 | ADF09842 | ADS84372 | ADR68514 | ADS84396 | ADR68538 | ADS84376 | ADS84368 | ADR68518 | ADR68510 | AAM51167 | AAE37209 | ADP22128 | ADK18593 | ADK18785 | ADK18858 | ADL25404 | ADP03979 | ADP03962 | ADP03963 | AAY93734 | AAE35889 | ADP22316 | ADP47227 |
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Match Length DB | 120 7 | 120 7 | 120 7 | _ | _ | _ | 123 8 | 123 8 | _ | 123 8 | 123 8 | | 144 6 | 122 8 | 126 7 | 126 7 | • | 126 8 | 121 7 | 121 7 | 126 7 | • | 451 6 | 125 8 | 121 8 |
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Match | 100.0 | 100.0 | 100.0 | 92.3 | 92.3 | 91.8 | 91.8 | 91.7 | 91.7 | 91.7 | 91.7 | 91.6 | 6.06 | 8.06 | 8.06 | 8.06 | 8.06 | 8.06 | 90.5 | 90.5 | 90.5 | 90.2 | | 89.9 | 89.8 |
| Score | 629 | 629 | 629 | 580.5 | 580.5 | 577.5 | 577.5 | 576.5 | 576.5 | 576.5 | 576.5 | 576 | 571.5 | 571 | 571 | 571 | 571 | 571 | 569.5 | 569.5 | 569 | 567.5 | 67. | ٠ | 265 |
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No. | 1 | 7 | e, | 4 | 9 | 9 | 7 | 8 | σ | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 |

| | _ | | Adg96547 Single ch | | Adp22222 Human ant | Abp45319 Human BLy | Adg96146 Single ch | Adk18821 Anti-huma | Adk18786 Anti-huma | Adk18822 Anti-huma | Adk18882 Anti-huma | Adk18601 Anti-huma | Adl25420 Human mAb | Adr38663 Mouse hea | Adp22348 Human ant | Adp03980 Murine-ex | Ade28451 Human ant | Ade28475 Human ant | Aaw13531 Anti-mela |
|----------|----------|----------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| ADA89238 | AAY82629 | ABP45720 | ADG96547 | ADR38664 | ADP22222 | ABP45319 | ADG96146 | ADK18821 | ADK18786 | ADK18822 | ADK18882 | ADK18601 | ADL25420 | ADR38663 | ADP22348 | ADP03980 | ADE28451 | ADE28475 | AAW13531 |
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| 124 | 143 | 252 | 252 | 122 | 126 | 247 | 247 | 126 | 126 | 126 | 126 | 126 | 126 | 122 | 134 | 127 | 125 | 470 | 123 |
| 89.8 | 8.68 | 89.6 | 9.68 | 89.5 | 89.5 | 89.5 | 89.5 | 89.3 | 89.3 | 89.3 | 89.3 | 89.3 | 89.3 | 89.2 | 89.2 | 89.1 | 0.68 | 0.68 | 88.9 |
| 565 | 265 | 563.5 | 563.5 | 563 | 563 | 563 | 563 | 562 | 562 | 295 | 562 | 562 | 562 | 561 | 561 | 560.5 | 559.5 | 559.5 | 559 |
| 56 | 1.7 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast; Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 29 ADC99800 standard; protein; 120 AA (first entry) lung cancer; human. 01-JAN-2004 ADC99800; RESULT 1 ADC99800

Homo sapiens.

WO2003057838-A2.

17-JUL-2003.

26-DEC-2002; 2002WO-US041581.

28-DEC-2001; 2001US-0346299P.

(ABGE-) ABGENIX INC

Gudas J;

WPI; 2003-587113/55. N-PSDB; ADC99802. New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.

Claim 1; SEQ ID NO 29; 78pp; English.

The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the pancreatic or condition two specifically melanoma, oesophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung canneer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody

Pred. No. 3.3e-47;

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Best Local Similarity
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                    120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a menoclonal antibody comprising a heavy chain amino acid, where the monoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has cytostatic and can be used in the production of a vaccine. The monoclonal antibodies against the MUC18 antigen are useful for diagnosing and treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or tumour metastasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-MUC18 antibody heavy chain, variable region,
                                                                                                                                                                                                            9
                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 29.
                                                                                                                                           1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY
                                                                                                                                                               1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY
                                                                                                         Gaps
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                                                                      DB 7;
                                                                                       3.3e-47;
                                                     100.0%; Score ... 3.3e-100.0%; Pred. No. 3.3e-100.0%; O; Mismatches
heavy chain protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 29; 87pp; English.
                                                                                                                                                                                                                                                                                                                                        ADD05404 standard; protein; 120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-DEC-2002; 2002WO-US041582
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                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                     Best Local Similarity 100.
Matches 120; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bar-Eli M;
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N-PSDB; ADD05406.
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                                   Sequence 120 AA;
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                                                                                                                                                                                                                                                                                                                                                                           ADD05404;
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                                                                      Query Match
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Length 120;

DB 7;

100.0%; Score 629;

Query Match

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                                                                                                                                       1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAFGKGLEWVAVISYDGSNKYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell proliferation inhibition; MUC18 tumour antigen;
anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
carcinoma; cancer; malignancy; heavy chain; human.
                                                                                                        QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY
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Pred. No. 3.3e-47;
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100.08; Pr.
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100.0%;
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Best Local Similarity
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the pharmaceutical composition comprising a therapeutic amount of the above antibody or antibody fragment, and a pharmaceutical excipient; (4) a pharmaceutical composition comprising a therapeutic amount of the above antibody or antibody fragment, and a pharmaceutical excipient; (4) an isolated and purified equence, and their fragments, romplements and degenerate codon equivalents; and (5) an isolated and purified amino acid sequence, and their fragments. The Epo receptor binding antibody has antianaemic, neuroprotective and vulnerary activities, and can be used in gene therapy. The compositions and methods from the present invention can be used for modulating an endogenous activity of a human EPO receptor or for treating mammals suffering from aplasia or anaemia. They may also be used for identifying mammals having a dystunctional EPO receptor. The composition may also be used in promoting wound healing or in protecting against neural cell and/or tissue damage resulting from brain/spinal cord injury, stroke and the like. The present sequence represents a human anti-EPO-R antibody heavy chain variable region, which is given in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes an antibody or its fragment that binds to or activates an endogenous activity of a human erythropoietin (BPO) receptor in a mammal, but does not interact with a peptide having a sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1) methods of modulating or activating an endogenous activity of a human EPO receptor in a mammal, comprising administering to the mammal a therapeutic amount of the above antibody or its fragment to modulate or activate the receptor; (2) a method of treating a mammal suffering from aplasia, comprising administering to the mammal a therapeutic amount of the above antibody or its fragment to modulate or activate the receptor;
                                                                                                                                                                                                                                                    erythropoietin receptor binding antibody; EPO receptor binding antibody, antianaemic; neuroprotective; vulnerary; gene therapy; aplasia; anaemia; wound healing; neural call damage protection; neural tissue damage protection; brain injury; spinal cord injury; stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.
                                                                                                                                                                                     Human anti-BPO-R antibody heavy chain variable region SEQ ID NO:11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antibodies that bind to or activate an endogenous human erythropoietin receptor, useful for diagnosing, preventing or tre disorders associated with dysfunctional erythropoietin receptor,
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                                                                                                                                                                                                                                 human; erythropoietin receptor; BPO receptor; erythropoietin receptor binding antibody; EPO
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                                             ADS84372 standard; protein; 123 AA.
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10-OCT-2003; 2003US-00684109
                                                                                                                                       (first entry)
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RESULT 4
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Sequence 123 AA;

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                                                                                                                                                                  61 ADSVKGRFTISRDNSKNTLYLQMNSLRVEDTAVYYCARDHGGRYVYDYGMDVWGQGTTVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antibody or its antibody fragment that activates an endogenous activity or is capable of binding to a human erythropoietin receptor in a mammal, useful for treating a mammal suffering aplasia or anemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antianaemic; respiratory; vulnerary; gene therapy; vaccine; erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia; hypoxaemia; chronic tissue hypoxa; blood circulation; blood flow; wound healing; neural cell damage; tissue damage, brain injury; spinal cord injury; stroke; anti-EPO-R-antibody; heavy chain;
                                                                                               QVQLVESGGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY
                                                                         1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY
                                                                                                                                              61 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCARSIFG-VVIDYGMDVWGQGTTVT
                                           Gaps
                                       1;
       Length 123;
                                       Indels
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Score 580.5; DB 8;
Pred. No. 5.7e-43;
0; Mismatches 7;
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   92.3%;
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Query Match 92.3
Best Local Similarity 93.4
Matches 113; Conservative
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(GREE/) GREEN L L
(WIEL/) WIELER J.
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ADR68514
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equivalents; and an isolated and purified amino acid sequence selected from 39 sequences comprising 27-552 amino acids (add SEQ ID NOs between SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or modulates the antibody or its antibody fragment that activates or modulates the activity of the receptor is useful in a method of treating a mammal suffering aplasia or anaemia. The antibodies are also useful for treating disorders characterised by decreased or subnormal levels of oxygen in the blood or tissue such as hypoxaemia or chronic tissue hypoxia and/or diseases characterised by inadequate blood circulation or reduced blood flow. They are also useful for promoting wound healing or for protecting against neural cell and/or tissue damage, resulting from brain/spinal cord mijury, stroke and the like. The antibodies are also useful for identifying or diagnosing mammals having dysfunctional errythropoletin receptor. This is the amino acid sequence of an anti-EPO-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ADSVKGRFTISRDNSKNTLYLQMNSLRVEDTAVYYCARDHGGRYVYDYGMDVMGQGTTVT 120
    and degenerate codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSIFG-VVIDYGMDVWGQGTTVT 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; erythropoietin receptor; EPO receptor; erythropoietin receptor binding antibody; erythropoietin receptor binding antibody; EPO receptor binding antibody; antianaemic; neuroprotective; vulnerary; gene therapy; aplasia; anaemia; wound healing; neural cell damage protection; neural tissue damage protection; brain injury; spinal cord injury; stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY
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                                                                                                                                                                                                                                                                                                                                                                                    Length 123;
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    complements,
                                                                                                                                                                                                                                                                                                                                                                               Score 580.5; DB 8;
Pred. No. 5.7e-43;
0; Mismatches 7;
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  specification, and their fragments,
                                                                                                                                                                                                                                                                                                    antibody heavy chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADS84396 standard; protein; 123 AA.
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10-OCT-2003; 2003US-00684109
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 93.4%;
Matches 113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-348433/32.
N-PSDB; ADS84395.
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                                                                                                                                                                                                                                                                                                                                            Sequence 123 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 V 120
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The present invention describes an antibody or its fragment that binds to or activates an endogenous activity of a human erythropoietin (BPO) areceptor in a mammal, but does not interact with a peptide having a creceptor in a mammal, but does not interact with a peptide having a creceptor in a mammal. Onc:, ADSB4362). Also described: (1) methods of modulating or activating an endogenous activity of a human BPO creceptor in a mammal. Comprising administering to the mammal a creceptor; (2) a method of treating a mammal suffering from aplasia, comprising administering to the mammal a therapeutic amount of the above antibody or its fragment to modulate or activate the receptor; (3) a pharmaceutical composition comprising a therapeutic amount of the above antibody or its fragment, and a pharmaceutical excipient; (4) a nisolated and purified polyuncleotide sequence, and their fragments, complements and degenerate codon equivalents; and (5) an isolated and purified polyuncleotide sequence, and their fragments. The BPO receptor building antibody has antianemic, neuroprotective and vulnerary activities, and can be used in gene therapy. The compositions and methods from the present invention can be used for identifying mammals having a dysfunctional BPO receptor or for treating mammals suffering from aplasia or anaemia. They may also be used for identifying mammals having a cetivity of a human BPO receptor or for treating mammals enfering and the composition may also be used in compassion may also be used in the present sequence represents a human anti-BPO-R antibody heavy compassion may also be used in the exemplification of the present sequence represents a human anti-BPO-R antibody heavy compassion in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCARSIFG-VVIDYGMDVWGQGTTVT 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY
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disorders associated with dysfunctional erythropoietin receptor, e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 577.5; DB 8; Length 123;
Pred. No. 1e-42;
1; Mismatches 7; Indels 1:
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                                                                  Claim 9; SEQ ID NO 35; 192pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADR68538 standard; protein; 123 AA.
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Best Local Similarity
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variable region.
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                            anemia.
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ADS84376;

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The invention describes an antibody or its fragment that activates an endogenous activity or capable of binding to a human erythropoietin receptor in a mammal, or that comprises at least one heavy or light chain covariable region having a sequence comprising 116 or 107 amino acids (SEQ ID NO: 3 or 5) given in the specification or its fragment, but does not interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also given in the specification. Also described are: a method of activating or modulating an endogenous activity of a human erythropoietin receptor in a modulating an endogenous activity of a human erythropoietin receptor in a manmal; a pharmaceutical composition comprising a therapeutic amount of an antibody or antibody fragment above and a pharmaceutical excipient; and an antibody or antibody fragment above and a pharmaceutical excipient; and an antibody or antibody fragment above selected from 28 sequences comprising 32-370 bp (even SEQ ID NOs between SEQ ID NO: 2-56) given in the specification, and their fragments, complements, and degenerace coden (equivalents; and an isolated and purified amino acid sequence selected from 35 sequences comprising 27-552 amino acids (odd SEQ ID NO: 55-68) given in the specification or their fragments. The antibody fragment that activates or modulates the activity of the receptor is useful in a method of treating a longerers characterised by decreased or subnormal levels of oxygen in the blood or tissue such as hypoxaemia or chronic tissue cure treating disorders characterised by inadequate blood circulation or reduced blood flow. They are also useful for pronormal levels are also useful for identifying or diagnosing mammals having dysfunctional erythropoietin receptor. This is the amino acid sequence of an anti-EPO-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antibody or its antibody fragment that activates an endogenous activity or is capable of binding to a human erythropoietin receptor in a mammal, useful for treating a mammal suffering aplasia or anemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Wieler J;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Green LL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; SEQ ID NO 35; 156pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                          Reilly EB,
10-OCT-2003; 2003US-00684109.
                                                                                 14-OCT-2002; 2002US-0418031P.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Ostrow DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-661369/64.
                                                                                                                                                                                                            OSTROW D H. REILLY E B.
                                                                                                                                                                                                                                                                                                  GREEN L L.
                                                                                                                                                                                                                                                                                                                                               WIELER J.
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(REIL/)
(GREE/)
(WIEL/)
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61 ADSVKGRFTISRDNSKNTLYLQMNSLRVEDTAVYYCAKDHGGRYVYDYGMDVWGQGTTVT 120
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                                                                        1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY
                                                                                                             61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSIFG-VVIDYGMDVWGQGTTVT
                              Gaps
                             ۲:
  Length 123;
                             Indels
91.8%; Score 577.5; DB 8; 92.6%; Pred. No. 1e-42;
                           7;
                           1; Mismatches
                           Conservative
           Best Local Similarity
Matches 112; Conserv
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activities, and can be used in gene therapy. The compositions and methods from the present invention can be used for modulating an endogenous activity of a human BPO receptor or for treating mammals suffering from applasta or anaemia. They may also be used for identifying mammals from a dysfunctional BPO receptor. The composition may also be used in promoting wound healing or in protecting against neural cell and/or tissue damage resulting from brain/spinal cord injury, stroke and the

tissue damage resulting from brain/spinal cord injury, stroke and the like. The present sequence represents a human anti-EPO-R antibody heavy chain variable region, which is given in the exemplification of the

present invention Sequence 123 AA;

chain

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The present invention describes an antibody or its fragment that binds to activates an endogenous activity of a human erythropoietin (BPO)

Creceptor in a mammal, but does not interact with a peptide having a sequence of 30 antino activating an endogenous activity of a human BPO receptor in a mammal, comprising administering to the mammal a therapeutic amount of the above antibody or its fragment to modulate or activate the receptor; (2) a method of treating a mammal suffering from aplasia, comprising administering to the mammal a therapeutic amount of the above antibody or its fragment to modulate or activate the receptor; (3) a pharmaceutical composition comprising a therapeutic amount of the above antibody or antibody fragment, and a pharmaceutical excipient; (4) an isolated and degenerate codon equivalents; and (5) an isolated and codo sequence, and their fragments, complements and degenerate codon equivalents; and (5) an isolated and purified amino acid sequence, and their fragments. The BPO receptor binding antibody has antianaemic, neuroprotective and vulnerary
                                                                                                                           human; erythropoietin receptor; EPO receptor; erythropoietin receptor binding antibody; erythropoietin receptor binding antibody; erythropoietin receptor binding antibody; antianaemic; neuroprotective; vulnerary; gene therapy; aplasia; anaemia; wound healing; neural cell damage protection; neural tissue damage protection; brain injury; spinal cord injury; stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antibodies that bind to or activate an endogenous human erythropoietin receptor, useful for diagnosing, preventing or treating disorders associated with dysfunctional erythropoietin receptor, e.g.
                                                                                          Human anti-EPO-R antibody heavy chain variable region SEQ ID NO:15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wieler J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reilly EB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 9; SEQ ID NO 15; 192pp; English.
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                                                                                                                                                                                                                                                                                                                                                                             14-OCT-2003; 2003WO-US032243.
                                                                                                                                                                                                                                                                                                                                                                                                                  14-OCT-2002; 2002US-00269711
10-OCT-2003; 2003US-00684109
                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-348433/32.
N-PSDB; ADS84375.
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                                                                                                                                                                                                                                                                 Homo sapiens.
                                                      18-NOV-2004
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1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60 Gaps 1; 8; Indels 0; Mismatches Matches 112; Conservative

1;

Length 123;

Score 576.5; DB 8;

91.7%;

Local Similarity

Query Match

Pred. No. 1.3e-42;

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ADS84376 standard; protein; 123 AA.

RESULT 8 ADS84376 ID ADS8

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ADR68518;
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(GREE/)
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Cor activates an endogenous activity of a human erythropoletin (EPO)

Cor ecceptor in a mammal, but does not interact with a peptide having a sequence of 30 amino acids (ESO ID NO:1, ADS84362). Also described: (1)

methods of modulating or activating an endogenous activity of a human EPO creceptor in a mammal, comprising administering to the mammal a creceptor; (2) a method of treating a mammal suffering from activate the receptor; (2) a method of treating a mammal suffering from aplasia, comprising administering to the mammal a therapeutic amount of the above antibody or its fragment to modulate or activate the receptor; (3) a pharmaceutical composition comprising a therapeutic amount of the above antibody or antibody fragment, and a pharmaceutical excipient; (4) a plasmaceutical composition comprising a therapeutic amount of the above antibody or antibody fragment, and a pharmaceutical excipient; (4) complements and degenerate codon equivalents; and (5) an isolated and composition and their fragments. Complements and degenerate codon equivalents; and (5) an isolated and compositions and methods from the present invention can be used for modulating an endogenous activity of a human EPO receptor or for treating mammals suffering from
                                                              ADSVKGRFTISRDNSKNTLYLQMNSLRVEDTAVYYCARDHGGRYVYDYGMDVWGQGTTVT 120
                   9
                                                                                                                                                                                                                                                                                                                                         receptor binding antibody;
therapy; aplasia; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antibodies that bind to or activate an endogenous human erythropoietin receptor, useful for diagnosing, preventing or treating disorders associated with dysfunctional erythropoietin receptor, e.g.
61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSIFG-VVIDYGMDVWGQGTTVT
                                                                                                                                                                                                                                                                                                                          human; erythropoietin receptor; EPO receptor; erythropoietin receptor binding antibody; EPO receptor binding antibody; EPO receptor binding antianamic; neuroprotective; vulnerary; gene therapy; aplasia; ans wound healing; neural cell damage protection; neural tissue damage protection; brain injury; spinal cord injury; stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.
                                                                                                                                                                                                                                                                                                Human anti-EPO-R antibody heavy chain variable region SEQ ID NO:7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reilly EB,
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                                                                                                                                                                                                            ADS84368 standard; protein; 123 AA.
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10-OCT-2003; 2003US-00684109
                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSIFG-VVIDYGMDVWGQGTTVT 119
aplasia or anaemia. They may also be used for identifying mammals having a dysfunctional BPO receptor. The composition may also be used in promoting wound healing or in protecting against neural call and/or tissue damage resulting from brain/spinal cord injury, stroke and the like. The present sequence reppresents a human anti-EPO-R antibody heavy chain variable region, which is given in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antianaemic; respiratory; vulnerary; gene therapy; vaccine; erythropoietin receptor; EPO-R, anti-EPO-R-antibody; aplasia; anaemia; hypoxaemia; chronic tissue hypoxa; blood circulation; blood flow; wound healing; neural cell damage; tissue damage; brain injury; spinal cord injury; stroke; anti-EPO-R-antibody; heavy chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLVESGGGVVQPGRSLRLSCVASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY
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                                                                                                                                                                                                                                                                                                                Score 576.5; DB 8;
Pred. No. 1.3e-42;
0; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; SEQ ID NO 15; 156pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reilly EB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADR68518 standard; protein; 123 AA.
                                                                                                                                                                                                                                                                                                                91.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                           Matches 112, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DH,
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OSTROW D H.
REILLY E B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Devries PJ, Ostrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-661369/64.
                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GREEN L L.
                                                                                                                                                                                            present invention
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                                                                                                                                                                                                                                                         Sequence 123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2004175379-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 V 120
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cc receptor in a mammal, or that comprises at least one heavy or light chain variable region having a sequence comprising 116 or 107 amino acids (SEQ ID No: 3 or 5) given in the specification or its fragment, but does not interact with a peptide comprising 30 amino acids (SEQ ID No: 1) also given in the specification. Also described are: a method of activating or modulating an endogenous activity of a human erythropoietin receptor in a mammal; a pharmaceutical composition comprising a therapeutic amount of an antibody or antibody fragment above and a pharmaceutical excipient, and mammal; a pharmaceutical composition comprising a therapeutic amount of an antibody or antibody fragment above and a pharmaceutical excipient, and mammal; a pharmaceutical excipient, and mammal; a pharmaceutical excipient, and an isolated and purified amino acid sequences comprising 322-370 bp (even SEQ ID Nos between SEQ ID No: 2-56) given in the specification or comprising 27-552 amino acid sequence selected from 3-57, and SEQ ID No: 58-68) given in the specification or complements; and an isolated and purified amino acid sequence selected from 3-57, and SEQ ID No: 58-68) given in the specification or mammal suffering aplasia or ansemia. The antibodies are also useful for treating disorders characterised by decreased or subnormal levels of oxygen in the blood or tissue such as hypoxaemia or chronic tissue changes, resulting from the protecting against neural cell and/or tissue damage, resulting from brain/spinal cord injury, stroke and the like. The antibodies are also useful for promoting wound healing or expincypoletin receptor. This is the amino acid sequence of an anti-EPO-R antibody when we thin variable residence when the mino acid sequence of an anti-EPO-R antibody when we thin variable residence. antibody heavy chain variable region. %\$GGGGGGGGGGGGGGGGGGGGGGGGGG

Sequence 123 AA;

61 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCARSIFG-VVIDYGMDVWGQGTTVT 119 61 ADSVKGRFTISRDNSKNTLYLQMNSLRVEDTAVYYCARDHGGRYVYDYGMDVWGQGTTVT 120 9 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 1 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVVISYDGSNKYY Gaps .. H Score 576.5; DB 8; Length 123; Pred. No. 1.3e-42; Query Match
91.7%; Score 576.5;
Best Local Similarity 92.6%; Pred. No. 1.3e
Matches 112; Conservative 0; Mismatches 120 V 120 121 V 121 Query Match 셤 ઠ 음 8 g ઠે

RESULT 11

ADR68510; ADR68510

ADR68510 standard; protein; 123 AA. (first entry) 02-DEC-2004

Anti-EPO-R-antibody heavy chain variable region segid 7.

antianaemic; respiratory; vulnerary; gene therapy; vaccine; erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia; hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow; wound healing; neural cell damage; tissue damage; brain injury; spinal cord injury; stroke; anti-EPO-R-antibody; heavy chain; variable region

Homo sapiens.

US2004175379-A1.

09-SEP-2004.

10-OCT-2003; 2003US-00684109.

14-OCT-2002; 2002US-0418031P

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The invention describes an antibody or its fragment that activates an endogenous activity or capable of binding to a human erythropoietin candogenous activity or capable of binding to a human erythropoietin cemperator in a mammal, or that comprises at least one heavy or light chain variable region having a sequence comprising 116 or 107 amino acids (SEQ ID NO: 3 or 5) given in the specification or its fragment, but does not interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also carriated in the specification. Also described are: a method of activating or modulating an endogenous activity of a human erythropoietin receptor in a martibody or antibody fragment above and a pharmaceutical excipient; an isolated and purified polynuclectide sequence selected from 28 sequences comprising 322-370 bp (even SEQ ID NOs between SEQ ID NOs 2-56) given in the specification, and their fragments, complements, and degenerate codon equivalents; and an isolated and purified amino acids sequence selected from 39 sequences comprising 27-55 amino acids sequence selected from 55 from 39 sequences comprising 27-55 amino acids (add SEQ ID NOs 3-57, and SEQ ID NO: 58-68) given in the specification or their fragments. The antibody or its antibody fragment that activates or modulates the activity of the receptor is useful in a method of treating a mammal suffering aplasia or anamia. The antibodies are also useful for the receptor is useful in a method of treating carments and an anamal suffering aplasia or anamia. The antibodies are also useful for the receptor is useful in a sequence of the receptor is useful in a method of treating aplasia or anamia. The antibodies are also useful for the receptor is useful in the specification or the receptor is useful in a method of treating the receptor is useful in a method of treating and an anamal suffering aplasia or anamial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oxygen in the blood or tissue such as hypoxaemia or chronic tissue thypoxia and/or diseases characterised by inadequate blood circulation or reduced blood flow. They are also useful for promoting wound healing or for protecting against neural cell and/or tissue damage, resulting from brain/spinal cord injury, stroke and the like. The antibodies are also useful for identifying or diagnosling mammals having dystunctional erythropoietin receptor. This is the amino acid sequence of an anti-EPO-R antibody heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                 New antibody or its antibody fragment that activates an endogenous activity or is capable of binding to a human erythropoietin receptor in a mammal, useful for treating a mammal suffering aplasia or anemia.
                                                                                                                                                                                     Wieler J;
                                                                                                                                                                                     Green LL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 6; SEQ ID NO 7; 156pp; English
                                                                                                                                                                                  Reilly EB,
                                                                                                                                                                                  Ostrow DH,
                         OSTROW D H. REILLY E B. GREEN L L.
                                                                                                                                                                                                                                           WPI; 2004-661369/64.
                                                                                                                     WIELER J.
                                                                                                                                                                                                                                                                        N-PSDB; ADR68509
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                                                                                                                  (WIET/)
                                                                                      (GREE/)
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1; 91.7%; Score 576.5; DB 8; Length 123; Indels ., Pred. No. 1.3e-42; 0; Mismatches 8 92.68; Query Match
Best Local Similarity 92.6
Matches 112; Conservative

Sequence 123 AA;

61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSIFG-VVIDYGMDVWGQGTTVT 119 120 9 61 ADSVKGRFTISRDNSKNTLYLQMNSLRVEDTAVYYCARDHGGRYVYDYGMDVWGQGTTVT g ઠે g

9

Gaps

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY

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AAM51167 standard; protein; 118 AA. AAM51167; AAM51167 XXXXXX

RESULT 12

(first entry) 10-JUN-2002

Tumour necrosis factor alpha, TNF; antibody, heavy chain, CDR; complementarity determining region; antirheumatic; antiarthritic; antialcer; antiathmatic; antiallergic; antiinflammatory; antisickling; antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropic; antianginal; cardiant; antibacterial; virucide; fungicide; antileprotic; protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic; human; diagnosis; therapy; DP-46. Novel isolated mammalian anti-tumor necrosis factor antibody, useful for treating sickle cell anemia, diabetes, atherosclerosis, restenosis, angina pectoris, myocardial infarction, leprosy. à Shealy 'n Scallon Human DP-46 heavy chain variable region. Heavner G, location/Qualifiers Example 3; Fig 4; 131pp; English. 50. .66 /label= CDR2 67. .98 /label= FR3 99. .107 /label= CDR3 108. .118 07-AUG-2000; 2000US-0223360P. 29-SEP-2000; 2000US-0236826P. 01-AUG-2001; 2001US-00920137. 07-AUG-2001; 2001WO-US024785 36. .49 /label= FR2 31. .35 /label= CDR1 .. .30 'label= FR1 108. .118 /label= J6 DM, Giles-Komar J, Knight (CENZ) CENTOCOR INC. WPI; 2002-217194/27, N-PSDB; ABL53507 WO200212502-A2 sapiens 14-FEB-2002 Region Region Region Region Region Region Region Ношо

The present sequence is that of a human DP-46 heavy chain variable region encoded by a human germline DP-46 gene in a transgenic mouse used in human monoclonal antibody (mab) construction. A Gentry fusion was performed using spleen cells from a hybrid mouse containing human variable and constant region antibody transgenes that was immunised with recombinant human tumour necrosis factor (TMF) alpha. Human makes were obtained that bound immobilised human TgG1, kappa isotype. Their heavy chain variable region deduced amino acid sequences (see AMMS1168-72) showed high similarity to the DP-46 sequence. The invention provides isolated human, primate, rodent, mammalian, chimeric, humanised and/or complementarity determining region (CDR)-grafted anti-TMF antibody compositions, encoding or complementary nucleic acids, vectors, immunoglobulins, and cleavage products and variants, as well as anti-TMF antibody compositions, formulations, devices, transgenic animals, cransgenic plants, and methods of making and using them. The anti-TMF antibody comprises at least a portion of an immunoglobulin molecule, especially the heavy chain and/or light chain variable regions given in the present sequence and in AMMS1165, or either all of the CDRs of the heavy chain (see AMMS118-60) or all of the CDRs of the heavy chain (see AMMS118-60) or all of the CDRs of the heavy chain (see AMMS118-60) or all of the CDRs of the heavy chain (see AMMS118-60) or all of the CDRs of the heavy chain and inhibit TMP-induced cell and in the composition. heavy chain (see AAM51158-60) or all of the CDRs of the light chain (se AAM51161-63). The antibodies may inhibit TNF-induced cell adhesion molecules, inhibit TNF binding to receptor, or provide Arthritic Index

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The invention relates to an antibody or its antigen-binding fragment which specifically binds to epitope on prostate specific membrane antigen (SPMA), and competitively inhibits the specific binding of a second antibody to its target epitope on PSMA. The invention is useful for diagnosing, treating or preventing PSMA-mediated disease such as prostate
                                                                                                                                                                                                                                                                                                                                                                                                                            120
                                                                                                                                                                                                                                                                                                                                                                                                                                                    in a mouse model. They are useful for diagnosing or treating of condition in a cell, tissue, organ or animal (claimed) such
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated antibody which binds to epitope on prostate specific membrane antigen, and competitively inhibits binding of second antibody to its target epitope on the antigen, useful for treating prostate
improvement in a mouse model. They are useful for diagnosing or treating a TNF related condition in a cell, tissue, organ or animal (claimed) su as rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis, crohn's pathology, sickle cell anaemia, diabetes, a cardiovascular disease such as arteriosclerosis, atherosclerosis, restenosis, angina pectoris or myocardial infarction, an infectious disease in a cell such as bacterial, viral, and fungal infections, pneumonia, leprosy and malaria, a malignant disease such as leukaemia, chronic myelocytic leukaemia, purkitis' s lymphoma and multiple myeloma, or a neurological disease such as multiple sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and Creutzfeldt-Jakob disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, Prostate specific membrane antigen; carcinoma; sarcoma; cancer; PSMA; melanoma; therapy; N-acetylated alpha-linked acidic dipeptidase; folate hydrolase; dipeptidal dipeptidase IV; gamma-glutamyl hydrolase; NAALADase; antibody; heavy chain variable region; VH.
                                                                                                                                                                                                                                                                                                                                                                      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSIFGVVIDYGMDVWGQGTTVTV
                                                                                                                                                                                                                                                                                                                                                1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY
                                                                                                                                                                                                                                                                                                            4; Gaps
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                                                                                                                                                                                                                                                                       Length 118;
                                                                                                                                                                                                                                                                     91.6%; Score 576; DB 5; Length 11
93.3%; Pred. No. 1.4e-42;
ive 1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE37209 standard; protein; 144
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07-MAR-2002; 2002US-0362747P.
20-SEP-2002; 2002US-0412618P.
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Matches 112; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PSMA-) PSMA DEV CO LLC
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N-PSDB; AAE56224
                                                                                                                                                                                                                                     Sequence 118 AA;
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                                                                                                                                                                                                                                                                       Query Match
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transitional cell carcinoma, panoreatic cancer including panoreatic duct carcinoma, lung carcinoma, ricluding non-small cell lung carcinoma, kidney carcinoma, lung carcinoma, kidney carcinoma, lung carcinoma, kidney cancer including conventional renal cell carcinoma, sarcoma including soft tissue sarcoma, breat cancer including glioblastoma multiforme, neuroendocrine carcinoma, colon cancer including glioblastoma multiforme, neuroendocrine carcinoma, colon testicular embryonal carcinoma, or melanoma including malignant melanoma. The invention is useful also for inhibiting or enhancing folate hydrolase activity of a NAALADase polypeptide alpha-linked acidic dipeptidase (NAALADase) activity of a NAALADase polypeptide, dipeptidase IV activity of a dipeptidy dipeptidase IV activity of a dipeptidy dipeptide, panama-glutamyl hydrolase activity of a gamma-glutamyl hydrolase activity of a gamma-glutamyl hydrolase polypeptide. The present sequence is human PSNA antibody heavy chain variable region (VH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anti-TNFa antibody; anabolic; antiarteriosolerotic; antiarthritic; antiboterial; antiarthritic; antiboterial; antiarthritic; eating-disorder; antiarthritic; eating-disorder; immunomodulator; immunosuppressive; nephrotropic; neuroprotective; vasotropic; antiapoptotic; TNFa antagonist; TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer; bladder cancer; lung cancer; glioblastoma; stomach cancer; endometrial cancer; immuno-mediated inflammatory disease; prostrate cancer; immuno-mediated inflammatory disease; restenosis; autoimmune disease; Crobn's disease; graft-host reaction; septic shock; cachexia; anorexia; multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSIFGVVI---DYGMDVWGQGTT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARVLVGALYYYNYYGMDVWGQGTT 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 QVQLVESGGGVVQPGRSLRLSCAASGFTFISYGMHWVRQAPGKGLEWVAVISYDGSNKYY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
  cancer or non-prostate cancer bladder chosen from cancer including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human anti-TNFa antibody heavy chain variable region SEQ ID NO:34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       monoclonal antibody; tumour necrosis factor-alpha; TNFa;
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Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee F
Manchulencho K, Faggioni R, Senaldi G, Qiaojuan JS;
                                                                                                                                                                                                                                                                                                                                                                                                             Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                      Score 571.5; DB 6;
Pred. No. 4.1e-42;
2; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADP22128 standard; protein; 122 AA.
                                                                                                                                                                                                                                                                                                                                                                                                   90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 90.2
Matches 111; Conservative
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                                                                                                                                                                                                                                                                                                                                                            Sequence 144 AA;
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The present interaction describes a righman monocloust annihold, in the present interaction describes a righman monocloust annihold, in the present interaction described to the monocloust annihold, in the level of Threa in a patient sample, comprising contacting with (I), and detecting the level of binding between the antibody and Thre in the level of Threa in a patient sample, comprising contacting with (I), and detecting the level of binding between the antibody and Thre in the sample; (2) a composition comprising the articlody or its functional fragment and a carrier; (3) treating (M2) an animal suffering from a neoplastic, or an immuno-mediated inflammatory disease by selecting an animal in need of treatment for the disease by administering the human monoclonal antibody of (I); and (4) inhibiting (M3) Threatment for Threa induced apoptosis by administering the human monoclonal antibody of (I); and (4) inhibiting (M3) Threatment for Threa induced apoptosis by administering the human monoclonal antibody of (I). (I) has anabolic, antiarteriosclerotic, antirheumatic, eating-contental, antihifammatory, antipsoriatic, antirheumatic, eating-contental, antihifammatory, antipsoriatic, antiheumatic, eating-contental, antihifammatory, antipsoriatic, antiheumatic, eating-contental, antihifammatory, antipsoriatic, antiheumatic, eating-contental, antihifammatory, antipsoriatic, antiheumatic, eating-contents, immunomodulator, immunomodula
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pancreatic cancer, and prostrate cancer; or immuno-mediated inflammatory diseases such as rheumatoid arthritis, glomerulonephritis, atherosclerosis, psoriasis, restenosis, autoimmune disease, crohn's disease, graft-host reactions, septic shock, cachexia, anorexia, and multiple sclerosis. The present sequence represents a human anti-TNFa antibody heavy chain variable region, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                            New recombinant human monoclonal antibody that specifically binds to Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such as cancers, or immuno-mediated inflammatory diseases such as rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSIFGVVIDYGMDVWGQGTTVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQDNWNYYYGMDVWGQGTTVTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.8%; Score 571; DB 8; Length 12 llarity 92.5%; Pred. No. 3.8e-42; Conservative 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-human PDGF-D antibody heavy chain protein sequence.
                                                                                                                                                                                                                                         Example 10; SEQ ID NO 34; 213pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADK18593 standard; protein; 126 AA
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                       WPI; 2004-480601/45.
N-PSDB; ADP22127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 122 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003057857-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111;
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The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEKZ93 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
                                                                                                                                                Weber R;
                                                                                                                                                                                                                                       New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.
                                                                                                                                                Gazit G,
                                                                                                                                                Chen F,
                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 17; 255pp; English
                                                                                                                                                Yang X,
                                                                                                                                                Feng X,
                                 06-JAN-2003; 2003WO-US000398
                                                                      07-JAN-2002; 2002US-00041860
                                                                                                                                                Corvalan JRF, Jia X,
                                                                                                                                                                                                        WPI; 2003-587119/55.
                                                                                                           (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 126 AA;
17-JUL-2003
                                                                                                                                                                   Bezabeh B;
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Search completed: November 9, 2005, 12:55:30 Job time: 74.985 secs

TVTV 120 |||| TVTV 124

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Query Match 90.8%; Score 571; DB 7; Length 126; Best Local Similarity 89.5%; Pred. No. 3.9e-42; Matches 111; Conservative 1; Mismatches 8; Indels

9

4; Gaps

Sequence

24, Appl 106, App 106, App 4, Appli 68, Appl 110, App 110, App 17, Appl

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

OM protein

Run on:

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61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSIFGVVI---DYGMDVWGQGTT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCARDPRGATLYYYYYGMDVWGQGTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Squence 70, Application US/09472087

Patent No. 668736

GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: MUBLIER, BILLER E.
APPLICANT: MUBLIER, BILLER E.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GILMAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PP1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT APPLICATION NUMBER: 60/113,647
PRIOR PILLOG DATE: 1999-12-23
PRIOR FILLING DATE: 1999-12-23
PRIOR FILLING DATE: 1008: 147

CURRENT FILLING DATE: 1008: 147

PRIOR PILLING DATE: 1008: 147

SOFFWARE: PatentIn Ver. 2.1
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US-09-456-090A-102
US-09-451-244-102
US-09-490-070A-24
US-09-490-153-24
US-09-490-153-24
US-09-490-153-24
US-09-456-090A-106
US-09-453-234-106
US-09-453-234-110
US-09-456-090A-110
US-09-456-090A-110
US-09-456-090A-14
US-08-862-124-14
US-08-862-124-14
US-08-862-124-14
US-09-456-090A-56
US-09-456-090A-56
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Patent No. 6140470
GENERAL INFORMATION:
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Best Local Similarity 90.2
Matches 111; Conservative
    APPLICANT: Alan Garen
APPLICANT: Xiaohong Cai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||||
VTV 123
    VTV 120
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US-09-472-087-70
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80, Appl

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108, App
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Sequence 6
Sequence 3
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629
1 QVQLVESGGGVVQPGRSLRL.....FGVVIDYGMDVWGQGTTVTV
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/cgn2 6/ptodata/1/iaa/5B_COWB.pep:*
/cgn2 6/ptodata/1/iaa/6A COWB.pep:*
/cgn2 6/ptodata/1/iaa/6B_COWB.pep:*
/cgn2 6/ptodata/1/iaa/PCTUS COWB.pep:*
/cgn2 6/ptodata/1/iaa/PCTUS COWB.pep:*
                                         GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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US-08-983-667-38
US-09-421-840B-6
US-07-942-245-35
US-08-331-398A-46
US-08-331-398A-46
US-08-759-804A-46
US-08-759-804A-46
US-09-260-198A-2
US-09-424-840B-16
US-09-424-840B-16
US-09-424-840B-16
US-09-424-840B-16
US-09-456-090A-92
US-09-456-090A-92
US-09-456-090A-92
US-09-453-234-108
US-09-473-234-108
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US-09-240-274-25
US-09-472-087-12
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length
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Minimum DB Maximum DB

Database

Searched:

567.

No.

Result

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3; Gaps

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APPLICANT: Havenga, Stefan
APPLICANT: Werlinden, Stefan
TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER
FILLE REFERENCE: 2183-4080US
CURRENT APPLICATION NUMBER: US/09/315,926A
CURRENT FILING DATE: 1999-05-20
PRIOR PELICATION NUMBER: EP 99201593.3
PRIOR PLICATION NUMBER: EP 98201693.3
PRIOR FILING DATE: 1999-05-20
PRIOR PLICATION NUMBER: EP 98201693.3
PRIOR FILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PACENTIN VERSION 3.0
SEQ ID NO 80
LENGTH. 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCARSIFGVVIDYGMDVWGQGTTVTV 120
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Fatent No. 679038
Fatent No. 679038
GENERAL INFORMATION:
APPLICANT: Berchtold, Peter
APPLICANT: Berchtold, Peter
TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
FILE REFERENCE: 100564-09049
CURRENT APPLICATION NUMBER: US/09/424,840B
FRIOR APPLICATION NUMBER: DE 19820663.1
PRIOR APPLICATION NUMBER: DE 19755227.7
PRIOR APPLICATION NUMBER: DE 19755227.7
FRIOR APPLICATION NUMBER: DE 19755227.7
FRIOR APPLICATION NUMBER: DE 1975527.7
FRIOR PRILING DATE: 1999-12-12
PRIOR APPLICATION NUMBER: DE 1975527.7
FRIOR PILING DATE: 1999-10-66
FRIOR APPLICATION NUMBER: DE 19753904.8
FRIOR FILING DATE: 1999-06-66
FRIOR PILING DATE: 1999-06-66
FRIOR APPLICATION NUMBER: DE 19723904.8
FRIOR FILING DATE: 1999-06-66
FRIOR APPLICATION NUMBER: DE 19723904.8
FRIOR FILING DATE: 1997-06-66
FRIOR APPLICATION NUMBER: DE 19723904.8
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OTHER INFORMATION: Description of Artificial Sequence: phage
NAME/KEY: PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (1)..(248)
; OTHER INFORMATION: /note="hCAT1 amino acid sequence"
US-09-315-926A-80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-424-840B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 248
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                                                                                                                                                                                                                              COMPUTER: United States of America
ZIP: 06520-8114
COMPUTER READABLE FORM:
MEDLING TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
COMPUTER: IBM PC
COMPUTER: IBM PC
COMPUTER: IBM PC
COMPUTER: MS DOS
SOFTWARE: Word Processing
CURRENTING SYSTEM: MS DOS
SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,607
FILING DATE: ADril 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
CLASSIFICATION NUMBER: 324,33
REFERENCE/DOCKET NUMBER: OCR-679
TELECHOMUNICATION INFORMATION:
TELECHOMUNICATION INFORMATION:
TELECHOMUNICATION INFORMATICS:
LENGTH: 123 residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: POLYPE:
DESCRIPTION: POLYPEPTION
CORGANISM: Homos capiens (melanoma patient
ORGANISM: Homos capiens (melanoma patient
ORGANISM: mimmized with autologous tumor cells)
INDIVIDUAL ISOLATE: CYTES
IMMEDIATE SOURCE:
LIBRARY: PMY:
      Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: Human Anti-Tumor Monoclonal TITLE OF INVENTION: bodies NUMBER OF SEQUENCES: 51 CORRESPONDENCE ADDRESS: ADDRESSE: Department of Molecular Biophysics ADDRESSEE: and Biochemistry, Yale University STREET: 266 Whitney Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIBRARY: DM414 scFv antibodies obtained from LIBRARY: fUSE5 fusion phage construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-315-926A-80
; Sequence 80, Application US/09315926A
; Patent No. 6498027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: heavy chain
                                                                                                                                                                         STREET: 266 Whitn
CITY: New Haven
STATE: Connecticu
COUNTRY: United S
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Gaps

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FitzGerald, David
Brinkmann, Ulrich
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61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSIFGVVIDYG----MDVWGQGTT 117
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88.6%; Pred. No. 1.9e-47;
ive 1; Mismatches 6; Indels 7
                                                                                                                                                                                                 APPLICANT: REES, Anthony R.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: GUILD, Braydon C.
TITLE OF INVENTION: SURRACE RESIDUE VENEERING OF RODENT
TITLE OF INVENTION: ANTIBODIES
                                                                                                                                                                                                                                                                                          ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas STREET: 2100 Pensylvania Avenue, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                        Stephen M.J.
                                                                                                                                Sequence 35, Application US/07942245
Patent No. 5639641
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: REASLE, Stephen M.J.
APPLICANT: REES, Anthony R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 88.6°
Matches 109; Conservative
                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
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                                         119 TV 120
                                                                 120 TV 121
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Sequence 46, Application US/08331398A Patent No. 5608039 GENERAL INFORMATION APPLICANT: Pastan, Ira APPLICANT: Willingham, Mark

US-08-331-398A-46

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Itai
Chimeric and Mutationally Stabilized Tumor-
Specific Antibody Fragments, Fusion Proteins, and Uses
Thereof
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ښ
APPLICANT: Pai, Lee
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
TITLE OF INVENTION: and Their Uses (as amended)
NUMBER OF SUCURICES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 86.6%; Score 544.5; DB 1; Length 119; Best Local Similarity 89.2%; Pred. No. 36-47; Matches 107; Conservative 1; Mismatches 9; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Human fetal immunoglobulin
56Pl'CL Variable Heavy chain (V-H)'
                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppdisk
COMPUTER: IBM PC compatible
SOCTAME: PAELCATION DATA:
APPLICATION NUMBER: US/08/31,398A
FILING DATE: 38-CCT-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/56,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REGISTRATION NUMBER: 015280-126110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-331-397B-46

Sequence 46, Application US/08331397B

Setent No. 5981726

GENERAL INFORMATION:

APPLICANT: Pastan, Ira

APPLICANT: Benhar, Itai

TITLE OF INVENTION: Chimeric and Mut

TITLE OF INVENTION: Specific Antibod

TITLE OF INVENTION: Thereof

NUMBER OF SEQUENCES: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1..119
OTHER INFORMATION:
OTHER INFORMATION:
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California
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US-09-227-693-46
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56P1'CL Variable Heavy chain (V-H)'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Willingham, Mark
APPLICANT: FitzGerald, David J.
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
CORRESPONDENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                             COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: BEATON BATON:
APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT-1994
CLASSIFICATION NUMBER: US 07/767,331
PRIOR APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION NUMBER: US 07/767,331
FILING DATE: 12-OCT-1990
ATTONNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 38,498
REGISTRATION NUMBER: 38,498
REGISTRATION NUMBER: 38,498
REGISTRATION NUMBER: 38,498
REGISTRATION NUMBER: 310-9600
TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
L'ENGTH: 119 amino acids
                  ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 119 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 89.24
Matches 107; Conservative
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MOLECULE TYPE: protein
CORRESPONDENCE ADDRESS:
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Protein
                                                                                     California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino
STRANDEDNESS:
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                                                                                   STATE: CE
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61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSIFGVVIDYGMDVWGQGTTVTV 120
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APPLICANT: PASTAN, Irai
APPLICANT: BENHAR, Itai
APPLICANT: BENHAR, Itai
APPLICANT: BENHAR, Eduardo A.
APPLICANT: JUG, Sun-Hee
APPLICANT: JUG, Sun-Hee
APPLICANT: LEE, BYUNGKOOK
TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND AND TOWNSEND T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ÷
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56Pl'CL Variable Heavy chain (V-H)"
                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,804A
FILING DATE: 03-DEC-1996
CLASSIFICATION NUMBER: US/08/759,804A
FILING DATE: 03-DEC-1996
CLASSIFICATION NUMBER: US/08/331,398
FILING DATE: 28-OCT-1994
PRIOR APPLICATION NUMBER: US/07/767,331
FILING DATE: 28-OCT-1991
PRIOR APPLICATION NUMBER: US/07/767,331
FILING DATE: 12-OCT-1990
ATTORNEY AGENT INFORMATION:
NAME: Weber: Ellen L.
REGISTRATION NUMBER: 015280-126140US
TELERDHONE: 415) 576-0300
INFORMATION FOR SEQ ID NO: 46: SEQUENCE CHARACTERISTICS:
CREMENTED OF THE CALL O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSEE: Townsend and Townsend Khourie and Crew F: Steuart Street Tower, One Market Plaza San Francisco California
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 89.2
Matches 107; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 1.119
OTHER INFORMATION:
OTHER INFORMATION:
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61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCART--GEYSGYDTSGVELMGQGTT 118
                                                                                                                                                                                                                                                                                                                                                61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSIFGVVIDY---GMDVWGQGTT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ADSVKGRFTISRDNSKQTLYLQMNSLRAEDTAVYYCARSIFGVVIDY----GMDVWGQGT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ADSVKGRFAISRDNSKWTLYLQMNSLRAEDTAVYYCAKD--GRSGSYARFDGMDVWGQGT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 26, Application US/09240274;
Patent No. 6255455;
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVKLLESGGGVVHPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVALISYDGSNKYY 60
                                                                                                                                                                                                                                                                               1 QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSIKYY
                                                                                                                                                                                                                                                     1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY
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                                                                                                                                                                                                             Gaps
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                                                                                                                                                           86.2%; Score 542.5; DB 4; Length 123; 87.0%; Pred. No. 5e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16, Application US/09424840B
Fatent No. 6790938
GENERAL INFORMATION:
FAPLICANT: BERCHCIOId, Peter
APPLICANT: BERCHCY, ROBERT F. A.
TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
FILE REFERENCE: 100564-09049
CURRENT APPLICATION NUMBER: US/09/424,840B
CURRENT APPLICATION NUMBER: US/09/424,840B
FRIOR APPLICATION NUMBER: DE 19820663.1
PRIOR FILING DATE: 1999-12-03
PRIOR PILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: DE 1975227.7
PRIOR APPLICATION NUMBER: DE 1975227.7
PRIOR APPLICATION NUMBER: DE 19752904.8
FRIOR PILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 538; DB 4; Length 124;
Pred. No. 1.4e-46;
4; Mismatches 8; Indels
                                                                                                                                                                                Pred. No. 5e-47;
5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.5%;
85.5%;
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                  Best Local Similarity 87.0 Matches 107; Conservative
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Best Local Similarity 85.5'
Matches 106; Conservative
                                                                TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-09-240-274-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCARR---SARTYYFDYWGQGTLVTV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVELVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
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Pred. No. 3e-47;
1; Mismatches 9; Indels 3
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APPLICANT: Wilton, Alison J
APPLICANT: Braddock, Peta SH
APPLICANT: Braddock, Peta SH
APPLICANT: Du Fou, Sarah L
APPLICANT: Conroy, Louise A
APPLICANT: Tempest, Philip R
TITLE OP INVENTION: Specific binding members for TGFbetal
FILE REFERENCE: 2011/35620A
CURRENT APPLICATION NUMBER: US/09/560,198A
CURRENT FILING DATE: 2000-04-28
PRIOR FILING DATE: 1999-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Human fetal immunoglobulin
56Pl'CL VH region"
                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/227,693
FILING DATE:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15280-126-1-3
                                                                                                                                                                                                                                                                                    PRICIA PAPELICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-007-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-126-1
TELECOMMUNICATION INFORMATION:
                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09560198A Patent No. 6492497 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (415) 543-9600
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TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 89.2
Matches 107; Conservative
                ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
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OTHER INFORMATION:
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APPLICANT: Holliger, Kasper
APPLICANT: Marks, James
APPLICANT: Clackson, Timothy
APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory
APPLICANT: Winter, Timothy
APPLICANT: Winter, Timothy
APPLICANT: Planchy
APPLICANT: Timothy
FITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 213819-00013
                                                                                                                                                                                                                                                      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSIFGVVID---YGMDVWGQGTT 117
                                                                                                                                                                                                                                                                                100 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR------DRGYYYMDVWGKGTT 152
                                                                                                                                                                                           40 QVQLVQSGGGVVQPGRSLRLSCAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYY 99
                                                                                                                                                                  1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY
                                                                                                                     Gaps
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88.0%; Pred. No. 1.5e-45;
iive 4; Mismatches 7; Indels 3.
                                                                    84.1%; Score 529; DB 3; Length 310;
85.4%; Pred. No. 3.1e-45;
tive 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cambridge Antibody Technology
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE KEKERENE: 213435-00013.

PILE KEKERENE: 213435-00013.

CURRENT FILING DATE: 2000-11-28

PRIOR PELING DATE: 1990-10-10.

PRIOR FILING DATE: 1990-10-10.

PRIOR PELING DATE: 1990-10-19

PRIOR PELING DATE: 1990-10-19

PRIOR PELING DATE: 1990-10-19

PRIOR APPLICATION NUMBER: GB 9022845.3

PRIOR PILING DATE: 1990-10-19

PRIOR PILING DATE: 1990-11-19

PRIOR PILING DATE: 1990-11-19

PRIOR PILING DATE: 1991-10-19

PRIOR PILING DATE: 1991-10-19

PRIOR PILING DATE: 1991-10-16

PRIOR FILING DATE: 1991-03-06

PRIOR FILING DATE: 1991-03-06

PRIOR PILING DATE: 1991-03-06

PRIOR PILING DATE: 1991-03-10

PRIOR APPLICATION NUMBER: PCT/GB91/01134

PRIOR PILING DATE: 1991-01-08

PRIOR PELING DATE: 1995-06-07

NUMBER OF SEQ ID NOS: 272

SOFTWARE: PATEUTIN VETSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 167, Application US/09726219A; Patent No. 6806079; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pope, Anthony
Johnson, Kevin
Hoogenboom, Hendricus
Griffiths, Andrew
                                                                        Query Match
Best Local Similarity 85.4
Matches 105; Conservative
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Best Local Similarity 88.0
Matches 103; Conservative
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US-09-726-219A-167
       TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                              153 VTV 155
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US-09-726-219A-167
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US-09-079-029-11
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 84.3%; Score 530; DB 3; Length 126; Best Local Similarity 81.2%; Pred. No. 9.1e-46; Matches 104; Conservative 7; Mismatches 5; Indels
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF;
CURRENT APPLICATION UNBER: US/09/240,274;
CURRENT PILLING DATE: 1999-01-29;
EARLIER PILLING DATE: 1998-04-10;
EARLIER PILLING DATE: 1998-04-10;
EARLIER PILLING DATE: 1998-10-11;
NUMBER OF SEQ ID NOS: 224;
SOFTWARE: PALENTIN Ver. 2.0;
SEQ ID NO 26;
LENGTH: 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
OTHER INFORMATION: anti-Rh(D) chain D31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Adams, Camilia W.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chuncharapai, Anan
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/09079029
Patent No. 6342369
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way CITY: South San Francisco CATAE: California COUNTRY: USA
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61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSIFGVVIDYGMD---VWGQGTT 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 83.7%; Score 526.5; DB 4; Length 123; Best Local Similarity 86.2%; Pred. No. 2e-45; Matches 106; Conservative 2; Mismatches 10; Indels 5;
                                                                                                                                                                                                                                              ; GENERAL INFORMATION;
; APPLICANT: Thompson, Julia E
; APPLICANT: Thompson, Julia E
; APPLICANT: Lennard, Simon N
; APPLICANT: Wilton, Alison J
; APPLICANT: Wilton, Alison J
; APPLICANT: Dr. Fou. Sarah L
; APPLICANT: Conroy, Louise A
; APPLICANT: Tempest, Philip R
; TITLE OF INVENTION: Specific binding members for TGFbetal
; FILE REFERENCE: 28111/35620A
; CURRENT APPLICATION NUMBER: US/09/560,198A
; CURRENT APPLICATION NUMBER: US 60/131,983
; PRIOR APPLICATION NUMBER: US 60/131,983
; PRIOR PILING DATE: 2000-04-28
; SOFTWARE: PatentIn Ver. 2.1
; SQ ID NO 4
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-560-198A-4
                                                                                                                                                                                 US-09-560-198A-4
Sequence 4, Application US/09560198A
Patent No. 6492497
GENERAL INFORMATION:
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Search completed: November 9, 2005, 11:46:41 Job time: 19.6466 secs

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Sequence 29, Appl
Sequence 11, Appl
Sequence 27, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 11, Appl
Sequence 106, Appl
Sequence 106, Appl
                                                                                                                            9, 2005, 11:40:37; Search time 66.6667 Seconds (without alignments) 753.137 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                     US-10-660-357A-29
629
1 QVQLVESGGGVVQPGRSLRL......FGVVIDYGMDVWGQGTTVTV 120
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1. (cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

1. (cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

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US-10-30-530-29
US-10-660-357-29
US-10-269-711-11
US-10-269-711-27
US-10-269-711-31
US-10-269-711-31
US-10-269-711-35
US-10-269-711-36
US-10-22-088-106
US-10-22-088-106
                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                 1867879 segs, 418409474 residues
GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published_Applications_AA:*
                                                                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 200000000
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| | ALIGNMENTS | | | | | |
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| equenc | S-10-293-418- | 12 | 222 | 89.6 | 563.5 | 4.4 |
| 115 | 11-031-485-115 | 7 50 | 117 | | 95 5 | 24.2 |
| 82, | 10-371-942-82 | 12 | 124 | σ. | 10 | 41 |
| 142 | 10-726-332-14 | 11 | 121 | 6 | | 40 |
| 222 | 10-727-155-2 | 11 | 125 | ė. | 65. | 39 |
| 107 | 10-292-088-10 | 15 | 125 | ö | 99 | 38 |
| 17, | 11-085-368-1 | 20 | 451 | ö | 67. | 37 |
| 70, | 10-776-649-7 | 16 | 451 | ö | 67. | 36 |
| 20, | 10-612-497-7 | 16 | 451 | ö | 67. | 35 |
| 17, | 10-153-382-1 | 14 | 451 | | | 34 |
| 47 | 11-009-731-47 | 20 | 117 | | 67. | 33 |
| Sequence 133, App | US-10-309-762-133 | ۲ ۱ | 126 | | ກິດ | |
| 149 | 10-309-762-14 | 12 | 121 | <i>。</i> | 69 | m (|
| 132 | -10-309-762-13 | 15 | 121 | ö | | 29 |
| 14, | -10-665-383-14 | 16 | 126 | ö | 57 | 28 |
| 282 | -10-041-860-2 | 14 | 126 | ö | 7 | 27 |
| | 10-041-860-20 | 14 | 126 | | _ | 26 |
| 17, | -10-041-860-1 | 14 | 126 | ö | 7 | 25 |
| 34 | -10-727-155-3 | 17 | 122 | ö | 57 | 24 |
| 31, | -10-976-352-3 | 18 | 144 | | 71. | 23 |
| 31, | -10-695-667-3 | 16 | 144 | 。 | 71. | 22 |
| 31, | -10-395-894-31 | 15 | 144 | 。 | | 21 |
| 117 | -10-292-088-11 | 15 | 123 | 4 | 72. | 20 |
| 115 | -10-292-088-1 | 15 | 123 | H | 74. | 19 |
| 116 | -11-031-485-11 | 50 | 122 | Н | 74. | 18 |
| 15, | -10-684-109- | 16 | 123 | 4 | 76. | 17 |
| | -10-684-109-7 | 16 | 123 | 91.7 | 76. | 16 |
| 15, | -10-269-711- | 15 | 123 | ۲. | 76. | 15 |
| 7 | -10-269-71 | 15 | 123 | Ξ. | 76. | 14 |
| 11, | -10-858-855- | 17 | 141 | 91.7 | 7 | 13 |
| 35, | -10-684-109-3 | 16 | 123 | 91.8 | | 12 |
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ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSIFGVVIDYGMDVWGQGTTVTV 120
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       ; Sequence 20, Application US/10330613; Sequence 20, Application No. US2003014780941; Bublication No. US2003014780941; GENERAL INFORMATION:
; APPLICANT: GLAGA, Jean
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN; FILE REFERENCE: ABGENIX.022A; CURRENT APPLICATION NUMBER: US/10/330,613; CURRENT FILING DATE: 2002-12-26; PRIOR FILING DATE: 2001-12-18; PRIOR FILING DATE: 2001-12-18; NUMBER OF SEQ ID NOS: 40; SEQ ID NOS: 40; SEQ ID NO 29; SEQ ID NO 29; LENGTH: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 629; DB 14;
100.0%; Pred. No. 3.6e-53;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 120; Conservative
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ORGANISM: Homo Sapiens
US-10-330-613-29
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      Sequence 29, Application US/10330530;
Publication No. US20030152514A1;
GENERAL INFORMATION:
APPLICANT: GUGAS, Jean
TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
FILE REFRERNCE: ABGENIX.031A;
CURRENT FILING DATE: 2002-12-26;
PRIOR APPLICATION NUMBER: US/10/330,530
CURRENT FILING DATE: 2001-12-26;
PRIOR APPLICATION NUMBER: US 60/346414;
PRIOR APPLICATION NUMBER: US 60/346414;
PRIOR SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 120
TYPE: PRT
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Sequence 20, Application US/10660357

Publication No. US20040115205A1

GENERAL INFORMATION:

APPLICANT: Bar-Eli, Menashe

APPLICANT: Bar-Eli, Menashe

TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18

TITLE OF INVENTION: ANTIGEN

FILE REFERENCE: ABGENIX.030C1

CURRENT APPLICATION NUMBER: US/10/660,357

CURRENT FILING DATE: 2003-09-10

PRIOR PILING DATE: 2002-12-26

NUMBER OF SEQ ID NOS: 40

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 29

LENGTH: 120
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Best Local Similarity 100.
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: Homo Sapiens
US-10-330-530-29
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US-10-660-357-29
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US-10-330-530-29
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US-10-269-711-11
Sequence 11, Application US/10269711
Sequence 11, No. US20040071694A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories

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61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSIFG-VVIDYGMDVWGQGTTVT 119
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A APPLICANT: Abbott Laboratories
APPLICANT: Reilly, Edward B.
APPLICANT: Ostrow, Dave
APPLICANT: Green, Larry
TITLE OF INVENTION: ENTYHROPOIETIN RECEPTOR BINDING
TITLE OF INVENTION: ANTIBODIES
FILE REFERENCE: 6989.US.O.
CURRENT FILING DATE: 2002-10-14
CURRENT FILING DATE: 2002-10-14
NUMBER OF SEC ID NOS: 57
SEC ID NO 23;
SEC ID NO 23;
SEC ID NO 23;
                                                                                                                                                                                                                                                                                                                                                                                                                   DB 15;
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                                                             APPLICANT: Wailer, James
APPLICANT: Green, Larry
TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
TITLE OF INVENTION: ANTHEODIES
FILE REFERENCE: 6989.US.O1
CURRENT APPLICATION UNDBER: US/10/269,711
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FASELSEQ for Windows Version 4.0
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93.4%; Pred. No. 1.9e
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    DeVries, Peter
Reilly, Edward
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ORGANISM: Homo sapiens
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DeVries,
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LENGTH: 123
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61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSIFG-VVIDYGMDVWGQGTTVT 119
                                                                                          61 ADSVKGRFTISRDNSKNTLYLQMNSLRVEDTAVYYCARDHGGRYVYDYGMDVWGQGTTVT 120
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1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.3%; Score 580.5; DB 15; Length 93.4%; Pred. No. 1.9e-48; ive 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Green, Larry L.
APPLICANT: Green, Larry L.
APPLICANT: Reilly, Edward B.
APPLICANT: Wieler, James
TITLE OF INVENTION: Erythropoietin Receptor Binding
TITLE OF INVENTION: Antibodies
TITLE OF INVENTION: Antibodies
TITLE OF INVENTION: Antibodies
TITLE OF INVENTION: Antibodies
TITLE OF INVENTION: MUMBER: US.0.2
CURRENT APPLICATION NUMBER: 10/269,711
PRIOR APPLICATION NUMBER: 10/269,711
PRIOR PILING DATE: 2002-10-14
NUMBER OF SEC ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Green, Larry
TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
TITLE OF INVENTION: ANTIBODIES
FILE REPERENCE: 6989 US.01
CURRENT APPLICATION NUMBER: US/10/269,711
CURRENT FILING DATE: 2002-10-14
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FRASESO for Windows Version 4.0
                                                                                                                                                                                                                                                                                                 Sequence 35, Application US/10269711; Publication No. US20040071694A1; GENERAL INFORMATION:
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PUBLICATION NO. US20040175379A1
GENERAL INFORMATION:
APPLICANT: DeVries, Peter J.
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Devises, Peter J.
APPLICANT: Reilly, Edward B.
APPLICANT: Weiler, James
APPLICANT: Weiler, James
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Matches 113; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 31, Application US/10269711
FUDLICATION NO. US20040071694A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Beilly, Edward B.
APPLICANT: Reilly, Edward B.
APPLICANT: Weiler, James
APPLICANT: Weiler, James
APPLICANT: Weiler, James
APPLICANT: Weiler, James
APPLICANT: Green, Larry
ITLE OF INVENTION: BYTHRODIES;
FILE OF INVENTION: ANTIBODIES;
FILE REFERENCE: 6989.US.OI
CURRENT APPLICATION NUMBER: US/10/269,711
CURRENT FILING DATE: 2002-10-14
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                            US-10-269-711-27
; Sequence 27, Application US/10269711
; Publication No. US20040071694A1
; GENERAL INFORMATION:
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Best Local Similarity 93.44
Matches 113; Conservative
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Best Local Similarity 93.44
Matches 113; Conservative
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US-10-269-711-27
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US-10-269-711-31
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LENGTH: 123
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LENGTH: 123
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LENGTH: 123
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                                                                                                                                                                                                                                                          61 ADSVKGRFIISRDNSKNTLYLQMNSLRVEDTAVYYCARDHGGRYVYDYGMDVWGQGTTVT 120
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                                                                               DB 16; Length 123;
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                                                                             Score 580.5; DB 16; Length
Pred. No. 1.9e-48;
0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 106, Application US/10292088
Publication No. US20030211100A1
GENERAL INFORMATION:
APPLICANT: BEDIAN, VAHE
APPLICANT: GLADUE, RONALD P.
APPLICANT: GLADUE, RONALD P.
APPLICANT: JIA, XIAO-CHI
APPLICANT: JIA, XIAO-CHI
APPLICANT: FENG, XIAO-CHI
COURRENT FENG, XIAO-CHI
CURRENT APPLICATION NUMBER: US/10/292,088
CURRENT APPLICATION NUMBER: 60/348,980
PRIOR APPLICATION NUMBER: 60/348,980
PRIOR APPLICATION NUMBER: 60/348,980
PRIOR APPLICATION NUMBER: 61/348,980
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 106
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; Sequence 43, Application US/10269711
; Publication No. US20040071694A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: DeVries, Peter J.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Weiler, James
                                                                           Query Match
Best Local Similarity 93.4%;
Matches 113, Conservative
TYPE: PRT
CORGANISM: Homo sapiens
US-10-684-109-11
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US-10-292-088-106
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61 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCARSIFG-VVIDYGMDVWGQGTTVT 119
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91.8%; Score 577.5; DB 15; Length 123;
Best Local Similarity 92.6%; Pred. No. 3.6e-48;
Matches 112; Conservative 1; Mismatches 7; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 35, Application US/10684109; Sequence 35, Application US/10684109; Publication No. US20040175379A1; GENERAL INFORMATION:
APPLICANT: Devries, Peter J.; APPLICANT: Green, Larry L.; APPLICANT: Really, Edward B.; APPLICANT: Really, Edward B.; APPLICANT: Really, Edward B.; TITLE OF INVENTION: Brythropoietin Receptor Binding; TITLE OF INVENTION: Brythropoietin Receptor Binding; FILE REFERENCE: 6989.US.O. CURRENT APPLICATION NUMBER: US/10/684,109; CURRENT FILING DATE: 2003-10-10; PRIOR FILING DATE: 2002-10-14; NUMBER OF SEQ ID NOS: 115; SOFFWARE: FastSEQ for Windows Version 4.0
APPLICANT: Green, Larry
TITLE OF INVENTION: BRYTHROPOIETIN RECEPTOR BINDING
TITLE OF INVENTION: ANTIBODIES
FILE REFERENCE: 6989.US.O1
CURRENT APPLICATION NUMBER: US/10/269,711
CURRENT PILING DATE: 2002-10-14
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FASTSEQ for Windows Version 4.0
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens US-10-269-711-43
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                            Sequence 11, Application US/10858855;
Publication No. US20050118651A1;
GENERAL INFORMATION:
APPLICANT: BASI, GUING
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE BETA
TITLE OF INVENTION: AMYLOID PEPTIDE
FILE REFERENCE: ELN-028;
CURRENT APPLICATION NUMBER: US/10/858,855;
CURRENT FILING DATE: 2004-06-01;
PRIOR PELLING DATE: 2003-05-30;
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 4.7e-48;
0; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Devies, Peter J.
APPLICANT: Reilly, Edward B.
APPLICANT: Ostrow, Dave
APPLICANT: Ostrow, Dave
APPLICANT: Green, Larry
TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
TITLE OF INVENTION: ANTIBODIES
FILE REFERENCE: 6989.US.Ol
CURRENT APPLICATION NUMBER: US/10/269,711
CURRENT PILING DATE: 2002-10-14
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 91.7%; Score 576.5; DB 1. Best Local Similarity 92.6%; Pred. No. 4.6e-48; Matches 112; Conservative 0; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/10269711 Publication No. US20040071694A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91.7%;
93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 93.33
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-10-269-711-7
                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: SIGNAL
; LOCATION: (1) ...(19)
US-10-858-855-11
                                                                                                                                                                                                                                                                                                            SEQ ID NO 11
LENGTH: 141
                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSIFG-VVIDYGMDVWGQGTTVT 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                        APPLICANT: Abbott Laboratories
APPLICANT: DeVries, Peter J.
APPLICANT: Devises, Peter J.
APPLICANT: Beilly, Edward B.
APPLICANT: Weiler, Dave
APPLICANT: Weiler, James
APPLICANT: Green, Larry
ITILE OF INVENTION: EXTYRACOPOIETIN RECEPTOR BINDING
ITILE OF INVENTION: ANTIBODIES
FILE REFERENCE: 6989.US.O1
CURRENT APPLICATION NUMBER: US/10/269,711
CURRENT FILING DATE: 2002-10-14
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FASELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.7%; Score 576.5; DB 1 92.6%; Pred. No. 4.6e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: November 9, 2005, 12:43:02 Job time : 67.6667 secs
; Sequence 15, Application US/10269711; Publication No. US20040071694A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 92.6
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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9, 2005, 12:25:58; Search time 12.9123 Seconds (without alignments) 892.802 Million cell updates/sec November Run on:

1 QVQLVESGGGVVQPGRSLRL.....FGVVIDYGMDVWGQGTTVTV 120 US-10-660-357A-29 629 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | dр | | | COLUMNIA | |
|---------------|-------|----------------|--------|----|----------|--------------------|
| Result
No. | Score | Query
Match | Length | DB | ΙD | Description |
| | 57 | | 1 | 7 | E36005 | Iq heavy chain V r |
| 7 | 559 | 88.9 | 128 | ~ | S48797 | heavy |
| m | LO. | 87.9 | 120 | 7 | S31112 | heavy |
| 4 | ö | 87.5 | 132 | ~ | S31603 | |
| Ŋ | • | 87.4 | 134 | N | S31679 | |
| 9 | 549 | 87.3 | 114 | ~ | S46390 | heavy |
| 7 | ė. | 86.9 | 121 | ~ | G36005 | |
| 80 | 545.5 | 86.7 | 119 | N | F36005 | heavy |
| თ | 543.5 | 86.4 | 123 | 0 | S38493 | heavy |
| 10 | 542 | 86.2 | 122 | N | 831117 | heavy |
| 11 | 540 | 'n | 118 | N | S31116 | heavy |
| | 539.5 | 85.8 | 121 | N | S19666 | |
| 13 | 537 | 85.4 | 114 | 7 | 846392 | heavy |
| 14 | 536.5 | 85.3 | 130 | 7 | S31601 | heavy |
| 15 | 535 | | 137 | ~ | S31701 | heavy |
| 16 | 532 | | 139 | 7 | S31674 | heavy |
| 17 | 529.5 | | 130 | ~ | PL0098 | |
| 18 | 524 | • | 140 | N | S70442 | heavy chain |
| 19 | 523.5 | 83.2 | 133 | N | A49028 | heavy cha |
| 20 | 522 | | 147 | N | 137780 | |
| 21 | 521.5 | | 135 | N | S31598 | heavy che |
| 22 | 521 | | 114 | 7 | S46391 | |
| 23 | 520 | | 133 | ~ | S31510 | |
| 24 | 517 | 82.2 | 118 | ~ | PH1660 | heavy chain V |
| 25 | 516.5 | 82.1 | 113 | 7 | S38490 | |
| 56 | | - | 160 | 7 | 805271 | Ig heavy chain pre |
| 27 | 516 | 82.0 | 122 | ~ | 831119 | heavy chain |
| 28 | 515.5 | 82.0 | 109 | α. | PH1644 | heavy cha |
| 53 | 514 | 81.7 | 122 | H | M3HUAM | Ig heavy chain V-I |

| Ig heavy chain V r | | | | | | | | | | Ig heavy chain - h | | | Ig heavy chain V r | | æ |
|--------------------|-----------|------------|------------|-----------|------------|-------------|------------|------------|------------|--------------------|------------|------------|--------------------|------------|--------|
| 46 | 46 | 45 | 643 | 116 | .677 | 1943 | 1642 | 0782 | 5270 | 111 | 794 | 9910 | 1688 | 1662 | 337455 |
| PH1646 | 8295 | PH16 | PHI | PLC | 831 | A6 0 | Н | 82 | 83 | 831 | S26 | 36 | 83 | Ы | S |
| 2 PH16 | 2 8295 | 2 PH16 | 2 PH1 | 2 PLC | 2 831 | 2 A60 | 2 PH: | 2 82 | 2 83(| 2 831 | 2 \$26 | 2 56 | 2 83 | 2 PH | 2 83 |
| 109 2 PH16 | 7 | ~ | 7 | 7 | 7 | 7 | 7 | ~ | 7 | 7 | 7 | 7 | 7 | 7 | 7 |
| 7 | 98 2 | 111 2 | 111 2 | 98 2 | 118 2 | 151 2 | 108 2 | 124 2 | 117 2 | 119 2 | 123 2 | 122 2 | 134 2 | 118 2 | 125 2 |
| 109 2 | 81.4 98 2 | 81.2 111 2 | 81.0 111 2 | 80.3 98 2 | 80.0 118 2 | 80.0 151 2 | 79.8 108 2 | 79.8 124 2 | 79.7 117 2 | 79.7 119 2 | 79.4 123 2 | 79.2 122 2 | 79.0 134 2 | 78.9 118 2 | 125 2 |

ALIGNMENTS

RESULT 1

| E36005 |
|---|
| Ig heavy chain V region (M72) - human |
| C;Species: Homo sapiens (man) |
| C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998 |
| C;Accession: E36005 |
| R;Schroeder Jr., H.W.; Wang, J.Y. |
| Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990 |
| A, Title: Preferential utilization of conserved immunoglobulin heavy chain variable |
| A; Reference number: A36005; MUID:90349571; PMID:2117273 |
| A;Accession: E36005 |
| A;Status: preliminary |
| A;Molecule type: mRNA |
| A;Residues: 1-122 <sch></sch> |
| A;Cross-references: GB:M34030 |
| C;Genetics: |
| A;Gene: GDB:IGH@; IGHDY1 |
| A;Cross-references: GDB:118731; OMIM:146910 |
| A;Map position: 14q32.33-14q32.33 |
| C; Superfamily: immunoglobulin V region; immunoglobulin homology |
| C; Keywords: heterotetramer; immunoglobulin |
| F;15-98/Domain: immunoglobulin homology <imm></imm> |
| 91.78; |
| Best Local Similarity 93.3%; Pred. No. 3.5e-45;
Matches 112; Conservative 0; Mismatches 8; Indels 0; Gaps 0; |
| Qy 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60 |
| |
| Db 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60 |
| Qy 61 ADSVKGRFTISRDNSKWTLYLQMNSLRAEDTAVYYCARSIFGVVIDYGMDVWGQGTTVTV 120 |
| nh 61 anguszpertrephuszkert. 11 mm marchanduszczervycznywy 130 |
| |

e gene

RESULT 2

19 deavy chain V region (anti-Sm, VH3/Dxp4/JH6) - human (fragment)
C)species: Homo saplens (man)
C)species: Homo saplens (man)
C;pacession: S48797; S26893
R)Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
R)Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
R)Mahmoudi, M.; Edwards J.; Cairns, Cotober 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: S48797
A;Accession:
```
Best Local Similarity 90.0
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: S31585
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-134 <CUI>
  A; Residues: 1-132 <CUI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-114 <FIG>
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Cidecesion: S31112
Expansion: S3112
Expansion: S3112
Expansion: S3112
A.Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A.Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A.Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A.Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A.Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A.A.Status: preliminary; nucleic acid sequence not shown; translation not shown A.Status: preliminary; nucleic acid sequence not shown; translation not shown A.Status: Experiment and sequence was submitted to the EMBL Data Library, October 1991 C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Superfamily: immunoglobulin homology <IMM>
F:15-98/Domain: immunoglobulin homology <IMM>
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C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: 831603
R;Culainier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: 831585
A;Accession: 831503
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       groups
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A;Title: The repertoire of human germline V(H) sequences reveals about fifty; A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26893
A;Molecule type: DNA
A;Residues: 1-98 <TOM>A;Residues: 1-98 <TOM>C;Superfemences: EMBL:Z12350; NID:g32922; PIDN:CAA78220.1; PID:g32923
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 02-Dec.1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                               QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYY
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Pred. No. 5.1e-43;
                                                                                                                                                                                                                                                  Score 559; DB 2;
Pred. No. 1.6e-43;
                                                                                                                                                                                                                                                                                                  1; Mismatches
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                                                                                                                                                                                                                                                    Score 559;
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Ig heavy chain V region - human
                                                                                                                                                                                                                                                                         Best Local Similarity 86.7
Matches 111; Conservative
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Best Local Similarity
Watches 108; Conserv
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C;Species: Homo sapiens (man)
C;Species: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31679
R;Culisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
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C;Date: 27-Jan-1995 #text_change 20-Jun-2000
C;Date: 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: $46590
C;Accession: $46590
J; Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by A;Reference number: $46390; MUD:94254092; PMID:8196048
A;Accession: $46390
A;Accession:
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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A)Cross-references: EMBL:Z14168; NID:g30999; PIDN:CAA78537.1; P:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;30-113/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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90.0%; Pred. No. 1.1e-42;
ive 2; Mismatches 2; Indels
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Pred. No. 9.4e-43;
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88.3%; Pred. No. >...
2; Mismatches
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Pred. No. 1.2
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Best Local Similarity 88.3
Matches 106; Conservative
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Matches 108; Conservative
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C.Species: How sapines (man)
C.Species: Mono sapines (man)
C.Species: Mono sapines
C.Superfamily: Mono sapines
C.Species
C.Superfamily: Mono sapines
C.Species
C.Superfamily: Mono sapines
C.Species
C.Superfamily: Mono sapines
C.Species
C.Speci
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C;Species: Homo sapiens (man)
C;Date:: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Datesion: 538493
C;Accession: 538493
A;Description: Human antibody fragments specific for human blood group antigens from a A;Reference number: 838488
A;Accession: 538493
A;Status: preliminary
A;Molecule type: DNA
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A;Cross-references: EMBL:Z23036; NID:g414033; PIDN:CAA80571.1; PID:g414034
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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Score 545.5; DB 2;
Pred. No. 2.4e-42;
1; Mismatches 9;
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88.3%; Pred. No. 5.1e-42;
iive 0; Mismatches 14;
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89.3%; Pred. No. 3.7e-42;
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      86.7%;
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Query Match
Best Local Similarity 89.2
Matches 107; Conservative
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Matches 106, Conservative
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Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: G36005
A;Statuus: preliminary
A;Statuus: preliminary
A;Residues: 1-121 <SCH>
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Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990

A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene A;Feference number: A36005; MUID:90349571; PMID:2117273

A;Accession: F36005

A;Status: preliminary

A;Molecule type: mRNA

A;Molecule type: mRNA

A;Residues: 1-119 <SCH>
A;Cross-references: UNIPROT:QBWUKL; GB:M34026
C;Genetics:
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                                                                   C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 09-Jul-2004
C;Accession: F36005
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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C,Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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Pred. No. 2e-42;
1; Mismatches
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C;Genetics:
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Best Local Similarity 88.6%;
Matches 109; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VIV 119
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Ig heavy chain V region (VH-28) - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: 846392
R;Figini, M; Marks, J.D.; Winter, G.; Griffiths, A.D.
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by A;Reference number: 846392
A;Accession: 846392
A;Accession: 846392
A;Accession: Preliminary
A;Molecule type: DNA
A;Residues: 1-114 <FIG.
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R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: 831585
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61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKT--GYSSGWGYFDYWGQGTLVT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSIFGVVIDYGMDVWGQGTTVTV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDSGG-----YWGQGTTVTV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: EMBL:Z31688; NID:g499306; PIDN:CAA83493.1; PID:g1335145 C,Superfamily: immunoglobulin V region; immunoglobulin homology C,Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.Species: Homo sapiens (man)
C.Date: 03-Mar.1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY
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A;Molecule type: mRNA
A;Residues: 1-130 <CUI>
A;Cross-references: EMBL:Z14192; NID:g31018; PIDN:CAA78561.1; PID:g31019
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;30-113/Domain: immunoglobulin homology <IMM>
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Pred. No. 1.38-41;
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Pred. No. 1.7e-41;
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87.5%; Pred. No. 1.76
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Best Local Similarity 87.5'
Matches 105; Conservative
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Best Local S:
Matches 106
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S31601
                                                                                                                                                                                                                                                                               RESULT 13
S46392
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J. Mol. Biol. 222, 58-597, 1991
J. Reference number: S19663, MUID:92085276; PMID:1748994
J. Reference number: MRA
J. Residues: 1-121 < MAR>
J. Residues: 1-121 < MAR>
J. Cross-references: EMBL:X61646; NID:937688; PIDN:CAA43827.1; PID:91335369
C. Superfamily: immunoglobulin nomology
C. Keywords: heterotetramer; immunoglobulin homology
F:15-98/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: 33116
R; Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman B; Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman B; Talmunol. 22, 247-251, 1992
A; Title: Restricted utilization of germ-line V(H) 3 genes and short diverse third complem A; Reference number: 331104; MUID:92111633; PMID:1730252
A; Accession: 53116
A; Acce
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C.Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
                                                QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYY
                                                                                                                                                                              ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCARDFFAPPNWSHFDYWGQGTLVTV
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             QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY
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Best Local Similarity 87.0%; Pred. No. 7.4e-42;
Matches 107; Conservative 1; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                 heavy chain - human
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19 heavy chain V region - human (fragment)
C.Bpecides: Homo sapiens (man)
R.C.Guishiner, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
R.C.Guishiner, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
A.Bescripticun: Mechanisms that generate human immunoglobulin diversity operate from the A.B. Patel unimary
A.Beference number: S31585
A.Bescripticulary
A.Beferences number: S31701
A.Status: predliminary
A.Molecule type: mRNA
A.Molecule type: ```

CLOS XIVI III III BURG CILL

mus musculu homo sapien homo sapien

Q6pdb8 Q6mzv7 Q6in78 Q6gmw7 P01764

P01781 Q6mzx9 099ka4 06p6c4 P01763

homo sapien nomo sapien homo sapien homo sapien mus musculu homo sapien

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Q68cn4 Q6mzq6 Q8ncl6

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TISSUB-Primary B.-Cells;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=124.79932; DOI=10.1073/pnas.242603899;

MAISCHOL S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Antschul S.F., Johnson E., Wander D., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Bronstein M.J., Uddin T.B., TOSHiyuki S., Carninori P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., N., Milahon D.K., Muzny D.M., Sodersgren E.J., Lu X., Gibbs R.A., Hulyk S.W., Villalon D.K., Muzny D.M., Sodersgren E.J., Lu X., Gibbs R.A., Hulyk S.W., Willahon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Merselly R.W., Touchman J.W., Green E.D., Dickson M.C., Schein J.E., Merselly R.W., Touchman J.W., Green E.D., Dickson M.C., Schein J.E., Grentzation and initial analysis of more than 15,000 full-length human and mouse C.D., Marselly R.M., Mallahon M.A., Mallahon M.A., Mallahon M.A., Mallahon M.A., Mallahon D.E., Schnerch A., Schein J.E., Grentzation and initial analysis of more than 15,000 full-length human and mouse C.D.A. Marselly R.M., Mallahon M.A., Mallahon
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 the EMBL/GehBank/DDBJ databases.
 Last sequence update)
Last annotation update)
 Proc. Natl. Acad. Sci. U.S.A. 99:16899:16903(2002)
 613 AA
 ALIGNMENTS
 068CN4
06MZQ6
08MCL6
06MZV7
06 PDB8
06MZV7
06 IN78
06 IN78
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9 HV3T HUMAN
 HV3B HUMAN
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Strausberg R.;
Submitted (DEC-2001) to the ENEMBL; BC020240; ARH20240.1; -PIR; F36005; F36005.
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 01-MAR-2002 (TrEMBLrel.
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01-MAR-2004 (TrEMBLrel.
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PH1643; PH1643.
PH1646; PH1645.
PH0098; PL0098.
PL0120; PL0120.
S15590; S15590.
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Homo sapiens (Human)
 S70442
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991.843 Million cell updates/sec
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 1 QVQLVESGGGVVQPGRSLRL......FGVVIDYGMDVWGQGTTVTV 120
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Q6pj95
Q6mzu6
Q96bb9
Q6n092
Q6gmx2
 Q6mzv6 |
P01773 |
Q8n5k4 |
 Q7z351
Q9u172
 28wuk1
 P01783
 29hcc1
 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 1612378 segs, 512079187 residues
 SUMMARIES
 Q6P181
HV3H HUMAN
Q9UL71
 Q9Y509
HV3J_HUMAN
 Q6GM<u>Y</u>2
HV3I_HUMAN
HV3K_HUMAN
 HV16 MOUSE
Q6MZV6
HV3L HUMAN
Q8N5K4
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 HV3G HUMAN
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Q9UL93
Q9UL90
 Q96BB9
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Q6GMX2
 BLOSUM62
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629
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 Score
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517.5
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499
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 495
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 Searched:
 Database
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Result Š.

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 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSIFGVVIDYG-----MDVWGQG 115
 ADSVKGRFTISRDNSKVTLYLQMNSLRAEDTAVYYCAK-----DWSEGVETFDIWGQG 132
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 113
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 79
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 Gaps
 12; Gaps
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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 Length 240;
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 Indels
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 Pfam; PF07654; Cl-set; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS500835; IG_LIKE; 5.
PROSITE; PS002290; IG MHC; UNKNOWN 3.
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 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;
 25-OCT-2004 (TrEMBLrel. 28, Created)
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25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Single-chain Fv (Fragment).
 DB 2;
 86.0%; Score 541; DB 2;
84.8%; Pred. No. 5.7e-48;
tive 3; Mismatches 4;
 Score 531.5; DB 2, Pred. No. 1.9e-47;
 5; Mismatches
 PRT;
 84.5%;
 Best Local Similarity 84.8
Matches 106, Conservative
 Matches 104; Conservative
 PRELIMINARY;
 240
 Homo sapiens (Human)
HSSP; P01861; 1ADQ.
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 133 TMVTV 137
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 Name=scFv;
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 1 VOLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYA 60
 62 DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSIFGVVIDYGMDVWGQGTTVTV 120
 VQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYA
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
 SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
MU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
 "Myosin-reactive autoantibodies in rheumatic carditis and normal
 5,
 Score 529.5; DB 2; Length 116;
Pred. No. 1.3e-47;
2; Mismatches 8; Indels 5;
 MEDLINE-98277139; PubMed-9614934; DOI=10.1006/clin.1998 4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
 Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
 0DA0348154DD6061 CRC64;
 Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, AF035021, AAD56257.1; -.
PIR, PH1644, PH1644.
PIR, PL0120; PL0120.
HSSP, P01772; 2FB4.
InterPro; IPR001396; Ig_v.
SMART; SM00406; IGv.
NON. MSSP, PS50835; IG_LIKE; 1.
 fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, FP035024; AAD56260.1; -.
EMBL, FP035024; AAD56260.1; -.
HSSP, P01772, 2FB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
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 116 116
116 AA; 12434 MW;
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 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2004 (TrEMBLrel. 26,
PRELIMINARY;
 Homo sapiens (Human)
 SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 TV 120
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 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKD------LNYWGQGTLVTV 111
 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARS--IFGVVIDY-GMDVWGQGTT 117
 9
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 1 QVELVESGGGVVZPGRSLRLSCAASGFTFSNYAMHWVRQPPGKGLEWVAVISYBGBBKYY
 Gaps
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 Lebman D.W., Putnam F.W.;

"Amino acid sequence of the variable region of a human mu chain:

"Coation of a possible JH segment.";

Proc. Natl. Acad. Sci. U.S.A. 77:3239-3343(1980).

-!- MISCELLANEOUS: This mu chain was isolated from the plasma of a patient with macroglobulinemia.

-!- SIMILARITY: Contains 1 immunoglobulin-like domain.

PIR; A02051; M3HUAM.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 82.3%; Score 517.5; DB 2; Length 113; 83.3%; Pred. No. 2.3e-46; ive 4; Mismatches 7; Indels 9
 81.7%; Score 514; DB 1; Length 122; 78.9%; Pred. No. 5.8e-46; ive 13; Mismatches 7; Indels
 Ig-like.
Pyrrolidone carboxylic acid.
 113 AA; 12437 MW; ED57FDD19086D07F CRC64;
 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;
 SMART; SM00406; ĬĠv; 1.
RNOSITE; PSS0835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin V region;
Pyrrolidone carboxylic acid.
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Homo sapiens (Human).
 122 AA
 GO; GO:000576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:imumne response; NAS.
InterPro; IPR007110; IG-like.
InterPro; IPR003596; IG-V.
 MEDLINE=81013859; PubMed=6774332;
PS50835; IG_LIKE; 1.
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Matches 100, Conservative
 Local Similarity 78.99
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 113
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1
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 118 VTV 120
 VIV 120
 HV3G HUMAN
P01768;
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TISSUE=Primary B-Cells;

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X ELTRAUSE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA STRAUSE=2388257; Debberg B.A. Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

BAD Jatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

BAD ALT S. S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S. S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

BOSAK S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RAID D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Ratkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schuutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Marra M.A.;

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.",

Lyco. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).
 Ţ
 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSIFGVVID--YGMDVWGQGTTV 118
 80 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAKHGSGSYIGYYYGMDVWGQGTTV 139
 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY
 20 EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGY
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
 DB 2; Length 573;
 13; Indels
 Strausberg R.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. Submitted (JAN-2002) to the EMBL; BC021276; AAH21276.1; -... PIR; S21205; S21205. PIR; S30532; S30532.
 Hypothetical protein.
SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;
 Last sequence update)
Last annotation update)
 79.3%; Score 499; DB 2; 79.5%; Pred. No. 1.3e-43; ive 10; Mismatches 13;
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 Local Similarity 79.5% tes 97; Conservative
PRELIMINARY;
 01-MAR-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
Hypothetical protein.
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 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSIFGVVIDYGMDVWGQGTTVTV 120
 61 ADSVKGRFTIFRDNSKNMMDLQMNSLRAEDTAVYYCAKDERGRLVGTYFDYWGQGTLVTV 120
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 1 EVQLVESGGGVVQPGRSLRLSCAASRFTFSNYGMHWVRQAPGKGLEWVAAISNDGSNKFY
 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY
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TISSUB=Human rectum tumor;
The German Human cDNA Consortium;
Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
Fobo G., Han M., Wiemann S.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX640627; CAE45781.1; --
HSSP; P01861; 1ADQ.
 Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
 "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035030; AAD56266.1; -.
HSSP; P01772; 2FB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGV; 1.
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 SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
 Score 495; DB 2; Length 122;
Pred. No. 5.7e-44;
7; Mismatches 17; Indels
 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
10-CYT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
(Fragment).
 Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M. Young D.C.,
 13579 MW; 36054D41366545B8 CRC64;
 Last sequence update)
Last annotation update)
 122 AA.
 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last ann
Hypothetical protein DKFZp686F15220.
Name=DKFZp686F15220;
 Created)
 PRT;
 PRT;
 InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig v.
Pfam; PF07654; Cl-set; 3.
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 PROSITE; PS50835; IG_LIKE; 1.
 (TrEMBLrel. 13, (TrEMBLrel. 13,
 Query Match
Best Local Similarity 80.09
PRELIMINARY;
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 SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 3.
SMART; SM00406; IGv; 1.
 Homo sapiens (Human).
 122 AA;
 NCBI_TaxID=9606;
 Q9UL84;
01-MAY-2000
 NON TER
NON TER
SEQUENCE
 06N089;
 680N90
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TISSUE=Primary B-Cells;

RX STEE=Primary B-Cells;

RX Strausberg R.L. Feingold E.A., Grouse L.H., Derge J.G.,

RIGURE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Strausberg R.L. Feingold E.A., Grouse L.H., Derge J.G.,

RIGURE R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatcherko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Porner R.A., Rubin G.M., Hong L.,

Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Rodergren E.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RIGHGUEZ A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Kzzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,

A Jones S.J., Marra M.A.;

R. "Generation and initial analysis of more than 15,000 full-length human
 61 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCARSIFGV--VIDYGMDVWGQGTTV 118
 80 ADSVKGRFTISRDNGKNSLYLQMNSLRAEDTALYYCAKEI-GAHNFYYYGMDVWGQGTTV 138
 79
 20 EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIAY
 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY
 Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 .,
,
 Length 472;
 Strausberg R.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
REMBL, BCO41037, AAH41037.1; -.
REMBL, BCO41037, AAH41037.1; -.
RICEPTO (PR003599; IG.
RICEPTO; IPR003599; IG.
RICEPTO; IPR003599; IG.
RICEPTO; IPR003599; IG.
RICEPTO; IPR003596; IG.
REMRT; SW004009; IG. 2.
REMRT; SW004009; IG. 2.
REMRT; SW004009; IG. 2.
 13; Indels
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS02290; IG_MHC; UNKNOWN_2.
HYPOCHELICAI protein.
SEQUENCE 412 AA; 51724 MW; 26CB340D0046D279 CRC64;
 Created)
Last sequence update)
Last annotation update)
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
 DB 2;
 Score 494.5; DB 2
Pred. No. 3.1e-43;
 478 AA
 9; Mismatches
 PRT;
 78.6%;
79.5%;
 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
 cDNA sequences.
 97; Conservative
 PRELIMINARY;
 TISSUE=Primary B-Cells;
 Hypothetical protein.
Homo sapiens (Human).
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 TV 120
 139 TV 140
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MEDLINE=96071149; PubMed=7475288;
Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
Lichtentein A.K., Berenson J.R.;
Lichtentein A.K., Berenson J.R.;
Lichtentein A.K., Berenson J.R.;
A CD10-positive subset of malignant cells is identified in multiple myeloma using PCR with patient-specific immunoglobulin gene primers.";
Leukemia 9:1948-1953(1995).
BMBL; 808860; AAD14339:1; -.
HSSP; P01842; LAQK.
GO; GO:0005887; C:integral to plasma membrane; NAS.
GO; GO:0016066; P:cellular defense response (sensu Vertebrata); NAS.
InterPro; IPR007110; 1g-like.
InterPro; IPR003196; Ig-v.
SMART; SM00406; IGv; 1.
 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY
 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSIFGVVIDYGMDVWGQGTTVTV
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Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 "Myosin-reactive autoantibodies in rheumatic carditis and normal
 DB 2; Length 121;
 MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
 Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
 16; Indels
 121 121
121 AA; 13154 MW; 2F045CCFASDS0736 CRC64;
 Created)
Last sequence update)
Last annotation update)
 Score 490.5; DB 2
Pred. No. 1.7e-43;
 Cin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035043; AAD56279.1; -.
HSSP; PO1852; INFD.
INTERPO; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
 121 AA.
 9; Mismatches
 147
 Created)
 PRT;
 PROSITE; PS50835; IG LIKE; 1.
 (TrEMBLrel. 12, C
(TrEMBLrel. 12, I
(TrEMBLrel. 25, I
 78.0%;
 (TrEMBLrel. 13,
 Conservative
 PRELIMINARY;
 PRELIMINARY;
 VH3 protein (Fragment).
 SMART; SM00406; IGV; 1
 Homo sapiens (Human)
 Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 01-NOV-1999
01-NOV-1999
 01-MAY-2000
 94;
 01-OCT-2003
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Matches 94
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 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCARSIFGVVIDYGMDVWGQGTTVTV 120
 9
 20 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYMMSWVRQAPGKGLEWVANIKQDGSEKYY
 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR----SIFGVVIDY---GMDVWG
 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY
 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY
 Gaps
 MEDLINE=74175307; PubMed=4208843;
Florent G., Lehman D., Putnam F.W.;
"The switch point in mu heavy chains of human IgM immunoglobulins.";
Blochemistry 13:2482-2488(1974).
-!- MISCELLANBOUS: This chain was isolated from a Waldenstrom's
 Gaps
 21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
19 heavy chân V-III region GA.
Homo sapiens (Human)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 7;
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 Score 493.5; DB 2; Length 478;
Pred. No. 4e-43;
7; Mismatches 13; Indels 7
 Length 122;
 Ig-like.
Pyrrolidone carboxylic acid.
 13; Indels
 al protein. -
478 AA; 52666 MW; 17BED38D917970D6 CRC64;
 122 AA; 13166 MW; 74E5B6959E84100A CRC64;
 macroglobulin.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02052; MHUGA.
HSSP; P01772; 2FB4.
 InterPro; 11.
Promit Proposition 1.
PROSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin V region;
Pyrrolidone carboxylic acid.
Pyrrolidone carboxylic Pyrrolidone carboxylic
 78.4%; Score 493; DB 1; 72.5%; Pred. No. 9.3e-44; ive 20; Mismatches 13.
 78.7%; Sco. No. 4c. 78.7%; Pred. No. 4c. 7; Mismatches
 122 AA
 GO; GO:0005576; C:extracellular; NAS. GO; GO:0003823; P:antigen binding; NAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR007110; IG-like.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 PRT;
 (Rel. 01, Created)
 87; Conservative
 Matches 100; Conservative
 STANDARD;
 :||||||
140 KGTTVTV 146
 QGTTVTV 120
 Similarity
 Similarity
 NCBI_TaxID=9606;
 Hypothetical
SEQUENCE 47
 HV3H HUMAN
P01769;
21-JUL-1986
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 120
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 61 AGSVKGRFTISRDNSKNTLYLONTSLRVEDTAVYCAKDGNYFDSVGYYYAGIDYWGOGT 120
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 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCAR--SIFGVVIDY--GMDVWGQGT
 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY
 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 MEDLINE=79124695; PubMed=420800;
Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
"Amino acid sequence of the VH region of human myeloma
cryoimmunoglobulin 1gG Hil.";
Biochemistry 18:553-560(1979).
 ij
 76.7%; Score 482.5; DB 1; Length 121; 75.8%; Pred. No. 1.2e-42; Live 10; Mismatches 18; Indels 1.
 17.7%; Score 489; DB 2; Length 147; larity 78.2%; Pred. No. 3e-43; Conservative 8; Mismatches 15; Indels
 Ig-like.
Pyrrolidone carboxylic acid.
 protein.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
-!- SIMILARITY: Contains 1 immunoglobuling.
-!- SIMILARITY: Inmunoglobuling.
-!- SIMILARIT
 147 147
147 AA; 15768 MW; 8489FCAAA7BC925C CRC64;
 121 AA; 13566 MW; 480FC53610EF5DAB CRC64;
 PROSITE; PSS0835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin V region;
Pyrrolidone carboxylic acid.
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Homo bapiens (Human).
 PROSITE; PS50835; IG_LIKE; 1.
 Conservative
 STANDARD;
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
 Local Similarity
nes 97; Conserv
 Local Similarity
ses 91, Conserv
 117 TVTV 120
 121 LVTV 124
 NCBI_TaxID=9606;
 HV3J HUMAN
P01771;
 MOD_RES
NON_TER
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TISSUB-Primary B-Cells;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MISCANI S.C., Zeeberg B.A., Grouse L.H., Derge J.G.,

Altschul S.E., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Heishe F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., McKerran K.J., Malke J.A., Gunaratne P.H.,

Raba S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu K., Gibbs R.A.,

Mylting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Makealey R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

""Generation and initial analysis of more than 15,000 full-length human
 ï
 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSIFGVVID-----YG 108
 80 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGGNGIAAAGRVVYAEDYYYYYG 139
 20 QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSSSYTNY 79
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 Gaps
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 12;
 Length 606;
 Score 481; DB 2; Length 606
Pred. No. 1.1e-41;
7. Wismatches 17; Indels
 Straubberg R.;
Submitted (UUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC037358; AH73758.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.
InterPro; IPR00306; Ig.MrC.
InterPro; IPR003596; Ig.
InterPro; IPR003596; Ig.
Pfam; PF07654; C1-set; 4.
 66184 MW; B6B38B51114E4C55 CRC64;
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 Last sequence update)
Last annotation update)
 7; Mismatches
 PROSITE; PS50835; IG LIKE; 5.
PROSITE; PS00290; IG MHC; UNKNOWN 3.
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Best Local Similarity 72.7%;
Matches 96; Conservative
 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
 mouse cDNA sequences.'
 MDVWGQGTTVTV 120
 MDVWGQGTTVTV 151
PRELIMINARY;
 IISSUE-Primary B-Cells;
 SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 4
SMART; SM00406; IGv; 1.
 Hypothetical protein.
 Hypothetical protein
 (Human)
 SEQUENCE FROM N.A
 NCBI_TaxID=9606;
 Homo sapiens
 140
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61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSIFGVVIDYGMDV--WGQGTTV 118
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 [1]
SEQUENCE.
MEDLINE-77070269; PubMed=826475;
MEDLINE-77070269; PubMed=826475;
Ponsting1 H., Hilschmann N.;
"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
 7; Gaps
 Dreker L., Schwarz J., Reichel W., Hilschmann N.;

"Rule of antibody structure. The primary structure of a monoclonal igd1 immunoglobulin (myeloma protein Nie), I: purification and characterization of the protein, the L- and H-chains, the cyanogen bromade cleavage products, and the disulfide bridges.";

Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).

-I- MISCELLANBOUS: This chain was isolated from an IgG1 myeloma
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
1g heavy chain V-III region NIE.
Howo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 DB 1; Length 119;
 Ig-like.
Pyrrolidone carboxylic acid.
 Query Match

76.4%; Score 480.5; DB 1; Length
Best Local Similarity 77.0%; Pred. No. 1.8e-42;
Matches 94; Conservative 9; Mismatches 12; Indels
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-!-SIMILARITY: Contains 1 immunoglobulin-like domain.
BISP, A91668; GHUMI.
BISP, P01772; ZFB4.
GO: GO: 0005576; C: extracellular; NAS.
GO: GO: GO: P: immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
 22 96
119 119
119 AA; 13242 MW; C96935A6E55E165B CRC64;
 Pfam; PF0047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin V region; Pyrrolidone carboxylic acid.
Illi Inc.
Providence carboxylic acid.
Illi Inc.
Providence carboxylic
 119 AA.
 PRT;
 MEDLINE=77070267; PubMed=1002129;
STANDARD;
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ADC99804 standard; protein; 117 AA.
 ADC99804;
 RESULT 1
 9, 2005, 11:43:32 ; Search time 72.1353 Seconds (without alignments) 627.306 Million cell updates/sec
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626
1 QVQLEQSGPGLVKPSETLSL......ARGGDGYRYWGQGTLVIVSS 117
 2105692
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 Total number of hits satisfying chosen parameters:
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GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
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 BLOSUM62
Gapop 10.0 , Gapext 0.5
 geneseqp2003as:*
geneseqp2003bs:*
 A_Geneseq_16Dec04:*
 geneseqp1980s:*
geneseqp1990s:*
 geneseqp2001s:*
geneseqp2002s:*
 geneseqp2004s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Description              |   | Adc99804 Anti-huma | Add05408 Anti-MUC1 | Adf09846 Human ant | Adc99776 Anti-huma | Add05380 Anti-MUC1 | Adf09818 Human ant | Adc99784 Anti-huma | Add05388 Anti-MUC1 | Adf09826 Human ant | Adp03968 Murine-ex | Adp03870 Murine-ex | Adp03974 Murine-ex | _        | Adp03869 Murine-ex | Aab62775 Human HIV | Adp03970 Murine-ex | Adj80377 Antibody | Aab62765 Human HIV | Aaw78433 Antibody | Abb97976 Heavy cha | Adg88414 anti-Ob-R | Adp03934 Murine-ex | Aab62745 Human HIV | Adp03935 Murine-ex | Adp03977 Murine-ex |
|--------------------------|---|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|-------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| ID                       |   | ADC99804           | ADD05408           | ADF09846           | ADC99776           | ADD05380           | ADF09818           | ADC99784           | ADD05388           | ADF09826           | ADP03968           | ADP03870           | ADP03974           | ADP03873 | ADP03869           | AAB62775           | ADP03970           | ADJ80377          | AAB62765           | AAW78433          | ABB97976           | ADG88414           | ADP03934           | AAB62745           | ADP03935           | ADP03977           |
| DB                       | i | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7        | 7                  | 4                  | 7                  | 7                 | 4                  | ~                 | ß                  | 7                  | 7                  | 4                  | 7                  | 7                  |
| Query<br>Match Length DB |   | 117                | 117                | 117                | 117                | 117                | 111                | 117                | 117                | 117                | 118                | 123                | 120                | 120      | 123                | 120                | 119                | 121               | 122                | 123               | 123                | 123                | 110                | 123                | 124                | 122                |
| Query<br>Match           |   | 100.0              | 100.0              | 100.0              | 96.5               | 96.5               | 96.5               | 7.06               | 7.06               | 90.7               | 88.3               | 88.2               | 87.8               | 87.8     | 87.5               | 96.6               | 86.4               | 86.3              | 86.1               | 86.1              | 86.1               | 86.1               | 85.9               | 85.9               | 85.9               | 85.7               |
| Score                    |   | 626                | 626                | 626                | 604                | 604                | 604                | 268                | 268                | 568                | 552.5              | 552                | 549.5              | 549.5    | 548                | 542                | 541                | 540.5             | 539                | 539               | 539                | 539                | 537.5              | 537.5              | 537.5              | 536.5              |
| esult<br>No.             |   | -                  | 7                  | m                  | 4                  | ហ                  | 9                  | 7                  | æ                  | σ                  | 10                 | 11                 | 12                 | 13       | 14                 | 15                 | 16                 | 17                | 18                 | 19                | 20                 | 21                 | 22                 | 23                 | 24                 | 25                 |

|                                                                                                                                                          | Adpusses Murine-ex<br>Aaw27554 Human Ab<br>Abj18676 Antibody |
|----------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------|
| ADP03981 AAU81276 ADP03871 AAY15126 ADP03868 ADP03875 ADP03875 ADP03875 ADP03875 ADP03875 ADP03875 ADP03875 ADP03875 ADP03983 ADP03981 ADP03981 ADP03981 | ADF03989<br>AAW27554<br>ABJ18676                             |
| L 20 L 20 L L L L 20 20 20 L L L L 20 L 10 L 1                                                                                                           | 0 70 ~                                                       |
| 125<br>125<br>125<br>125<br>125<br>127<br>123<br>123<br>123<br>123<br>123<br>123<br>123<br>123<br>123<br>123                                             | 119                                                          |
| 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8                                                                                                                    | 84.7<br>84.7                                                 |
| 536<br>536<br>536<br>537<br>537<br>537<br>537<br>537<br>537<br>537<br>537<br>537<br>537                                                                  | 530<br>530<br>530                                            |
| 2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3                                                                                                                  | 4 4 4<br>5 4 5                                               |

## ALIGNMENTS

anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast; Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 33 26-DEC-2002; 2002WO-US041581 28-DEC-2001; 2001US-0346299P (first entry) WPI; 2003-587113/55. (ABGE-) ABGENIX INC lung cancer; human. N-PSDB; ADC99806 WO2003057838-A2. Homo sapiens. 01-JAN-2004 17-JUL-2003. Gudas J; 

New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.

Claim 1; SEQ ID NO 33; 78pp; English.

The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the pancreatic or condition tumours, specifically melanoma, ossophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung cannoer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody

Pred. No. 1.8e-46;

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117; Conservative
 Best Local Similarity
 12-FEB-2004
 17-JUL-2003
 Gudas J;
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 The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the monoclonal antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has orycestatic and can be used in the production of a vaccine. The monoclonal antibodies against the MUC18 antigen are useful for diagnosing and treating tumours, inhibiting cumour growth (e.g. melanoma, lung tumour or tumour metasteasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-MUC18 antibody heavy chain, variable region,
 9
 9
 monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
 Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
 HNPSLKSRITISVDTSKNQFSLKLSSVTAADTAVYYCARGGDGVRYWGQGTLVTVSS 117
 HINDELKERITISVDTSKNOFSLKLSSVTAADTAVYYCARGGDGYRYWGQGTLVTVSS 117
 Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 33.
 1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY
 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY
 Gaps
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 Length 117;
 100.0%; Score 626; DB 7; 100.0%; Pred. No. 1.8e-46;
 0; Mismatches
heavy chain protein of the invention.
 Claim 1; SEQ ID NO 33; 87pp; English
 ADD05408 standard; protein; 117 AA
 26-DEC-2002; 2002WO-US041582
 28-DEC-2001; 2001US-0346460P
 (first entry)
 protein of the invention
 Conservative
 Bar-Eli M;
 2003-577496/54.
 (ABGE-) ABGENIX INC.
 Best Local Similarity
Matches 117, Conserv
 WPI; 2003-577496/
 metastatic tumor.
 Sequence 117 AA;
 Sequence 117 AA;
 WO2003057006-A2
 Homo sapiens
 01-JAN-2004
 ADD05408;
 61
 Gudas J,
 Query Match
 RESULT
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Length 117;

DB 7;

Score 626;

100.08;

Query Match

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 The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid sequence represents a heavy chain from an MUC18 tumour antigen-specific
 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYLYYSGSTY 60
 ۰۵,
 9
 9
 Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.
 HNPSLKSRITISVDTSKNQFSLKLSSVTAADTAVYYCARGGDGYRYWGQGTLVTVSS 117
 61 HNPSLKSRITISVDISKNOFSLKLSSVTAADTAVYYCARGGDGYRYWGQGTLVTVSS 117
 61 HNPSLKSRITISVDTSKNQFSLKLSSVTAADTAVYYCARGGDGYRYWGQGTLVTVSS 117
 HNPSLKSRITISVDTSKNQPSLKLSSVTAADTAVYYCARGGDGYRYWGQGTLVTVSS 117
 1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY
 1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY
 1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY
 cell proliferation inhibition; MUC18 tumour antigen;
anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
carcinoma; cancer; malignancy; heavy chain; human.
 Gaps
 Gaps
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 ;
0
 Length 117;
 Indels
 Indels
 Human anti-MUC18 monoclonal antibody heavy chain #9.
 cch 100.0%; Score 626; DB 7; al Similarity 100.0%; Pred. No. 1.8e-46; 117; Conservative 0; Mismatches 0;
 ö
 Mismatches
 Claim 1; SEQ ID NO 33; 83pp; English.
 Z
100.08;
 ADF09846 standard; protein; 117
 28-DEC-2001; 2001US-0346414P.
 26-DEC-2002; 2002WO-US041580.
 (first entry)
 monoclonal antibody.
 WPI; 2003-598367/56
 (ABGE-) ABGENIX INC
 Query Match
Best Local Similarity
 N-PSDB; ADF09848
 Sequence 117 AA;
 WO2003057837-A2
 Homo sapiens
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monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.

26-DEC-2002; 2002WO-US041582 28-DEC-2001; 2001US-0346460P

WO2003057006-A2.

17-JUL-2003

Homo sapiens.

Gudas J, Bar-Eli M; WPI; 2003-577496/54.

N-PSDB; ADD05382.

(ABGE-) ABGENIX INC.

Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 5.

(first entry)

01-JAN-2004

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anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
 New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.
 Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 5.
 ADC99776 standard; protein; 117 AA.
 Claim 1; SEQ ID NO 5; 78pp; English
 26-DEC-2002; 2002WO-US041581.
 28-DEC-2001; 2001US-0346299P.
 (first entry)
 WPI; 2003-587113/55.
N-PSDB; ADC99778.
 (ABGE-) ABGENIX INC.
 lung cancer; human
 Sequence 117 AA;
 WO2003057838-A2
 Homo sapiens
 01-JAN-2004
 17-JUL-2003
 ADC99776;
 Query Match
 Gudas J;
RESULT .4
ADC99776
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Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a

Claim 1; SEQ ID NO 5; 87pp; English.

metastatic tumor.

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The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds too MUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the cell surface such as tumnours, specifically melanoma, oseophageal, pancreatic or colorectal tumnours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody heavy chain protein of the invention.
 ö
 1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY 60
 9
 HNPSLKSRITISVDTSKNOFSLKLSSVTAADTAVYYCARGGDGYRYWGQGTLVTVSS 117
 1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY
 Gaps
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 96.5%; Score 604; DB 7; Length 117; 94.0%; Pred. No. 1.4e-44; ive 7; Mismatches 0; Indels
 Matches 110; Conservative
 Local Similarity
 61
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ADD05380 standard; protein; 117 AA

RESULT 5 ADD05380

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ADD05380;

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 The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds WGC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody mas cytostatic and can be used in the production of a vaccine. The monoclonal antibodies against the WGC18 antigen are useful for diagnosing and treating tumours, inhibiting cell invasion associated with melanoma, or tumour metastasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-WGC18 antibody heavy chain, variable region,
 9
 9
 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGGGYKYWGQGTLVTVSS 117
 HNPSLKSRITISVDTSKNOFSLKLSSVTAADTAVYYCARGGDGYRYWGQGTLVTVSS 117
 1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY
 0; Gaps
 Score 604; DB 7; Length 117;
Pred. No. 1.4e-44;
7; Mismatches 0; Indels
 cell proliferation inhibition; MUC18 tumour antigen;
 Human anti-MUC18 monoclonal antibody heavy chain #2.
 Ź
 ADF09818 standard; protein; 117
 Query Match
Best Local Similarity 94.0%;
Matches 110; Conservative
 (first entry)
 protein of the invention.
 Sequence 117 AA;
 ADF09818;
 61
 RESULT 6
 ADF09818
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New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g.
 a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds too MVC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the cell surface such as tumours, specifically melanoma, oscophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including
 invention relates to a novel isolated monoclonal antibody comprising
 YNPSLKSRVIISVDISKNOPSLKLSSVIAAADIAVYYCAREGDGFDYWGQGILVIVSS 117
 61 HNPSLKSRITISVDTSKNQFSLKLSSVTAADTAVYYCARGGDGYRYWGQGTLVTVSS 117
 Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 13.
 QVQLQESGPGLVXPSQTLSLTCTVSGGSISSGGYWTWIRQHPGKGLEWIGFIYYSGSTY
 QVQLEQSGPGLVKPSETLSLTCTVSGGS1SSGTYHWSW1RQHPGRGLEW1GY1YYSGSTY
 colorectal, breast or lung caneer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody
 monoclonal antibody; tumour; MUC18; proliferation; cytostatic; antigen; tumour metastasis; melanoma; metastatic; human; heavy
 90.7%; Score 568; DB 7; Length 11.
 tumors, cancers, and other malignancies.
 heavy chain protein of the invention.
 Claim 1; SEQ ID NO 13; 78pp; English.
 ADD05388 standard; protein; 117 AA.
 28-DEC-2001; 2001US-0346460P.
 26-DEC-2002; 2002WO-US041582
26-DEC-2002; 2002WO-US041581
 28-DEC-2001; 2001US-0346299P
 (first entry)
 Best Local Similarity 88.9
Matches 104; Conservative
 WPI; 2003-577496/54.
N-PSDB; ADD05390.
 WPI; 2003-587113/55
 (ABGE-) ABGENIX INC
 (ABGE-) ABGENIX INC
 Sequence 117 AA;
 N-PSDB; ADC99786
 WO2003057006-A2
 Homo sapiens
 01-JAN-2004
 17-JUL-2003.
 Gudas J,
 Query Match
 Gudas J;
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 ADD05388
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 The invention comprises a method for inhibiting cell proliferation associated with expression of MUCI8 tumour antigen. The method involves administering anti-MUCI8 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUCI8 tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid sequence represents a heavy chain from an MUCI8 tumour antigen-specific monoclonal antibody.
 anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
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 Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-
 HNPSLKSRITISVDTSKNOFSLKLSSVTAADTAVYYCARGCDGYRYWGOGTLVTVSS 117
 1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY
 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTY
anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour; carcinoma; cancer; malignancy; heavy chain; human.
 Gaps
 Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 13
 ö
 Score 604; DB 7; Length 117;
Pred. No. 1.4e-44;
7; Mismatches 0; Indels
 Pred. No. 1.467; Mismatches
 Claim 1; SEQ ID NO 5; 83pp; English.
 ADC99784 standard; protein; 117 AA.
 96.5%;
94.0%;
 26-DEC-2002; 2002WO-US041580
 28-DEC-2001; 2001US-0346414P
 01-JAN-2004 (first entry)
 WUC18 monoclonal antibody
 Conservative
 WPI; 2003-598367/56.
 (ABGE-) ABGENIX INC
 Similarity
 lung cancer; human
 N-PSDB; ADF09820
 Sequence 117 AA;
 WO2003057838-A2.
 WO2003057837-A2
 Homo sapiens
 Homo sapiens
 Best Local Simi
Matches 110;
 17-JUL-2003
 17-JUL-2003
 ADC99784;
 61
 Query Match
 antigen,
 Sudas J;
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Gaps

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Length 117;

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vaccine;

RESULT 7 ADC99784

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The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises tumour growth in an animal. The tumour inhibition process comprises comprised an electing an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the anipody comprises of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has artibodies against the MUC18 antigen are useful for diagnosing and treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or tumour metastasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-MUC18 antibody heavy chain, variable region,
 Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
 HNPSLKSRITISVDTSKNOFSLKLSSVTAADTAVYYCARGGDGYRYWGQGTLVTVSS 117
 1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY
 ; Score 568; DB 7; Length 117;
; Pred. No. 1.8e-41;
10; Mismatches 3; Indels
 Human anti-MUC18 monoclonal antibody heavy chain #4.
 Claim 1; SEQ ID NO 13; 87pp; English.
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 ADF09826 standard; protein; 117
 90.78;
 88.98;
 Query Match
Best Local Similarity 88.99
Matches 104; Conservative
 (first entry)
 protein of the invention.
 metastatic tumor.
 Sequence 117 AA;
 12-FEB-2004
 61
 ADF0982
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Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.
 cell proliferation inhibition; MUC18 tumour antigen; anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour; carcinoma; cancer; malignancy; heavy chain; human.
 26-DEC-2002; 2002WO-US041580.
 28-DEC-2001; 2001US-0346414P.
 WPI; 2003-598367/56.
 (ABGE-) ABGENIX INC
 N-PSDB; ADF09828.
 WO2003057837-A2
 Homo sapiens
 17-JUL-2003
 Gudas J;
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associated with expression of MUCIS tumour antigen. The method involves administering anti-MUCIS monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUCIS tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting in the present aminours, carcinomas, cancer and other malignancies. The present amino acid sequence represents a heavy chain from an MUCIS tumour antigen-specific
                                                                     comprises a method for inhibiting cell proliferation
                       Claim 1; SEQ ID NO 13; 83pp; English.
                                                                                                                                                                                                                                                                                             monoclonal antibody
                                                                     The invention
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Sequence 117 AA;

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                                                                                                                                             61 HNPSLKSRITISVDTSKNQFSLKLSSVTAADTAVYYCARGGDGYRYWGQGTLVTVSS 117
                                                                      QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGY1YYSGSTY
                                                                                      1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY
                                             Gaps
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               Length 117;
Score 568; DB 7; Length Land Pred. No. 1.88-41; Pred. Transpers 3; Indels
                                        10; Mismatches
                                                                                                                                                                                                                                  ADP03968 standard; protein; 118 AA
               90.7%;
                                           Conservative
                            Similarity
       Query Match
Best Local Simi]
Matches 104; (
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Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 138. monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen; cytostatic; colorectal neoplasm; renal call carcinoma; cervical intraepithelial squamous neoplasia; cervical intraepithelial glandilar neoplasia; oesophageal; breast gene therapy; murine; mouse; human; heavy chain variable domain. (first entry) 29-JUL-2004 ADP03968;

Unidentified

02-DEC-2002; 2002WO-US038550 WO2003048328-A2. 12-JUN-2003.

03-DEC-2001; 2001US-0337275P

(ABGE-) ABGENIX INC

Ξ Gallo Gudas J, Foltz I, Handa M,

WPI; 2003-523295/49.

colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical intraepithelial squamous and glandular neoplasia or esophageal tumors. New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.

Example 2; SEQ ID NO 138; 89pp; English.

The invention relates to a novel isolated monoclonal antibody (mAb) comprising a heavy chain polypeptide and light chain polypeptide having a sequence chosen from one of 53 fully defined anino acid sequences given in the specification, where the antibody specifically binds carbonic anhydrase IX (GA IX) tumour antigen. The antibody of the invention demonstrates cytostatic activity and may be useful for treating a tumour,

transgenic mouse strain.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen; cytostatic; colorectal neoplasm; renal cell carcinoma; cervical intraepithelial squamous neoplasia; cervical intraepithelial glandular neoplasia; oesophageal; breast cancer; gene therapy; murine; mouse; human; heavy chain variable domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel isolated monoclonal antibody (mab) comprising a heavy chain polypeptide and light chain polypeptide having sequence chosen from one of 53 fully defined amino acid sequences given in the specification, where the antibody specifically binds carbonic anhydrase IX (CA IX) tumour antigen. The antibody of the invention demonstrates cytostatic activity and may be useful for treating a tumour, such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma, cervical intraepithelial squamous and glandular neoplasia, osesophageal tumour or breast cancer, possibly via gene therapy. The current sequence is that of a murine-expressed anti-human CA IX monoclonal antibody WH (heavy chain variable domain) protein of the invention. The protein was generated via the introduction of the human CA IX protein into
              cervical intraepithelial squamous and glandular neoplasia, oesophageal tumour or breast cancer, possibly via gene therapy. The current sequence is that of a murine-expressed anti-human CA IX monoclonal antibody VH (heavy chain variable domain) protein of the invention. The protein was generated via the introduction of the human CA IX protein into a
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                                                                                                                                                                                                                                                                                                                                                       61 HNPSLKSRITISVDTSKNQFSLKLSSVTAADTAVYYCAR-GGDGYRYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                           OVOLOESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New anti-CA IX monoclonal antibody, useful for treating a tumor e.g., colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical intraepithelial squamous and glandular neoplasia or esophageal tumors.
                                                                                                                                                                                                                                                                            OVOLEOSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIROHPGRGLEWIGYIYYSGSTY
such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                       Ä
                                                                                                                                                                                                 Length 118;
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                             7,
                                                                                                                                                                                                                                     2
                                                                                                                                                                                             Score 552.5; DB Pred. No. 4e-40; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallo M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 10; 89pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ą.
                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADP03870 standard; protein; 123
                                                                                                                                                                                             88.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                           Query Match
Best Local Similarity 89.0
Matches 105; Conservative
                                                                                                                 transgenic mouse strain.
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                                                                                                                                                          Sequence 118 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
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monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen; cytostatic; colorectal neoplasm; renal cell carcinoma; cervical intraepithelial squamous neoplasia; cervical intraepithelial glandilar neoplasia; oesophageal; breast cancer; gene therapy; murine; mouse; human; heavy chain variable domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel isolated monoclonal antibody (mAb) comprising a heavy chain polypeptide and light chain polypeptide having a sequence chosen from one of 53 fully defined amino acid sequences given in the specification, where the antibody specifically binds carbonic anhydrase IX (CA IX) tumour antigen. The antibody of the invention demonstrates cytostatic activity and may be useful for treating a tumour, such as colorectal neoplasm, renal cell carcinoma, cervical intraepithelial squamous and glandular neoplasia, osesophageal tumour or breast cancer, possibly via gene therapy. The current sequence is that of a murine-expressed anti-human CA IX monoclonal antibody VH (heavy chain variable domain) protein of the invention. The protein was generated via the introduction of the human CA IX protein into
                                                                                                                                                                                                                   61 HNPSLKSRITISVDTSKNQFSLKLSSVTAADTAVYYCARGGDGY-----RYWGQGTLVT 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
intraepithelial squamous and glandular neoplasia or esophageal tumors.
                                                                                                                                                                1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTY
                                                                                                                                             1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New anti-CA IX monoclonal antibody, useful for treating a tumor e.g., colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
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                                                                     Score 552; DB 7; Length 123; Pred. No. 4.6e-40;
                                                                                                       7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                     ADP03974 standard; protein; 120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-DEC-2002; 2002WO-US038550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-DEC-2001; 2001US-0337275P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Handa M,
                                                                       88.2%;
                                                                                            85.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                           Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transgenic mouse strain.
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                                                                                        Similarity
                                                                                                                                                                                                                                                                                          VSS 117
                                                                                                                                                                                                                                                                                                                            121 VSS 123
                                   AA;
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                                   Sequence 123
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                                                                       Query Match
                                                                                            Local
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Length 120;

DB 7;

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29-JUL-2004
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 Query Match
Best Local S
Matches 105
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                                                                                                                                HNPSLKSRITISVDTSKNOFSLKLSSVTAADTAVYYCARGGDGYRY-----WGQGTLVTV 115
                                                                                                                                                                                                                                                                                                                                           monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen; cytostatic; colorectal neoplasm; renal cell carcinoma; cervical intraepithelial squamous neoplasia; cervical intraepithelial glandular neoplasia; oesophageal; breast cancer; gene therapy; murine; mouse; human; heavy chain variable domain.
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                                                                                                                                                                                                                                                                                                                      Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 13.
                                                                                1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 intraepithelial squamous and glandular neoplasia or esophageal tumors
                                                                     1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIROHPGRGLEWIGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumors, cervical carcinoma, cervical
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.
                                               7;
                          Length 120;
                                               Indels
                         DB 7;
                        Score 549.5; DB 7
Pred. No. 7.3e-40;
}; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallo M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 13; 89pp; English.
                                                                                                                                                                                                                                                 ADP03873 standard; protein; 120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neoplasms, colorectal
                                             8;
                        87.8%;
86.1%;
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                                                                                                                                                                                                                                                                                               (first entry)
                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transgenic mouse strain.
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                                   Similarity
Sequence 120 AA;
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                                    Best Local Sim
Matches 105;
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                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel isolated monoclonal antibody (mAb) comprising a heavy chain polypeptide and light chain polypeptide having sequence chosen from one of 53 fully defined amino acid sequences given in the specification, where the antibody specifically binds carbonic anhydrase IX (CA IX) tumour antigen. The antibody of the invention demonstrates cytostatic activity and may be useful for treating a tumour, such as colorectal nooplasm, renal cell carcinoma, cervical intraepithelial squamous and glandular neoplasia, oesophageal tumour or breast cancer, possibly via gene therapy. The current sequence is that of a murine-expressed anti-human CA IX monoclonal antibody WH (heavy chain variable domain) protein of the invention. The protein was generated via the introduction of the human CA IX protein into
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                                                                                                                                                                                                                                                                                 1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY
                                                                                                                                                           QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTY
                                                                                                                                                                                                                                                 61 HNPSLKSRITISVDTSKNQFSLKLSSVTAADTAVYYCARGGDGYRY-----WGQGTLVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New anti-CA IX monoclonal antibody, useful for treating a tumor e.g., colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical intraepithelial squamous and glandular neoplasia or esophageal tumors.
                                                                  Gaps
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                                                                  Indels
                                                            . 7
Score 549.5; DB 7
Pred. No. 7.3e-40;
8; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADP03869 standard; protein; 123 AA.
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                                  86.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                               105; Conservative
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                                  Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                      SS 117
                                                                                                                                                                                                                                                                                                                                                                                                                               SS 120
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Job time : 73.1353 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human monoclonal antibody immunoreactive with human immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1 in biological sample and providing passive immunotherapy to HIV-1
                            1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY
                                            1 QVQLEQSGPGLVKPSQTLSLTCTVSGGSISSGGRYWSWIRQHPGKGLEWIGYIYYSGSTY
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   6; Gaps
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86.6%; Pred. No. 3.3e-39;
ive 9; Mismatches 5; Indels
6; Indels
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6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JUN-2000; 2000WO-US017327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0141701P
                                                                                                                                                                                                                                                                                                          (first entry)
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Matches 103; Conservative
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Watkins BA, Reitz MS;
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N-PSDB; AAF29076.
                                                                                                                                                                        121 VSS 123
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infected mammal.
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Run on:

Sequence:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: PERFORMS-DOS
SOFTWARE: PATEMEN PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAWE: James F. Haley, Jr., Esq.
FILING DATE: 1NFORMATION:
NAWE: James F. Haley, Jr., Esq.
FILEDROMINICATION NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPRAX: (212)596-900
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TTYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 530; DB 3; Length 119;
Pred. No. 3.3e-45;
7; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Knappik, Achim
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: 11ag, Vic
APPLICANT: Ge, Liming
APPLICANT: Plueckthun, Andreas
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
           US-09-138-091A-77
US-09-474-840B-20
US-09-472-087-86
US-08-545-809A-116
US-08-545-809A-12
US-08-545-809A-12
US-08-545-809A-12
US-08-545-809A-12
US-08-545-809A-12
US-08-545-809A-12
US-08-545-809A-12
US-08-545-809A-12
US-08-545-809A-12
US-08-545-809A-14
US-08-545-809A-14
US-08-545-809A-14
                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                          Sequence 39, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
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Best Local Similarity 86.8%;
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-025-7698-39
                                                                                                                                                                                                                                                                                                                               RESULT 1
US-09-025-769B-39
November 9, 2005, 11:29:55; Search time 18.1805 Seconds (without alignments) 480.403 Million cell updates/sec
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Sequence 65,
Sequence 39,
Sequence 65,
Sequence 11,
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Sequence 39,
Sequence 65,
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Sequence 1
Sequence 2
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1 QVQLEQSGPGLVKPSETLSL.....ARGGDGYRYWGQGTLVTVSS
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-025-769B-39
US-09-025-769B-65
US-09-490-070A-39
US-09-490-153-39
US-09-490-153-65
US-09-490-153-65
US-09-490-124-65
US-09-014-65-11
US-08-10-125-11
US-09-017-62B-11
US-09-017-62B-11
US-09-014-880-11
US-09-450-363-11
US-09-450-363-11
US-09-450-363-11
US-09-450-363-11
US-09-450-363-11
US-09-450-363-11
US-09-450-363-11
US-09-450-363-11
US-09-450-363-145
US-09-017-62B-5
US-09-017-62B-25
US-09-017-93-35
US-09-018-25
US-09-018-25
US-09-018-25
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                                                                                                                                                                                                                                                         513545 segs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length
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Minimum DB Maximum DB

Database

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                                                                                                                                                            1 QVQLQESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYSGSTN 58
                                     1 QVQLQESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYSGSTN 58
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ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: 19M PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REFERENCE/DOCKT NUMBER: 7094

REFERENCE/DOCKT NUMBER: MORPHO/5

TELECOMMUNICATION INPORMATION:

TELECOMMUNICATION INPORMATION:

TELECHONE: (212)596-9090

"FILEPHONE: ARCHIVER: AR
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Pred. No. 3.3e-45;
7; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ling, Vic
APPLICANT: Ling, Vic
APPLICANT: Pluckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                              61 HNPSLKSRITISVDTSKNQFSLKLSSVTAADTAVYYCAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-025-769B-65; Sequence 65, Application US/09025769B; Patent No. 6300064
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Best Local Similarity 86.8
Matches 105; Conservative
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61 HNPSLKSRITISVDTSKNOFSLKLSSVTAADTAVYYCAR-GGDGY---RYWGQGTLVTVS 116
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                                                                                                                                                                                                                                                                                               ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 119;
                                                                                                                                                                                                                          TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
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86.8%; Pred. No. 3.3e-45;
tive 7; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: BP 95 11 3021.0 FILING DATE: 18-AUG-1995 ATTORNEY, AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-070A-39
Sequence 39, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Ranappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-09-490-070A-65
; Sequence 65, Application US/09490070A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 86.8
Matches 105; Conservative
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61 HNPSLKSRITISVDTSKNQFSLKLSSVTAADTAVYYCAR-GGDGY---RYWGQGTLVTVS 116
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Fatent No. 6706484
GENERAL INFORMATION:
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSE: James F. Haley, Jr., Esq. c/o Fish & Neave
                                                                             c/o Fish & Neave
                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION NUMBER: US_09/490,153
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         TITLE OF INVENTION: Protein/(Poly)peptide libraries
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86.8%; Pred. No. 3.3e-45;
tive 7; Mismatches 3
                                                                        ADDRESSEE: James F. Haley, Jr., Esq. STREET: 1251 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27, 794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-153-39
                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 24-Jan-2000 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 39
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                                                 CORRESPONDENCE ADDRESS
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Best Local Similarity 86.87
Matches 105; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQESGPGLVXPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYSGSTW 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Is is tabley used.

COMPUTER: Is MP FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 1A ANG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31.298
REFERENCE/DOCKET NUMBER: 31.299
REFERENCE/DOCKET NUMBER: 31.299
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (222. 91.2-2000
                                                                                                                                                                                                                                                ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                 Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
CORRESPONDENCES: 373
                                                                                                                                                                                                                                                                                               STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 530; DB 4;
Pred. No. 3.3e-45;
7; Mismatches 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 39, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 119 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (202) 912-2020
                                            APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 86.8%;
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                CITY: Washington
STATE: D.C.
COUNTRY: USA
Patent No. 6696248
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20006
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59 YNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCARWGGDGFYAMDYWGQGTLVTVS 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 65, Application US/09490324

Patent No. 6828422

GENERAL INFORMATION:

APPLICANT: Knappik, Achim
Pack, Peter

Ilaq, Vic

Ge, Liming
Moroney, Simon
Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly) peptide libraries

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
              CURRENT APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-dan-2000
PRIOR APPLICATION NUMBER: US/09/490,324
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELEPOMUNICATION INFORMATION:
TELEPRAX: (212) 596-9000
TELEFRAX: (212) 596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 530; DB 4;
Pred. No. 3.3e-45;
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86.8%; Pred. No. 3...
7; Mismatches
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APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 86.8
Matches 105; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                           CURRENT APPLICATION DATA:

SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:

PRIDICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY'AGENT INFORMATION:

REGISTRATION NUMBER: 27,794
TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.7%; Score 530; DB 4; Length 119; 86.8%; Pred. No. 3.3e-45; 1.ve 7; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                 COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-153-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 39, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212) 596-9000
                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 119 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FELEFAX: (212)596-9090
V FOR SEQ ID NO: 65:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 86.8
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New York
  STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ilag,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR
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28

Gaps

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REGISTRATION NUMBER: 33,367
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Patent No. 5567246

GENERAL INFORMATION:
APPLICANT: Saixch HOSOKAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: Wasuhiro NAGAIKE
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 805 Fifteenth Street, N.W., #700
CITTL MASHINGTON
CONTENTION OF SECURITY MASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 HNPSLKSRITISVDTSKNQFSLKLSSVTAADTAVYYCAR-GGDGY---RYWGQGTLVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 84.7%; Score 530; DB 4; Length 119; Best Local Similarity 86.8%; Pred. No. 3.3e-45; Matches 105; Conservative 7; Mismatches 3; Indels
                                                                                     NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27, 794
REFERENCE DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPRONE: (212) 596-9000
TELEFAX: (212) 596-9000
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acids
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: D.C. COUNTRY: U.S.A. ZIP: 2005
COUNTRY: U.S.A. ZIP: 20005
COMPUTER READABLE FORM: 6.25 inch, 500 kb COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 65: US-09-490-324-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 S 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s 119
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US-08-360-125-11
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61 HNPSLKSRITISVDTSKNOFSLKLSSVTAADTAVYYCARGG-DGYRY----WGQGTLVTV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGSIYYSGSTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Indels
                                                                                                                                                                                                                                                                                                                                TISSUE TYPE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 520.5; DB 1;
Pred. No. 2.9e-44;
8; Mismatches 8;
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; Sequence 11, Application US/08450578
; Patent No. 5837845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-11
TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                         INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 82.8%;
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
AUTHORS:
                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
                                                                                                                                 single
                                                                                                                                                                                                                                                               STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                 ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
                                                                                                                                                                                               ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOCUMENT NUMBER:
                                                                                                                               STRANDEDNESS:
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                                TELEFAX:
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VOLUME:
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Gaps

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61 HNPSLKSRITISVDTSKNOFSLKLSSVTAADTAVYYCARGG-DGYRY----WGQGTLVTV 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/09017628

Patent No. 5990287

GENERAL INFORMATION:

APPLICANT: HOSOKAWA, Saiko

APPLICANT: HOSOKAWA, Yoko

APPLICANT: HOSOKAWA, Yoko

APPLICANT: ITO, No. 59902871hiko

APPLICANT: HIRAKAWA, Yoko

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO

TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE

FILE REFERENCE: 177/52731KH

CURRENT APPLICATION NUMBER: US/09/017,628

CURRENT APPLICATION NUMBER: 08/360,125

EARLIER FILING DATE: 1994-12-20

NUMBER OF SEQ ID NOS: 42

SEQUENCE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 83.1%; Score 520.5; DB 2; Length 122; Best Local Similarity 82.8%; Pred. No. 2.9e-44; Matches 101; Conservative 8; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Hybridoma producing human antibody 1-3-1
US-09+017-628-11
                                                                                                             YOLUME:
FORDES:
DATE:
DATE:
FILING DATE:
FUBLICATION DATE:
FREEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SS 117
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                                                                            TITLE:
JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 11
LENGTH: 122
                                                           AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116
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APPLICANT: Saiko HOSOKAWA

APPLICANT: Toshiaki TAGAWA

APPLICANT: Yoko HIRAKAWA

APPLICANT: No. 581748451hiko ITO

APPLICANT: Kazuhiro NAGAIKE

ITTLE OF INVENTION: Human Monoclonal Antibody

TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer

TITLE OF INVENTION: Call Membrane

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderath

STRPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HARLOTYPE:
TISSUE TYPE:
CELL LINE:
ORGANELLE:
IMBEDIATE SOURCE:
LIBRARY:
CLONE:
                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,578
FILING DATE: May 25, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
                                                                                                                                                                                                                                           STREET: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11:
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SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                     STATE: D.C. COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY:
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7

Gaps

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APPLICANT: Saiko HOSOKAWA
APPLICANT: Saiko HOSOKAWA
APPLICANT: Yoshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: Wo. 6436434ihiko ITO
APPLICANT: Wo. 6436434ihiko ITO
APPLICANT: Wo. 6436434ihiko ITO
APPLICANT: Wazuhiro NaGalfe
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: Wenderoth, Lind & Ponack
CITY: Washington
STREET: U.S.A
ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAPLOTYPE:
TISSUB TYPE:
TESL TYPE: Hybridoma producing human antibody 1-3-1
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: IEM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/450,363 FILING DATE: MAY 25, 1995 CLASSIFICATION DATA: APPLICATION NUMBER: 08/360,125 FILING DATE: December 20, 1994 FILING DATE: December 20, 1994 FILING DATE: December 20, 1994 FILING DATE: June 29, 1992 ATORNEY AGENT INFORMATION: NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367 REGISTRATION NUMBER: 33,367 REGISTRATION NUMBER: 33,367 REGISTRATION NUMBER: 33,367 RELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acid
TYPE: amino acid
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NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANELLE:
MMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 OVOLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY 60
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                                                                                                                    Sequence 11, Application US/09014880

Patent No. 5990297

GENERAL INFORMATION:

APPLICANT: Salko HOSOKAWA et al.

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY

TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE

NUMBER OF SEQUENCES:

ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.

STREET: 2033 K Street, N.W., #800

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.
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; ORIGINAL SOURCE:

; CELL TYPE: Hybridoma producing human antibody 1-3-1

US-09-014-880-11
                                                                                                                                                                                                                                                                                                                                                                                                                   CCUNTRY: U.S.A.

ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OFERATING SYSTEM: MS-DOS
SOFTWARE: Wordsperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/450,578
FILING DATE: January 28, 1995
FILING DATE: December 20, 1995
FILING DATE: December 20, 1994
FILING DATE: December 20, 1994
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 37,955
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: 33,367
REFERENCE/DOCKET NUMBER: TELEPHONE: 202-721-8250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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US-08-450-363-11

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1 OLOLOESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGSIYYSGSTY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                    INDIVIDUAL ISOLATE: «Unknown»

BAPECPUEDMENTAL STAGE: «Unknown»

HAPLOTYPE: «Unknown»

TISSUE TYPE: «Unknown»

TELL TYPE: Hybridoma producing human antibody 1-3-1

CELL LINE: «Unknown»

ORGANELLE: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 520.5; DB 4; Length
Pred. No. 2.9e-44;
8; Mismatches 8; Indels
     APPLICATION NUMBER: JP158861/1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                        NAME: Warren M.Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE DOCKET NUMBER: <U
TELECOMMINICATION INFORMATION:
TELEPHONE: 202-721-8200
                       FILING DATE: June 28, 1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                               TELERAK: «Unknown»
TELEX: «Unknown»
TELEX: «Unknown»
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHROMOSOME/SEGMENT: <Un
MAP POSITION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: «Unknown»
ANTI-SENSE: «Unknown»
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.1%;
82.8%;
                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: <Unknown>
STRAIN: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
   LIBRARY: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLONE: <Unknown>
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 83.1
Best Local Similarity 82.8
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNITS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-467-903-11
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Kazuhiro NAGAIKE
KAzuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
Specifically Binding to Surface Antigen of Cancer
Cell Membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                      1 QLQLQESGPGLVKPSETLSLTCTVSGGSISSSYYWGWIRQPPGKGLEWIGSIYYSGSTY 60
                                                                                                                                                                                                                                                                                                                                                                   1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                              2,
                                                                                                                                                                                                                                                                                          Length 122;
                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDPETFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/467,903
FILING DATE: 21-Dec-1999
CLASSIFICATION: cUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                        DB 4;
                                                                                                                                                                                                                                                                                      Score 520.5; DB 4
Pred. No. 2.9e-44;
8; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 42
CORRESPONDENCE MADRESSE: Wanderoch, Lind & Ponack
STREET: 2033 K Street, N.W., #800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/450,363
FILING DATE: MAY 25,1955
FILING DATE: December 20, 1954
FILING DATE: December 20, 1994
FILING DATE: Due 29, 1992
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1991
APPLICATION NUMBER: JP188859/1991
FILING DATE: June 28, 1991
FILING DATE: June 28, 1991
FILING DATE: June 28, 1991
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DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
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Patent No. 6787133
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
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Yoko HIRAKAWA
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82.8%;
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COMPUTER READABLE FORM:
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Best Local Similarity 82.8
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: D.C. COUNTRY: U.S.A.
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
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                                                        TITLE:
JOURNAL:
VOLUME:
ISSUE:
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Gaps

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61 HNPSLKSRITISVDISKNOFSLKLSSVTAADTAVYYCAR-----GGDGYRYWGQGTLV 113
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                                                                                       GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Tang, Y. Tom
APPLICANT: Gorley, Meil C.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STREET: 30 Alto
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: DOS
SOFTWARE: FASESCO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: HEREWITH
CLASSIPICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER:
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Best Local Similarity 81.5%; Pred. No. 1.9e-43;
Matches 101; Conservative 7; Mismatches 9; Indels 7.
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Sequence 4, Application US/09049672A
Patent No. 613541
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
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LENGTH: 473 amino acids
TYPE: amino acidd
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PANCTUTO1
CLONE: 1513264
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ORGANISM:
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                                                      November 9, 2005, 11:40:37; Search time 65 Seconds (without alignments) 753.137 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-330-530-33
US-10-60-357-33
US-10-330-613-5
US-10-330-530-5
US-10-60-357-5
US-10-330-613-13
US-10-60-357-13
US-10-60-357-13
US-10-309-762-13
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Maximum Match 100%
Listing first 45 summaries
                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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626
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Perfect score:
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22, Appl

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Fublication No. US20030147809A1
GENERAL INFORMATION:
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
FILE REFERENCE: ABGENIX.022A
CURRENT APPLICATION NUMBER: US/10/330,613
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: 60/346299
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
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100.0%; Pred. No. 6.4e-48;
iive 0; Mismatches 0;
                      US-10-300-762-149
US-10-300-762-149
US-10-910-901-253
US-10-910-901-253
US-10-993-576-37
US-10-994-960A-26
US-10-994-960A-56
US-10-98-137-137
US-10-98-137-191
US-10-98-137-191
US-10-98-137-191
US-10-98-137-191
US-10-98-137-191
US-10-98-137-191
US-10-309-762-147
US-10-309-762-147
US-10-309-762-11
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US-10-988-360-8
US-10-309-762-12
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        Query Match 100.
Best Local Similarity 100.
Matches 117; Conservative
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US-10-330-530-33

Sequence 33, Application US/10330530

j Bublication No. US20030152514A1

j GENERAL INPORMATION:

APPLICANT: Gudas, Jean

TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES

FILE REFERENCE: ABGRIX.031A

CURRENT APPLICATION NUMBER: US/10/330,530

CURRENT PILING DATE: 2002-12-26

PRIOR APPLICATION NUMBER: US 60/346414

PRIOR FILING DATE: 2001-12-18

NUMBER OF SEQ ID NOS: 40

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 117;
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Sequence 33, Application US/10660357

Publication No. US20040115205A1

GENERAL INFORMATION:
APPLICANT: Bar-Eli, Menashe
APPLICANT: Green, Larry L.
TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
TITLE OF INVENTION: ANTIGEN
FILE REFERENCE: AGGENIX: 030-C1
CURRENT APPLICATION NUMBER: US/10/660,357
CURRENT FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-12-26
NUMBER OF SEQ ID NOS: 40

SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 6.4e-48;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 626; DB 16; Best Local Similarity 100.0%; Pred. No. 6.4e-48; Matches 117; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 5, Application US/10330613; Publication No. US20030147809A1 GENERAL INFORMATION: APPLICANT: Gudas, Jean
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Best Local Similarity 100.0%;
Matches 117; Conservative 0
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US-10-660-357-33
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LENGTH: 117
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                                                                                                                                                                                                                                                                                             SEQ ID NO 33
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1 QVQLEQSGPGLVXPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY 60
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Sequence 5, Application US/10330530;
Publication No. US20030152514A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
FILE REFERENCE: ABGENIX.031A
CURRENT APPLICATION NUMBER: US/10/330,530
CURRENT FILING DATE: 2002-12-26;
PRIOR APPLICATION NUMBER: US 60/346414
FRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 6.0
                                                                                                                                                                                                                                                                                                                                                                      Length 117;
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TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN FILE REFERENCE: ABGENIX.022A
CURRENT APPLICATION NUMBER: 105/10/330,613
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: 60/34629
PRIOR APPLICATION NUMBER: 60/34629
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 5, Application US/10660357
GENERAL INFORMATION:
APPLICANT: Bar-B1, Menashe
APPLICANT: Green, Larry L.
TITLE OF INVENTION: BAR OF ANTIBODIES AGAINST THE MUC18
TITLE OF INVENTION: ANTIGEN
FILE REFERENCE: ABGENIX.030C1
CURRENT APPLICATION NUMBER: US/10/660,357
CURRENT FILING DATE: 2003.09-10
PRIOR APPLICATION NUMBER: 10/330,580
                                                                                                                                                                                                                                                                                                                                                                 Score 604; DB 14;
Pred. No. 5.8e-46;
7; Mismatches 0;
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Pred. No. 5.8e-46;
7; Mismatches 0;
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94.0%;
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Best Local Similarity 94.0
Matches 110; Conservative
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Best Local Similarity 94.0
Matches 110; Conservative
                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo Sapiens
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                          SEQ ID NO 5
LENGIH: 117
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1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY 60
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APPLICANT: Guidas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Handa, Masahisa
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: ABGENTX.027A
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR PLING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 138
LENGTH: 118
                                                   DB 14; Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.7%; Score 568; DB 16; Length 117; larity 88.9%; Pred. No. 9e-43; Conservative 10; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                     Sequence 13, Application US/10660357

Publication No. US20040115205A1

GENERAL INFORMATION:

APPLICANT: Bar-Bil, Menashe

APPLICANT: Green, Larry L.

TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18

TITLE OF INVENTION: ANTIGEN

FILE REFERENCE: ABGENIX.030C1

CURRENT APPLICATION NUMBER: US/10/660,357

CURRENT FILING DATE: 2003-09-10

PRIOR FILING DATE: 2003-12-26
                                                                                            Indels
                                               90.7%; Score 568; DB 14
88.9%; Pred. No. 9e-43;
                                                                                            10; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 117
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                                               Query Match
Best Local Similarity 88.99
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo Sapiens
US-10-660-357-13
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CRGANISM: Homo sapiens
US-10-309-762-138
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        US-10-330-530-13
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Publication No. US20030152514A1

GENERAL INFORMATION:

APPLICANT: Gudas, Jean

TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES

FILE REFERENCE: ABGENTX.031A

CURRENT FILING DATE: 2002-12-26

PRIOR APPLICATION NUMBER: US 60/346414

PRIOR APPLICATION NUMBER: US 60/346414

PRIOR APPLICATION NUMBER: US 60/346414

NUMBER OF SEQ ID NOS: 40

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                 Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.7%; Score 568; DB 14; Length 117; 88.9%; Pred. No. 9e-43;
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Publication No. US20030147809A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUCI8 ANTIGEN
FILE REFERENCE: ABGENIX.022A
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: 60/346299
PRIOR FILING DATE: 2001-12-18
                                                                                                                                                                                            Query Match 96.5%; Score 604; DB 16; Best Local Similarity 94.0%; Pred. No. 5.8e-46; Matches 110; Conservative 7; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Mismatches
PRIOR FILING DATE: 2002-12-26
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 5
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SOFTWARE: FastSEQ for Windows Version 4.0
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Matches 104; Conservative
                                                                                                         TYPE: PRT
ORGANISM: Homo Sapiens
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ORGANISM: Homo Sapiens
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US-10-330-613-13
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LENGTH: 117
                                                                                       LENGTH: 117
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LENGTH: 117
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61 HNPSLKSRITISVDTSKNOFSLKLSSVTAADTAVYYCARGGDGYRY-----WGQGTLVTV 115
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                                                                                                                                                                                                                                                                                                                   1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTY 60
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JATORATION
JAPPLICANT: Grandas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Holtz, Ian
APPLICANT: Holts, Ian
APPLICANT: Holts
APPLICANT: Holts
APPLICANT: Holts
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
TITLE OF INVENTION: (CA IX)
CURRENT PELICATION NUMBER: US/10/309,762
CURRENT PILING DATE: 2002-12-02
PRIOR FILING DATE: 2001-12-03
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSEQ for Windows Version 4.0
IENGTH: 120
                                                                                                                            Length 120;
                                                                                                                                                                 2; Indels
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                                                                                                                     Score 549.5; DB 15;
Pred. No. 4e-41;
8; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/10309762; Publication No. US20040018198A1 GENERAL INFORMATION: APPLICANT: Gudas, Jean APPLICANT: Foltz, Ian APPLICANT: Handa, Masahisa APPLICANT: Gallo, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.8%;
                                                                                                                        Query Match 87.8%;
Best Local Similarity 86.1%;
Matches 105; Conservative
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ORGANISM: Homo sapiens
                                TYPE: PRT
CRGANISM: Homo sapiens
US-10-309-762-13
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Best Local Similarity
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SEQ ID NO 13
LENGTH: 120
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                                                                                                      1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTY 60
                                                                                                                                                                                         61 HNPSLKSRITISVDTSKNQFSLKLSSVTAADTAVYYCAR-GGDGYRYWGQGTLVTVSS 117
                                                                                                                                                                                                             61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYYGSGSDYWGQGTLVTVSS 118
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                                                               1; Gaps
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Sequence 10, Application US/10309762

Publication No. US20040018198A1

GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2001-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR APPLICATION NUMBER: 60/337275
SEQ ID NO 10
SEQ ID NO 10
HANDER OF SEQ ID NOS: 246
SEQ ID NO 10
HANDER OF EASTSEQ FOR Windows Version 4.0
SEQ ID NO 10
HANDER OF EASTSEQ FOR Windows Version 4.0
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Fublication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michals
TITLE OF INVENTION: ANTHEODIES AGAINST CARBOXIC ANHYDRASE IX
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFRERNCE: ABGRIXX.027A
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/33725
PRIOR APPLICATION NUMBER: 60/33725
PRIOR APPLICATION NUMBER: 60/33725
PRIOR APPLICATION NUMBER: 60/33725
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSEQ for Windows Version 4.0
                   Score 552.5; DB 15; Length 118; Pred. No. 2.1e-41; 7; Mismatches 5; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.2%; Score 552; DB 15; Length 123; 85.4%; Pred. No. 2.5e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Mismatches
                     88.3%;
               Query Match
Best Local Similarity 89.0%
Matches 105; Conservative
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Matches 105; Conservative
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US-10-309-762-10
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APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Cher, Ianyam
APPLICANT: Foltz, Ian
APPLICANT: Foltz, Ian
APPLICANT: Foltz, Ian
APPLICANT: Tee, Kam Fai
APPLICANT: Greffers, Michael
APPLICANT: Starling, Gary
APPLICANT: Starling, Gary
APPLICANT: Starling, Gary
APPLICANT: Khramtsov, Nikolia
TITLE OF INVENTION: ANTIBODIES AGAINST T CELL IMMUNOGLOBULIN
TITLE OF INVENTION: ANTIBODIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HNPSLKSRITISVDTSKNOFSLKLSSVTAADTAVYYCARGG------DGYRYWGQGTLV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLEQSGPGLVKPSQTLSLTCTVSGCSISSGGRYWSWIRQHPGKGLEWIGYIYYSGSTY 60
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87.3%; Score 546.5; DB 17; Length 125;
Best Local Similarity 83.1%; Pred. No. 7.7e-41;
Matches 103; Conservative 9; Mismatches 5; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 548; DB 15; Length 123;
Pred. No. 5.6e-41;
6; Mismatches 6; Indels
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN FILE REFERENCE: ABGENIX.027A CURRENT APPLICATION NUMBER: US/10/309,762 CURRENT FILING DATE: 2002-12-02 PRIOR APPLICATION NUMBER: 60/337275 PRIOR APPLICATION NUMBER: 60/337275 NUMBER OF SEQ ID NOS: 246 SOFTWARE: FRAESEQ FOR Windows Version 4.0 SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 53, Application US/10805177 Publication No. US20050084449A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 87.5%;
Best Local Similarity 85.4%;
Matches 105; Conservative
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CORGANISM: Homo Sapiens
US-10-805-177-53
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-9
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114 TVSS 117
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121 TVSS 124

Search completed: November 9, 2005, 12:43:03 Job time : 66 secs

Color Service : The Color

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Compugen Ltd.
version -
GenCore
(c) 1993
       Copyright
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sw model OM protein - protein search, using 9, 2005, 12:25:58 ; Search time 12.609 Seconds (without alignments) 892.802 Million cell updates/sec November Run on:

Title: Perfect score:

US-10-660-357A-33
626
1 QVQLEQSGPGLVKPSETLSL.....ARGGDGYRYWQQGTLVTVSS 117 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | neaction | g heavy cha | Ig variable region | g mu chain | Ig heavy chain V r | . o | g heavy chain | g heavy chain - | g heavy | יסו | Ig heavy chain V r | g heavy | | g heavy | g heavy | g heavy | g heavy chain | g heavy | Ig heavy chain V r | ס | g heavy | g heavy | Ig heavy chain V r | 0 | o | Ig heavy chain pre | g heavy chain | מ | b | g heavy chain |
|-----------|----------|-------------|--------------------|------------|--------------------|--------|---------------|-----------------|---------|--------|--------------------|---------|--------|---------|---------|---------|---------------|---------|--------------------|--------|---------|---------|--------------------|-----|--------|--------------------|---------------|--------|-----|---------------|
| SUMMARIES | | S13519 | 7 | S37456 | 831690 | S78051 | S44113 | 831511 | 831512 | S31586 | S26801 | S30534 | 831514 | S26802 | S26803 | S44114 | A26340 | 830530 | 809711 | 869912 | S31676 | 809710 | A49045 | 3 | 844125 | S78052 | _ | S44110 | - | S31604 |
| 2 | | | | | | | | | | | | | | | | | | | 7 | | | | | | | | • | • | | |
| 1,000,1 | Tagrand | 147 | 140 | 116 | 130 | 135 | 121 | 155 | 155 | 139 | 66 | 130 | 128 | 66 | 66 | 129 | 118 | 123 | 146 | 122 | 137 | 146 | 140 | 139 | 105 | 140 | 66 | 110 | 145 | 135 |
| Query | יימיכוו | | • | | 81.5 | | | 79.6 | | | | • | | | 77.3 | | | | 76.0 | | 75.8 | • | • | | 74.8 | | | 74.2 | ٠ | 74.1 |
| 97 | 2000 | 523 | 514 | 510 | 510 | 507 | 503 | 498 | 496 | 493.5 | 493 | 492.5 | 488 | 484 | 484 | 480.5 | 479 | 479 | 476 | 474.5 | 474.5 | 474 | 472 | 470 | 468 | 467.5 | 467 | 464.5 | • | 464 |
| Result | 2 | 1 | 7 | m | 4 | വ | ø | 7 | 8 | σ | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 |

| Ig heavy chain V r | Ig heavy chain V r | heavy | Ig heavy chain pre | Ig heavy chain V r | Ig heavy chain V r | Ig heavy chain V r | Ig mu chain precur | Ig heavy chain V r | Ig heavy chain V r | Ig heavy chain V r | Ig heavy chain V4. | hypothetical hybri | heavy chain | Ig heavy chain V r | Ig heavy chain V r |
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| 826906 | S19668 | S12412 | B26340 | S31585 | S20780 | S12416 | PT0370 | S26807 | S26800 | S31684 | S47010 | A24770 | E34964 | S24443 | \$26899 |
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| 97 | 127 | 66 | 116 | 137 | 118 | 97 | 120 | 66 | 66 | 124 | 126 | 140 | 117 | 118 | 66 |
| 73.8 | 73.8 | 73.6 | 73.6 | 73.6 | 73.4 | 73.3 | 73.3 | 73.2 | 73.2 | 73.2 | 72.9 | 72.7 | 72.4 | 72.4 | 72.4 |
| 462 | 462 | 461 | 461 | 460.5 | 459.5 | 459 | 459 | 458 | 458 | 458 | 456.5 | 455 | 453.5 | 453.5 | 453 |
| 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

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S13519
Ig heavy chain V region precursor - human
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4; Gaps Length 147; Query Match
83.5%; Score 523; DB 2; Length 14'
Best Local Similarity 82.6%; Pred. No. 4.2e-39;
Matches 100; Conservative 10; Mismatches 7; Indels

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9 1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY g ઠે ò

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117 \$ 117

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RESULT 2 I37782

Ig variable region (VDJ) (clone T23-9) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
C;Accession: 137782; 825476
R;Demaison, C:; Chastagner, P:; Theze, J:; Zouali, M.
R;Demaison, C:; Chastagner, P:; Theze, J:; Zouali, M.
A;Title: Somatic diversification in the heavy chain variable region genes expressed by A;Reference number: A36876; MUID:94119917; PMID:8290556

A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-140 <RES> A;Cross-references: BMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583 C;Superfamily: immunoglobulin V region; immunoglobulin homology

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Ig heavy chain precursor V-D-J region (clone mAB 61VH) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession 1578051; S23716
R;Harindranath, N.
S;Bharindranath, N.
S;Bharindranath, N.
S;Bharindranath, N.
S;Bharindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkin R; Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkin Int. Immunol. 3, 865-875, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Int. Immunol. 3, 865-875, 1991 A/Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and V(L) and V(L) regions of low- and V(L) and V(L) regions of low- and V(L)
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44113
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable A;Reference number: S44105
A;Accession: S44113
A;Accession: S44113
A;Accession: preliminary
A;Accession: preliminary
A;Residues: 1-121 < HAM>
                                                                                                                              61 HNPSLKSRITISVDTSKNQFSLKLSSVTAADTAVYYCARGG-----DGYRYWGQGTLVT 114
                                                     6 QVQLQESGPGLVKPSETLSLTCTVSGGSISS--YYWSWSRQPPGKGLEWIGYIYYSGSTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 QLQLQESGPGLVKPSETLSLTCTVSGGSISRGSHYWGWIRQPPGKGLEWIGSIYYSGNTY
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A; Residues: 13-111 < HAW>
A; Cross-references: EMBL:X54437
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin
C; Keywords: immunoglobulin
F; 1-13 / Domain: signal sequence (fragment) #status predicted <SIG>F; 14-135 / Product: Ig heavy chain (fragment) #status predicted <MAT>F; 27-111 / Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.0%; Score 507; DB 2; Length 135; 79.7%; Pred. No. 9.7e-38; ive 9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: S23716; MUID: 92031262; PMID: 1718404
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Matches 98; Conservative
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C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Accession: 837456
R.McIntosh, R.S.; Tandon, N.; Weetman, A.P.
Submitted to the EMBL Data Library, September 1993
A.P.
Scription: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from A.Reference number: 837453
A.Accession: 837456
A.Status: preliminary
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Cross-references: EMBL:X75024; NID:g404313; PIDN:CAA52932.1; PID:g758095
C.Supperfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C. Accession: S1690
R. Custinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A. Description: Mechanisms that generate human immunoglobulin diversity operate from the A. A. Secession: S1885
A. Accession: S1690
A. Status: preliminary
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                                                                                                                                                                                                                                                                                                 10 GLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTYHNPSLKSRI 69
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C.Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
                                                                                                                                                          1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY
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A; Residues: 1-130 <CUI>
A; Residues: 1-130 <CUI>
A; Cross-references: EMBL:214199; NID:g30984; PIDN:CAA78568.1; PID:g30985
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 20-102/ Domain: immunoglobulin homology <IMM>
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                                                  Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 510; DB 2; Length 116; Pred. No. 4.5e-38;
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                                                                                                     Indels
                                                                                                        9
                                               Score 514; DB 2;
Pred. No. 2.4e-38;
7; Mismatches 6
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F;46-128/Domain: immunoglobulin homology <IMM>
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83.6%;
                                               Query Match
Best Local Similarity 82.9%;
Matches 102; Conservative
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Best Local Similarity 83.63
Matches 97; Conservative
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Best Local Similarity 79.5
Matches 101; Conservative
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immunoglobulin V region;
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81.1%;
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97; Conservative
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99; Conservative
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A;Status: preliminary
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    C; Superfamily:
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Best Local S:
Matches 97
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Best Local S
Matches 99
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession. 231512
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
Submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autc
A;Accession: 331512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C'Species: Homo sapiens (man)
C'Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: 831511
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
A;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
A;Reference number: S31509
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                                                                                                                                                                                                                     1 QVQLQESGPGLVKPSETLSLTCTVSGGYISSSSYYWGWTRQPPGKGLEWIGSIYYSGSTY
                                                                                                                                                                                            1 OVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY
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A;Cross-references: EMBL;Z31389; NID:g472967; PIDN:CAA83264.1; PID:g940524 (S.Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heteroretramer; immunoglobulin F;15-99/Domain: immunoglobulin homology <IMM>
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A;Molecule type: mRNA
A;Residues: 1-155 <CHA>
A;Cross-references: EMBL:X69860; NID:g33082; PIDN:CAA49494.1; PID:g33083
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Pred. No. 6.9e-37;
8; Mismatches 9; Indels 10;
                                                                                    ; DB 2; Le._
. 1.9e-37;
. 12; Indels
                                                                                                          Length 121;
                                                                                                        Score 503; DB
Pred. No. 1.9e-
9; Mismatches
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                                                                                                        Query Match
Best Local Similarity 79.3%;
Matches 96; Conservative
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Best Local Similarity 78.4
Matches 98; Conservative
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A; Residues: 1-155 < CHA>
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Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31586
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C. submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
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C;Date: 13-Jan: 1995 #sequence_revision 25-Oct-1996 #text_change 20-Jun-2000
C;Date: 13-Jan: 1995 #sequence_revision 25-Oct-1996 #text_change 20-Jun-2000
C;Accession: S;8601; S26900
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Eur. J. Immunol. 22, 1075-1082, 1992
A;FitLe: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A;Reference number: S26800; MUID:92201299; PMID:1348029
                                                                                                                                                                                                                                                            33 QVQLQESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLEWIGYIYYTGSAT
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A;Residues: 1-99 verB>>
A;Cross-references: EMBL:Z14237; NID:g37706; PIDN:CAA78606.1; PID:g1335372
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
                                                                                                                                                             Gaps
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                                                                                           Length 155,
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Pred. No. 1.5e-36;
8; Mismatches 8; Indels
                                                                                                                                                          9; Indels
                                                                                                  DB 2;
                                                                                               Score 496; DB 2;
Pred. No. 1e-36;
9; Mismatches
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C; Keywords: heterotetramer; immunoglobulin
F;47-129/Domain: immunoglobulin homology <IMM>
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A;Residues: 1-128 <CHA>
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                       A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: $26885; MUID:93021117; PMID:1404388
A;Accession: $26900
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-99 <TOM>
A;Residues: 1-90 <TOM
A;Residue
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C'Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C'Accession: S31514
R'Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A';Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA A';Reference number: S31509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGSYYWSWIRQPAGKGLEWIGRIYTSGSTN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Species: Howo sapiens (man)
C.Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
C.Accession: S30534
R.Mariette, X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 HNPSLKSRITISVDTSKNQFSLKLSSVTAADTAVYYCAR 99
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                                                                                                                                                                                                                                                                                                                                                                                          Score 493; DB 2;
Pred. No. 1.2e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      78.8%;
ilarity 91.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S30534
Ig heavy chain V region - human
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                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 91, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S31514
Ig heavy chain - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: S31514
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61 HNPSLKSRITISVDTSKNQFSLKLSSVTAADTAVYYCARGGDGYRY----WGQGTLVTVS 116
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: $2680.
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A;Reference number: $26800; MUID:92201299; PMID:1348029
A;Accession: $26802
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C;Daceles: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Dacession: S5603
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Eur. J. Immunol. 22, 1075-1082, 1992
A;Fitle: Polymorphism of human immunoglobulin V(H) 4 germ-line genes.
A;Reference number: S26800; MUID:92201299; PMID:1348029
                                                                                                                                                                                                                                                                                                                                                               8 QVQLQESGPGLVRPSQTLSLTCTVSGGSISSGGFYWSWIRQHPGMALEWIAHIYFSGSTY
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A;Molecule type: DNA
A;Residues: 1-99 «WEN>
A;Cross-references: EMBL:Z14238; NID:g37710; PIDN:CAA78607.1; PID:g1335374
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                      1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY
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A,Cross-references: EMBL:X69862; NID:g33086; PIDN:CAA49496.1; PID:g33087
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;22-106/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 90.9%; Pred. No. 7.4e-36;
Matches 90; Conservative 7; Mismatches 2; Indels
                                                                                                                                                                                                                                                     11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66
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                                                                                                                                                                        78.0%; Score 488; DB 2; 76.0%; Pred. No. 4.3e-36; iive 14; Mismatches 11
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                                                                                                                                                                                                                                                     92; Conservative
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Best Local Similarity
Matches 92; Conserv
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Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: 544114
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL bata Library, March 1994
A;Bescription: Idiotypic vaccination against human B-cell lymphoma: rescue of variable x
A;Reference number: 544105
A;Accession: 544114
A;Accession: 644114
A;Ac
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                                                                                                  0; Gaps
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              Length 99;
                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  YNPSLKSRVIISVDTSKNQFSLKLSSVTAADTAVYYCAR 99
                                                                                                                                                                                                                                                                                                                                                               61 HNPSLKSRITISVDTSKNOFSLKLSSVTAADTAVYYCAR 99
    77.3%; Score 484; DB 2;
90.9%; Pred. No. 7.4e-36;
tive 7; Mismatches 2.
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Query Match
Best Local Similarity 90.99
Matches 90; Conservative
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With John Collect Coll

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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 9, 2005, 11:46:52; Search time 60.406 Seconds (without alignments) 991.843 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-660-357A-33 626 1 QVQLEQSGPGLVKPSETLSL.....ARGGDGYRYWGQGTLVTVSS 117

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| SUMMAKIES | DB ID Description | 2 O6GMX1 O6cmx1 homo sanien | 072379 homo | OEGMX6 Domod Segmx6 Domod | 09ul73 homo | Q6GMX7 homo | 095973 homo | Q96KX8 homo | Q96ey0 homo | Q6P4I8 Q6p4i8 homo | Q8IZD7 Q8izd7 homo | Q7z374 homo | Q86SX2 homo | JMAN P01824 homo | Q6NYH3 Demo | Q8wux4 homo | Q6gmx5 homo | Omod 01bulo | Q96aa6 homo | JMAN P06331 homo | Q9BQB8 homo | Melpde mns m | | | HV2G_HUMAN P01825 homo | Q9UL75 homo | 76 Q7z3y6 homo | HV46 MOUSE P01822 mus n | mus | Q6MZX7 | 1 HV47 MOTISE D01823 mis miscul |
|-----------|-------------------------|-----------------------------|-------------|---------------------------|-------------|-------------|-------------|-------------|-------------|--------------------|--------------------|-------------|-------------|------------------|-------------|-------------|-------------|-------------|-------------|------------------|-------------|--------------|-----|-------|------------------------|-------------|----------------|-------------------------|------|--------|---------------------------------|
| | Query
Match Length D | 476 | 478 | 465 | 119 | 477 | 150 | 496 | 620 | 576 | 130 | 492 | 139 | 129 | 478 | 595 | 597 | 597 | 625 | 146 | 597 | 136 | 479 | 473 | 117 | 122 | 116 | 137 | 262 | 476 | 113 |
| de | Query | 85.1 | 81.2 | 77.9 | 77.8 | 77.4 | 76.1 | 76.0 | S | 'n | 75.5 | 4 | | | σ. | 8 | 68.8 | 68.89 | 68.8 | 68.5 | 67.9 | | ŝ | ŝ | 'n | ď. | ë. | ۳, | 63.3 | ď. | 62.3 |
| | Score | 533 | 508.5 | 487.5 | 487 | 484.5 | 476.5 | 475.5 | 474.5 | 473.5 | 472.5 | 466 | 462 | 440 | 436 | 431 | 431 | 431 | 431 | 428.5 | 425 | 417.5 | 411 | 410.5 | 409 | 408.5 | 398 | 397 | 396 | 393 | 390 |
| | Result
No. | 1 | 2 | e | 4 | ഗ | 9 | 7 | 8 | σ | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 |

| P18532 mus musculu P18531 mus musculu Q90196 homo sapien Q81105 mus musculu Q91x92 mus musculu P01819 mus musculu P20957 xenopus lae Q99ng4 homo sapien Q61m78 homo sapien Q61m78 homo sapien Q9193 homo sapien Q9509 homo sapien Q9509 homo sapien Q9509 homo sapien Q9509 | |
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| HV61 MOUSE
HV60 MOUSE
Q91U56
Q91U56
Q91U5
Q91U32
Q91U32
MV02 XENLA
Q99NG4
Q99NG4
Q9NG4
Q9UC3
Q9UC33
Q9CUS3 | |
| | |
| 1116
1211
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1210
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1106 | |
| 500 500 500 500 500 500 500 500 500 500 | |
| 367.5
366.5
342
339.5
337.5
336.5
320
320
3116.5
314.5 | |
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ALIGNMENTS

| ID Q6GMX1; AC Q6GMX1; | Q6GMX1
Q6GMX1;
Q6GMX1; | PRELIMINARY | RY; | PRT; | 476 AA. | AA. | | |
|----------------------------|--|---|--------------------|----------------------|----------------|---|---|------------|
| 05-30
05-30 | 05-JUL-2004
05-JUL-2004
05-JUL-2004 | | | Last sequent | sence
otati | ed,
sequence update)
annotation update) | | |
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Homo :
Eukary | Hypothetical
Homo sapiens
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letazoa: Ch | ordata | ı: Craniat | V : 6: | ertebrata: | Cranjata: Vertebrata: Ruteleogromi: | |
| Mamma | Mammalia, Euther
NCBI TaxID=9606: | ia; | Primates; (| s, Catarri | ini, | Catarrhini; Hominidae; Homo | Ношо. | ì |
| [1] | [1]CEOURNCE EDOW N N | | | | | ٠ | | |
| TISSUE | TISSUE=Spleen; | | | | | | | |
| MEDLI | NE=2238 | 18257; Publ | Med=124 | 177932; DC | 01=10 | MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899 | 242603899; | |
| Strau | Sberg R | .L., Feing | Joid E. | .A., Grou | e.
L | H., Derge | r. G,
Sabiilor | c |
| Altsch | nl S.F | ., Zeeberc | 4 B E | Suetow K. | | chaefer C.1 | . Schulei | |
| Hopkii | 18 R.F. | , Jordan F | T., Moc | ore T., Ma | X S | I., Wang J | , Hsieh F. | |
| Diate | nenko L | ., Marusir | la K., | Farmer A | 4. | Rubin G.M. | Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., | 6 |
| Stapie | ston M. | , Soares r | | Tochica M | | Casavant T | L., Scheet | . T.E. |
| Raha | 3.S. 1 | ocuellano | N. A. | Peters G | , i | , Carninci
Abramson R | P., Frange | بر
نه ر |
| Bosak | S.A., | McEwan P.J | 1., Mck | Cernan K. | Σ | alek J.A., | Gunarathe | |
| Richa | rds S., | Worley K. | С., На | ile S., G | arcia | A.M., Gay | L.J., Huly | . S.W. |
| Fahev | J., He | lton E K | O.M., S
Kettema | sodergren
n M Mac | E.J. | , Lu X., G | Villaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahev J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A. | A 291 |
| Whitir | ng M., | Madan A., | Young | A.C., She | vche | nko Y., Bou | iffard G.G. | |
| Blake | sley R. | W., Touchn | nan d.k | f., Green | Δ F | , Dickson N | 1.C., | ن
د |
| Krzywi | nski M | .i. Skale | aka u | Smailus | | Schnerch | A Schein | ο
- α |
| Jones | S.J., | Jones S.J., Marra M.A.; | | | 1 | | | |
| "Gene | ration | and initia | 1 anal | ysis of n | ore | than 15,000 | "Generation and initial analysis of more than 15,000 full-length human | h hume |
| and mc | onse co | and mouse cDNA sequences."; | ses | | | | | |
| Froc. | Nat1. | Proc. Nati. Acad. Sci. U.S.A. | . U.S.A | 1. 99:168 <u>:</u> | 91-6 | 99:16899-16903(2002). | | |
| SEOTEN | SECTIENCE PROM N.A | A N | | | | | | |
| TISSUE | TISSUE=Spleen; | ű, | | | | | | |
| Strausberg | sberg R | R.; | | | | | | |
| Submitted | ted (J | | the co | EMBL/Gent | 3ank/ | to the EMBL/GenBank/DDBJ databases | ses. | |
| EMBL; | BC0737 | EMBL; BC073773; AAH73773.1; | 73.1; | ; | | | | |
| Inceri | ro; IF | 1003599; I | 5 | | | | | |
| InterPro; | | 1PR00/110; 1 |); IG-11Ke. | • | | | | |
| InterPro; | | IPR003006; I | MHC. | | | | | |
| InterPro; | | 359 | > | | | | | |
| | PF07654; | <u>1</u> | ا
سا | | | | | |
| Pfam; | | | | | | | | |
| SMART; | | 09; IG; 2. | | | | | | |
| CMADT. | SM00407; | 1001 | ٠,
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| PROSITE | E PSS | 10.15 | TKE | | | | | |
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1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 HNPSLKSRITISVDTSKNOFSLKLSSVTAADTAVYYCARGGDGY-RYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073766; AAH73766.1; -.
InterPro; IPR001599; Ig. C1.
InterPro; IPR001599; Ig. C1.
InterPro; IPR001596; Ig. MHC.
InterPro; IPR001596; Ig. V.
Pfam; PF07654; C1-set; 3.
Pfam; PF00047; ig; 4.
SWART; SM00409; IGc; 2.
SWART; SM00406; IGC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butel
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51083 MW; B3A9B7D0FDB1386E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 83.1
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
     Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 465 AA;
                                 (Human)
                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9UL73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09UL73
     DDE STANDER ST
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                                                                                                                                                                                                                                                                                                        61 HNPSLKSRITISVDTSKNOFSLKLSSVTAADTAVYYCARG---GDGYRYWGQGTLVTVSS 117
                                                                                                                                                                               9
                                                                                                                                                                                                                             79
                                                                                                                                                                            1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY
                                                                                                                                                                                                      20 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGDYYWSWIRQPPGKGLEWIGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY
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                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Minan rectum tumor;
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
Robo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
BMBL; BX38066; CAD97996.1; -.
HSSP; P01820; 1G7J.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig-CI.
InterPro; IPR003596; Ig-CI.
InterPro; IPR003596; Ig-V.
Fam; PF07654; CI-set; Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                              10;
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                                                                          Length 476;
                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
Hypothetical protein.
SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp686K04218 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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                                                                                                    Pred. No. 3.3e-45;
                                                                             .;
7
                                                                          85.1%; Score 533; DB 78.0%; Pred. No. 3.3e-
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                                                                                                                           13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.3%;
                                                                                               Local Similarity 78.0% tes 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                            |:|||||
TMVTVSS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aypothetical protein
                                                                                                                                                                                                                                                                                                                                                                              111 TLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=DKFZp686K04218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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05-JUL-2004
05-JUL-2004
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Q7Z379 Q7Z379;

RESULT 2

Q72379

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QEGMX6

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RESULT 3 Q6GMX6

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Best Loca Matches

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61 HNPSLKSRITISVDTSKNQFSLKLSSVTAADTAVYYCARGGD---GYRYWGQGTLVTVSS 117
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    "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Potential.
VH4 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 77.4%; Score 484.5; DB 2; Length 1 Similarity 78.3%; Pred. No. 2.5e-40; 94; Conservative 12; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Indels
                                                                                                                         Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
Subnitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF103795; AAC79084.1; -.
PIR; S31673; S31673.
PIR; S31673; S31673.
HSSP, P01880; 1673.
                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00230; IG_MHC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CFP85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 19 Potential.
20 >150 WH4 heavy chain variable.
150 150 MW, 85664E04938AA7C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
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1 Similarity 77.1%; Pred. No. 4.7e-40;
91; Conservative 14; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                          EMBL, BCO73765; AAH73765.11. -...
INLEPTO; IRR003599; IG.
INLEPTO; IPR003109; IG-like.
INLEPTO; IPR003106; IG-like.
INLEPTO; IPR003066; IG-WHC.
INLEPTO; IPR003596; IG-WHC.
INLEPTO; IPR003596; IG-WHC.
Fam; PP07654; CL-Set; Z.
Pfam; PF07654; IG-Set; Z.
SMART; SM00407; IG-1; 3.
SMART; SM00407; IG-1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                   SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                           and mouse cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON TER
SEQUENCE
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TISSUE=PRIMARY B-Calls;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MAISCHOL S.F., Zeeberg B.A., Garden C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
MATSIAN R.F., Jordan H., Moore T., Mang J., Haieh F.,
MATSIAN Saares M.B., Bonaldo M.F., Carninci P., Frange C.,
Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Matting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Markaley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Raywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                          Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
                                                                             SEQUENCE FROM N.A.
MEDILLE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.8%; Score 487; DB 2; Length 11 79.3%; Pred. No. 3.2e-41; Live 10; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                             fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AR035041; AAD56277.1; -.
PIR; PH0876; PH0876.
PIR; S12416; S12416.
                                                                                                                                                                                                                                                                               HSSP, P01820, 1G7J.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596, Ig_v.
SMART; SM00406, Igv, 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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Matches
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TISSUB-Primary B-Cells;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MISCHOLS R.D., Collins F.S., Magner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heiseh F.,

MISCHOLD M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Braha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

MISCHARGS S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

N. Helton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mitching M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Makealey R.W., Touchman J.W., Gareen E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

M. Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 HNPSLKSRITISVDTSKNQFSLKLSSVTAADTAVYYCAR----GGDGYRYWGQGTLVTV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY 60
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                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | HSSP, PO1820; 1G7J. |
| InterPro; IPR003599; IG. |
| InterPro; IPR003190; Ig-like. |
| InterPro; IPR003190; Ig-like. |
| InterPro; IPR0031006; Ig_MHC. |
| InterPro; IPR003596; Ig_WC. |
| Roan; PF07654; Cl-set; 4. |
| Roan; Romo406; IG2, 2. |
| R SMART; SM00406; IG2, 1. |
| R SMART; SM00406; IGV. |
| R PROSITE; PS002590; IG_MHC; UNKNOWN 3. |
| R PROSITE; PS00290; IG_MHC; IG_MHC; UNKNOWN 3. |
| R PROSITE; PS00290; IG_MHC; IR PROSITE; IR PROSITE; PS00290; IG_MHC; IR PROSITE; PS00290; IG_MHC; IR PROSITE; PS00290; IR PROSITE; PS00290; IR PROSITE; PS00290; IR PROSITE; PS00290; IR PS0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: BC011857; AAH11857.2; -.
PIR; S15590; S15590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                   620 AA
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                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences."
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                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                     IGHM protein.
Homo sapiens (Human)
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     TVSS 117
                                                         TVSS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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Best Local S
     114
                                                            140
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                                                                                                                                          RESULT
Q96EY0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., As Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., As Raha S.S., Morley K.C., Meters G.J., Abramson R.D., Mullahy S.J., Maray D.M., Sodergien B.J., Lu X., Gibbs R.A., Nilalon D.K., Muzny D.M., Sodergien B.J., Lu X., Gibbs R.A., Halton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Abraeley R.W., Touchman J.W., Green B.D., Dickson M.C., Arzyunski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., K. Green S.J., Marza M.A., Abraeley R.W., Sudes S.J., Marza M.A., Abraeley R.W., Schmutz J., Wyers R.M., Butterfield Y.S., R. Green S.J., Marza M.A., Smailus D.E., Schnerch A., Schein J.E., Scha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ï
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 QLQLQESGPGLVKSSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIANTYYSGITY 79
HNPSLKSRITISVDTSKNOFSLKLSSVTAADTAVYYCARGGDG-YRYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Straubberg N.;
Straubberg N.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC016369; AAH16369.1; -.
HSSP; P01876; 10W0.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_C1.
InterPro; IPR003006; Ig_WHC.
InterPro; IPR003596; Ig_W.
Pfam; PP07654; C1-set; Z.
SWART; SM00406; IGV; I...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
SEQUENCE 496 AA; $3391 MW; D346929849040D69 CRC64;
                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                 496 AA
                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences."
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                                                                                                                                                                                                                                                                                 PRELIMINARY;
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61 SGSPYYAPSLRSRVIISVDTSKNQLSLRLSSVTAADTAVYYCASPTHCSGGGCYAFFOHW 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGST-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 ----YHNPSLKSRITISVDTSKNOFSLKLSSVTAADTAVYYCA-----RGGDGY----RYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Human rectum tumor;
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
Fobo G., Han M., Wiemann S.;
Submitted (JUN-2013) to the EMBL/GenBank/DDBJ databases.
EMBL; BX538077; CAD98001.1; -.
HSSP; P01820; 1G7J.
                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 75.5%; Score 472.5; DB 2; Length 130; Local Similarity 73.1%; Pred. No. 1e-39; Nes 95; Conservative 11; Mismatches 11; Indels 13;
                                                                                                                                                                                                                                                                                                        01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Anti-thyroglobulin heavy chain variable region (Fragment).
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jang Y.-J., Chung J., Park J.-Y.,
Submirted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY145445, AAN64329.1; --
HSSP, P01820; 1G7J.
HIGEPPO: IPR007110; Ig-like.
InterPro: IPR003596; Ig-v.
SWART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13901 MW; 036131FC6EC1551E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein DKFZp686C02218 (Fragment)
Hypothetical protein DKFZp686C02218 (Fragment)
Homo sapiens (Human)
Bukaryota; Metayora
                                                                                                                                                                                                                                            130 AA.
                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23.
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                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GOGFLVTVSS 130
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130 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                        117 S 117
                                                                                                                     146 S 146
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SEQUENCE
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Q8IZD7
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MEDLINE=22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;

METAUSPER R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MAIschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Districhenco L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Motigue A.C., Galmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Mother A.C., Galmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Mones S.J., Marra M.A.,

Jones J.J., Mellon B. M.,

Jones J.J., Marra M.A.,

Jones J.J., Marra M.J.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC063384; AAH63384.1; -.
HSSP; P01820; 1A7N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWART; SW00409; IG; I.
SWART; SW00407; IGc1; 3.
SWART; SW00407; IGc1; 3.
SWART; SW00406; IGV; I.
PROSITE; PS00290; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
SEQUENCE 576 AA; 63363 MW; FBB97C949D720F1E CRC64;
                                                                                                                                                                                                       Q6P418;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                        576 AA
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ses 95, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA sequences.
                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF07654; C1-set;
Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                      117
                                                              SS 146
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                                                                                                                                                                                                                                                                                                          IGHD protein.
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                   116
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Matches
                                                                                                                                      RESULT 9
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Gaps

29 9

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61 HNPSLKSRITISVDTSKNOFSLKLSSVTAADTAVYYCARGG------DGYRYWG 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 OVOLEOSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                         Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.; "Complete amino acid sequence of the delta heavy chain of human immunoglobulin D.";
                                                                                                                                                                                                                                                                                                                                                                                                                                    myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Matl. Acad. Sci. U.S.A. 79:2850-2854(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R GO; GO:0005576; C:extracellular; NAS.
R GO; GO:000576; C:extracellular; NAS.
R GO; GO:0006955; F:antigen binding; NAS.
R GO; GO:0006955; P:immune response; NAS.
R InterPro; IPR00310; Ig-1ike.
R InterPro; IPR003596; Ig-v.
R Ffam; PF00047; ig; I.
R SMART; SM00406; IGv; I.
R PROSITE; PS50315; IG_LIKE; I.
DDOMAIN.
I 113 Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 AA; 14117 MW; D5D53D47ABE51319 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.3%; Score 440; DB 1; 64.3%; Pred. No. 1.9e-36;
                                                                                                                    Last sequence update)
Last annotation update)
                                                 129 AA
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15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                         MEDLINE=82222235; PubMed=6806818;
                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seque
05-JUL-2004 (Rel. 44, Last anno
1G heavy chain V-II region WAH.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83; Conservative
                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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HSSP; P01820; 1G7J.
GlycoSuiteDB; P01824; -.
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Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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                                                 HV2F HUMAN
P01824;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                 SEQUENCE
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ID Q
                                                     DDT TALE SELECTION OF THE SELECTION OF T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            92 YSPSLKSRLTIFVDTSKNHFSLRLTSVTAADTAVYYCVRHVEGPYGWFDPWGQGTLVTVS 151
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
Full-length cDNA clone CSODL004YM19 of B cells (Ramos cell line)
Homo sapiens (human) (Fragment).
                                                                                                                                                                                                                                                                                                    4
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                                                                                                                                                                                                                                                / Match 74.4%; Score 466; DB 2; Length 492; Local Similarity 72.7%; Pred. No. 1.9e-38; Indels 88; Conservative 16; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 73.8%; Score 462; DB 2; Length 139; Local Similarity 89.9%; Pred. No. 1.2e-38; nes 89; Conservative 6; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genoscope;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX248300; CAD62627.1;
INTERPRO; IG7J.
INTERPRO; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SWART; SW00406; IGV; I...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUBE cells;
Li W B., Gruber C., Jessee J., Polayes D.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                      492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam, PF07654; Cl-set; Z.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50835; IG_LIKE; 1.
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                                                                                                                                                       Hypothetical protein.
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SEQUENCE
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Latchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rabey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Blakesbey R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
manne GDNA sequences.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYIYYSGSTY
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Catarrhini; Hominidae; Homo.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR00110; Ig-like.
InterPro; IPR00110; Ig-like.
InterPro; IPR003599; Ig.
InterPro; IPR003596; Ig_w1.
InterPro; IPR003596; Ig_w2.
InterPro; IPR003596; Ig_w2.
InterPro; IPR00499; IG; 4.
SWART; SW00409; IG; 4.
SWART; SW00406; IGv; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypotherical protein.
SEQUENCE 478 AA; 51856 MW; SF8B98F60F077256 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Indels
                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL: BCO66594; AAH66594.1; -.
HSSP; P01820; 1A7N.
                                                                                                                                                                                                                                                                                                    Sci. U.S.A. 99:16899-16903(2002).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 69.6%; Score 436; DB 2; Local Similarity 70.2%; Pred. No. 1.9e-35; Ne 85; Conservative 19; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      595 AA
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Mammalia; Butheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26,
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Altschul S.F., Zeeberg B., Buecow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buecow K.H., Schaefer C.F., Bhat N.K.,
Appkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Robards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S.M., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Annara M.A.,
Jones S.J., Marra M.A.,
Generation and initial analysis of more than 15,000 full-length human
and mouse CDNA sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143
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    Schuler G.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC1019235; AAH19235.2; -
PIR; G34964; G34964.
R FSR; PO1961; 1ADQ.
R SKARP; SM00409; IG; 2.
R SMARF; SM00409; IG; 2.
R SMARF; SM00405; IGC; 1.
R SMARF; SM00406; IGC; 1.
R PROSITE; PS50835; IG_LIKE; 5.
R PROSITE; PS60299; IG_MC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
SEQUENCE 595 AA; 65290 MW; 0D4B50776545714E CRC64;
                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 68.8%; Score 411; DB 2; Local Similarity 71.9%; Pred. No. 7.9e-35; hes 92; Conservative 7; Mismatches 15
Collins F.S., Wagner L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Search completed: November 9, 2005, 13:05:51 Job time: 60.406 secs

144 GTTVTVSS 151

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                  Copyright
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- protein search, using sw model OM protein November 9, 2005, 11:43:32; Search time 74.6015 Seconds (without alignments) 627.306 Million cell updates/sec Run on:

US-10-660-357A-37 651 1 QVQLQESGFGLVKRSETLSL......WLVPDAFDIWGQGTMVSVSS 121 Title: Perfect score: Sequence:

Scoring table:

2105692 seqs, 386760381 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

2105692

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* A Geneseq 16Dec04: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | ф | | | | |
|---------------|-------|----------------|--------------------------|----|----------|--------------------|
| Result
No. | Score | Query
Match | Query
Match Length DB | DB | ΠD | Description |
| | 651 | 100.0 | 121 | 7 | ADC99808 | Adc99808 Anti-huma |
| 7 | 651 | 100.0 | 121 | 7 | ADD05412 | Add05412 Anti-MUC1 |
| m | 651 | 100.0 | 121 | 7 | ADF09850 | |
| 4 | 598 | 91.9 | 121 | 7 | ADC99780 | Adc99780 Anti-huma |
| 2 | 598 | 91.9 | 121 | 7 | ADD05384 | Add05384 Anti-MUC1 |
| 9 | 598 | 91.9 | 121 | 7 | ADF09822 | Adf09822 Human ant |
| 7 | 597 | 91.7 | 121 | 7 | ADC99772 | Adc99772 Anti-huma |
| 80 | | 91.7 | 121 | 7 | ADC99788 | Adc99788 Anti-huma |
| 6 | 597 | 91.7 | 121 | 7 | ADD05376 | |
| 10 | 597 | 91.7 | 121 | 7 | ADD05392 | Add05392 Anti-MUC1 |
| 11 | 597 | 91.7 | 121 | 7 | ADF09814 | Adf09814 Human ant |
| 12 | 597 | 91.7 | 121 | 7 | ADF09830 | Adf09830 Human ant |
| 13 | 562.5 | 86.4 | 243 | œ | ADO58076 | Ado58076 S9 cell d |
| 14 | 554 | 85.1 | 125 | 7 | ADP03871 | Adp03871 Murine-ex |
| 15 | 547 | 84.0 | 121 | ß | ABG92884 | |
| 16 | 546 | 83.9 | 123 | 9 | ADA89258 | Ada89258 Human ant |
| 17 | 544.5 | 83.6 | 121 | ß | ABB07171 | Abb07171 ebvHigM M |
| 18 | 544.5 | 83.6 | 121 | œ | ADI26658 | Adi26658 Human ant |
| 19 | 543 | 83.4 | 125 | 7 | ADP03868 | Adp03868 Murine-ex |
| 20 | 543 | 83.4 | 125 | 7 | ADP03876 | Adp03876 Murine-ex |
| 21 | 541.5 | 83.2 | 122 | 7 | ADP03885 | Adp03885 Murine-ex |
| 22 | 541.5 | 83.2 | 122 | 7 | ADP03889 | Adp03889 Murine-ex |
| 23 | 539 | 82.8 | 125 | 7 | ADP03983 | Adp03983 Murine-ex |
| 24 | 539 | 82.8 | 446 | œ | ADK52356 | Adk52356 Human ant |
| 25 | 538.5 | 82.7 | 120 | 7 | AAW90287 | Aaw90287 Human ant |
| | | | | | | |

| Adp22272 Human ant
Adp03887 Murine-ex
Adp03931 Murine-ex
Adp03884 Murine-ex
Adp03884 Murine-ex | | Adp03864 Murine-ex
Adp03862 Murine-ex
Ads19313 Heavy cha
Adp03933 Murine-ex | Adp03973 Murine-ex
Adi22106 Anti-plat
Ade28491 Human ant
Ade28471 Human ant | Adp03984 Murine-ex
Abg92888 Human imm
Aay15126 Anti-muri
Ade28447 Human ant |
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| ADP22272
ADP03887
ADP03931
ADP03884 | ABJ36929
ABP43199
AAW27554
ABJ18676 | ADP03864
ADP03862
ADS19313
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33 | 36
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41 | 4 4 4 4
2 6 4 3 |

ALIGNMENTS

anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast; Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 37. ADC99808 standard; protein; 121 AA. (first entry) lung cancer; human. 01-JAN-2004 ADC99808; RESULT 1 ADC99808

Homo sapiens

WO2003057838-A2

17-JUL-2003.

26-DEC-2002; 2002WO-US041581.

28-DEC-2001; 2001US-0346299P.

(ABGE-) ABGENIX INC

Gudas J;

WPI; 2003-587113/55.

N-PSDB; ADC99810

New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.

Claim 1; SEQ ID NO 37; 78pp; English.

The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the pancreatic or colorectal tumours, specifically melanoma, oesophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and centers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody

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WPI; 2003-598367/56.
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              Sequence 121 AA;
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                                          Query Match
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                                                                                                                                                                                61 PSLKSRVIVSVDTSKNQFSLKLNSVTAADTAVYYCARDPGQWLVPDAFDIWGQGTMVSVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                             monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
                                                                                                                         1 QVQLQESGBGLVKPSETLSLTCTVSGGSISTYYWSWIRQPPGKGLEWIGYIYYTGNTYYN
                                                                                                                                                                 PSLKSRVTVSVDTSKNQFSLKLNSVTAADTAVYYCARDPGQMLVPDAFDIWGQGTMVSVS
                                                                                                                                                                                                                                                                                                                                                                                                     Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 37.
                                                                                                            1 QVQLQESGPGLVKPSETLSLTCTVSGGSISTYYWSWIRQPPGKGLEWIGYIYYTGNTYYN
                                                                                 Gaps
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                                                      Length 121;
                                                                                 Indels
                                                    / Match 100.0%; Score 651; DB 7; Local Similarity 100.0%; Pred. No. 2.7e-47; hes 121; Conservative 0; Mismatches 0;
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 heavy chain protein of the invention.
                                                                                                                                                                                                                                                                                                                  ADD05412 standard; protein; 121 AA.
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                           Sequence 121 AA;
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                                                                                                                                                                                                                                                                            61 PSLKSRVTVSVDTSKNQFSLKLNSVTAADTAVYYCARDPGQWLVPDAFDIWGQGTMVSVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell proliferation inhibition; MUC18 tumour antigen;
anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
carcinoma; cancer; malignancy; heavy chain; human.
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   Length 121;
                                                                       Indels
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100.0%; Score 651; DB 7;
100.0%; Pred. No. 2.7e-47;
ive 0; Mismatches 0;
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                                Best Local Similarity 100.
Matches 121; Conservative
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Best Local Similarity 100.
Matches 121; Conservative
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                                                                                                                                     61 PSLKSRVTVSVDTSKNQFSLKLNSVTAADTAVYYCARDPGQMLVPDAFDIWGQGTMVSVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention demonstrates cytostatic activity and may be useful for treating ad disease or condition associated with the expression of WUCIB on the cell surface such as tumours, specifically melanoma, oesophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human WUCIB monoclonal antibody heavy chain protein of the invention.
                                                                                                                                                                                                                                          anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;
cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.
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            QVQLQESGPGLVKPSETLSLTCTVSGGSISTXYWSWIRQPPGKGLEWIGYIYYTGNTYYN
                                                                                                                                                                                                                      Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 9.
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Pred. No. 7.9e-43;
7; Mismatches 4;
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                                                                                                                                                        ADC99780 standard; protein; 121 AA.
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Best Local Similarity
Matches 110; Conserv
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PSLKSRVTVSVDTSKNQFSLKLNSVTAADTAVYYCARDPGQWLVPDAFDIWGQGTMVSVS 120
                                   61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
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Matches 110; Conservative
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Best Local Similarity 90.9
Matches 110; Conservative
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                                                                                                                                                                                           lung cancer; human
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121 S 121
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                                  RESULT 7
                                               ADC99772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention comprises a method for inhibiting cell proliferation associated with expression of WIC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid sequence represents a heavy chain from an MUC18 tumour antigen-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCARDQQQNLLPDAFDIWGQGTWVTVS 120
           61 PSLKSRVTVSVDTSKNQFSLKLNSVTAADTAVYYCARDPGQWLVPDAFDIWGQGTMVSVS 120
PSLKSRVTVSVDTSKNOFSLKLNSVTAADTAVYYCARDPGQWLVPDAFDIWGQGTMVSVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTTNYN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVQLQESGPGLVKPSETLSLTCTVSGGS1STYYWSW1RQPPGKGLEW1GY1YYTGNTYYN
                                                                                                                                                                                                                          cell proliferation inhibition; MUC18 tumour antigen; anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour; carcinoma; cancer; malignancy; heavy chain; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 598; DB 7; Length 121;
Pred. No. 7.9e-43;
7; Mismatches 4; Indels
                                                                                                                                                                                                     Human anti-MUC18 monoclonal antibody heavy chain #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 9; 83pp; English.
                                                                                                                              ADF09822 standard; protein; 121 AA.
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                                                                                                                                                                                                                                                                                                                                                                       28-DEC-2001; 2001US-0346414P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigen, involves incubatir
MUC18 monoclonal antibody.
                                                                                                                                                                               (first entry)
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Best Local Similarity 90.9
Matches 110; Conservative
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N-PSDB; ADF09824.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 121 AA;
                                                                                                                                                                                                                                                                                                  WO2003057837-A2
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                                                                                                         RESULT
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The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the pancreatic or condition associated with the expression of MUC18 on the pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.
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                                                                                                                                                                                                                                                                     Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 1.
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Pred. No. 9.6e-43;
7; Mismatches 4; Indels
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ADC99772 standard; protein; 121 AA.
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01-JAN-2004
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                                                                                                     anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;
cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the pancreatic or condition associated with the expression of MUC18 on the pancreatic or colorectal tumours, specifically melanoma, oesophageal, pancreincomas and cervical intraopithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                  New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSLKSRVTVSVDTSKNOFSLKLNSVTAADTAVYYCARDPGOWLVPDAFDIWGQGTWVSVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQESGPGLVKPSETLSLTCTVSGGSISTYYWSWIRQPPGKGLEWIGYIYYTGNTYYN
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                                                                               Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 597; DB 7; Length 121;
Pred. No. 9.6e-43;
7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heavy chain protein of the invention.
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           ADC99788 standard; protein; 121 AA.
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90.9%;
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                                                        01-JAN-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                 WPI; 2003-587113/55.
                                                                                                                                                                                                                                                                                  (ABGE-) ABGENIX INC
                                                                                                                                           lung cancer; human
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                                                                                                                                                                                      WO2003057838-A2.
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                                  ADC99788;
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Matches
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ID ADD0
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ADC99788
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The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises cumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the cantibody consists of any one of 10 fully defined sequences of 117-123 antibody consists of any one of 10 fully defined sequences of 117-123 canno acids given in the specification, and where the monoclonal antibody bus inhibited proliferation of the cells. The monoclonal antibody has cytostatic and can be used in the production of a vaccine. The monoclonal antibodies against the MUCI8 antigen are useful for diagnosing and cureating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or tumour metastasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-MUCI8 antibody heavy chain, variable region,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61. PSLKSRVTVSVDTSKNQFSLKLNSVTAADTAVYYCARDPGQWLVPDAFDIWGQGTMVSVS 120
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                                                                                                                                                              monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN
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                                                                            Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 1; 87pp; English.
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ADD05392
ID ADD05392 standard; protein; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-DEC-2001; 2001US-0346460P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-DEC-2002; 2002WO-US041582
(first entry)
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                                                                                                                                                                                                                                                                                     Homo sapiens.
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Gudas J,

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The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PSLKSRVTISVDTSKNQFSLRSSVTAADTAVYXCARDQGQWLLPDAFDIWGQGTMVTVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell proliferation inhibition; MUCI8 tumour antigen;
anti-MUCI8 monoclonal antibody; tumour metastasis inhibition; tumour;
carcinoma; cancer; malignancy; heavy chain; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVQLQESGPGLVKPSETLSLTCTVSGGSISTYYWSWIRQPPGKGLEWIGYIYYTGNTYYN
                                                                                  anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour; carcinoma; cancer; malignancy; heavy chain; human.
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                                                             cell proliferation inhibition; MUC18 tumour antigen;
                     Human anti-MUC18 monoclonal antibody heavy chain #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 597; DB 7;
Pred. No. 9.6e-43;
7; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 1; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADF09830 standard; protein; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.7%;
                                                                                                                                                                                                                                                                                               26-DEC-2002; 2002WO-US041580.
                                                                                                                                                                                                                                                                                                                                         28-DEC-2001; 2001US-0346414P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antigen, involves incubatir
MUC18 monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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Best Local Similarity 90.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-598367/56.
                                                                                                                                                                                                                                                                                                                                                                                      (ABGE-) ABGENIX INC
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                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                  17-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Gudas J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADF09830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has cytostatic and can be used in the production of a vaccine. The monoclonal antibodies against the MUC18 antigen are useful for diagnosing and treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or tumour metastasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-MUC18 antibody heavy chain, variable region, protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVS 120
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                                                                                       monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
                                       Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 597; DB 7;
Pred. No. 9.6e-43;
7; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 17; 87pp; English
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90.9%;
                                                                                                                                                                                                                                                                                               26-DEC-2002; 2002WO-US041582
                                                                                                                                                                                                                                                                                                                                         28-DEC-2001; 2001US-0346460P
01-JAN-2004 (first entry)
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Matches 110; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                   (ABGE-) ABGENIX INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                metastatic tumor
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                                                                                                                                                                                                     WO2003057006-A2
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                                                                                                                                                             Homo sapiens
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ADF09814;

RESULT 11 ADF09814

121 121

Query Match

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Gaps ; 0 Weinberger S, Kischel R;

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Identifying a B cell carrying a surface immunoglobulin molecule having binding site for an antigen of interest, useful for constructing therapeutic antibodies, comprises contacting a sample with the antigen
                        12-NOV-2003; 2003WO-EP012664.
                                                 13-NOV-2002; 2002EP-00025335
                                                                                               Baeuerle P, Hoffmann P,
                                                                                                                      WPI; 2004-449579/42.
                                                                        (MICR-) MICROMET AG
                                                                                                                                  N-PSDB; ADO58077
                                                                                                                                                                                             and a receptor.
   27-MAY-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                    The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid sequence represents a heavy chain from an MUC18 tumour antigen-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSLKSRVTVSVDTSKNQFSLKLNSVTAADTAVYYCARDPGGWLVPDAFDIWGGTWVSVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTWVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B cell; surface immunoglobulin; Ig; binding site; antigen; human CD28; closed system; detection laser-beam; catcher tube; electrochemical device; fluorescence activated cell sorter; FACS; antibody variable region; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QVQLQESGPGLVKPSETLSLTCTVSGGSISTYYWSWIRQPPGKGLEWIGYIYYTGNTYYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 597; DB 7;
Pred. No. 9.6e-43;
7; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S9 cell derived human scFvVL-VH protein.
                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 17; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADO58076 standard; protein; 243 AA.
                                                                               26-DEC-2002; 2002WO-US041580.
                                                                                                        28-DEC-2001; 2001US-0346414P.
                                                                                                                                                                                                                                                                                                                                                                                                                                              91.7%;
90.9%;
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Matches 110; Conservative
                                                                                                                                                                             WPI; 2003-598367/56.
                                                                                                                                (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                   monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                         N-PSDB; ADF09832
                                  WO2003057837-A2
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 121 AA;
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            Homo sapiens
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                                                          17-JUL-2003
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                                                                                                                                                       Gudas J;
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The invention relates to a novel method for identifying a B cell carrying a surface immunoglobulin (Ig) molecule having a binding site for an autigen of interest. The method comprises contacting a sample putatively containing the B cell with the antigen of interest and with a receptor containing the B cell with the antigen of interest and with a receptor specifically binding to the Ig molecule, and assessing the presence of the detectable signal. The invention further comprises: an antibody generated by the method above which is specific for human CDSB or comprising an amino acid(s) sequence(s) also given in the specification; and advice for assessing the presence of a detectable cy signal defined above, where the device comprises a closed system for the detection laser-beam and a catcher tube, and where the B cell of interest can be collected as a single cell by means of an electrochemical device, which is triggered by an electric signal generated by the fluorescence convers the nozale of the steady catcher tube liquid stream for a crivated cell sorter (FACS) device, where the electrochemical device moves the nozale of the steady catcher tube liquid stream for a programmed time over a collecting tube, microtiter plate or other container after a B cell is sorted. The method is useful for identifying a triable regions from the identified B cells, which may subsequently be container of entiveryons useful in therapeutic approaches. The method is also useful as an alternative to phage display for the gain of antibodies or its fragments. This sequence represents an S2 cell derived human container container after an expresents an S2 cell derived human container container and the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
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Pred. No. 1.6e-39;
8; Mismatches 5; Indels
Claim 22; SEQ ID NO 76; 156pp; English.
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Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         $ 243
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Best Local S
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ADP03871
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Immunoglobulin, variable heavy chain, variable light chain, human, G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation; fimunologic deficiency syndrome; blood protein disorder; nephritis; ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease; histlocytosis; chemotaxis; infectious disease; autoimmune disease; hadison's disease; dermatitis; rheumatoid arthitis; allergy; neurodegenerative disorder; viral infection; poxvirus infection; HU; human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma; pheumocystis carnii infection; cardiovascular disorder; atherosclerosis;

lymphocytopenia

WO200264612-A2

22-AUG-2002

Homo sapiens

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comprising a heavy chain polypeptide and light chain polypeptide having a sequence chosen from one of 53 fully defined amino acid sequences given in the specification, where the antibody specifically binds carbonic anhydrase. IX (CA IX) tumour antigen. The antibody of the invention demonstrates cytostatic activity and may be useful for treating a tumour, such as colorectal neoplasm, renal cell carcinoma, cervical arcinoma, cervical intraepthelial squamous and glandular neoplasia, osesophagaal tumour or breast cancer, possibly via gene therapy. The current sequence is that of a murine-expressed anti-human CA IX monoclonal antibody WH (heavy chain variable domain) protein of the invention. The protein was generated via the introduction of the human CA IX protein into
                                                                               cytostatic; colorectal neoplasm; renal cell carcinoma; cervical intraepithelial squamous neoplasia; cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
                 Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
intraepithelial squamous and glandular neoplasia or esophageal tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New anti-CA IX monoclonal antibody, useful for treating a tumor e.g., colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
                                                           monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
                                                                                                                                               gene therapy; murine; mouse; human; heavy chain variable domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention relates to a novel isolated monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 554; DB 7;
Pred. No. 4.1e-39;
8; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallo M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 11; 89pp; English.
                                                                                                                                                                                                                                                                                                                 02-DEC-2002; 2002WO-US038550
                                                                                                                                                                                                                                                                                                                                                           03-DEC-2001; 2001US-0337275P
                                                                                                                                                                                                                                                                                                                                                                                                                                               Handa M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transgenic mouse strain.
                                                                                                                                                                                                                                                                                                                                                                                                     (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-523295/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Foltz I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 125 AA;
                                                                                                                                                                                                                               WO2003048328-A2
                                                                                                                                                                                     Jnidentified.
                                                                                                                                                                                                                                                                         L2-JUN-2003
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The invention describes an isolated polynuclectide encoding a first antibody at least 95-100% identical to a second antibody consisting of an anino acid sequence comprising at least one, two or three CDR regions of a variable heavy (VH) or variable light (VL) domain of the antibody care seed by a hybridoma cell line consisting of XP3.5F1.XF1.1F8, XF2.728.36.728.XF2.728.3F1.0F8, XF2.728.25.36.06. XF2.728.36.05. XF2.728.38.36.06. XF2.728.36.05. XF2.728.38.38.2 The antibody is useful treating, preventing, ameliorating, prognosing or monitoring cancers or other diseases or disorders e.g. immunologic deficiency syndromes such as blood protein disorders e.g. immunologic deficiency.

Cancers or other diseases or disorders e.g. immunologic deficiency cancers or other diseases, conditions associated with an increase in certain haematopoletic cells such as histicocycosis, defective or aberrant certain haematopoletic cells such as histicocycosis, defective or aberrant channel disease, an autofimmune disease such as Addison's disease, dermatitis and rheumatoid archritis, alleagies, a neurodegenerative disorder, a viral infection e.g. HIV infection, cytomegalovirus or cardiovascular disorders such as atherosciencial, whomen General infection, a premucocytic central infection, a premucocytic cannii infection, cytomegalovirus or cardiovascular disorders such as atherosciences; lymphocytopenias, or disease or disorder associated with aberrant expression of novel human General control or disorder associated with aberrant expression of novel human General control or disorder associated with aberrant expression of novel human General control or disorder associated with aberrant expression of novel human General control or disorder associated with aberrant expression of novel human General control or disorder second co protein chemokine receptor (CCR5) HDGNR10. This is the amino acid sequence of human immunoglobulin sequence associated with the antibodies Length 121; Indels 6 84.0%; Score 547; DB 5; 86.0%; Pred. No. 1.6e-38; 8; Mismatches Matches 104; Conservative Best Local Similarity Sequence 121 AA; sednence of Query Match ð YNPSLKSRITISVDTSKNQFSLKLSSVTAADTAVYYCARTYYDFLTGYPDAFDIWGQGTM 120 YNPSLKSRVTVSVDTSKNQFSLKLNSVTAADTAVYYCARDPGQWLV--PDAFDIWGQGTM 116

9

Gaps

4,

Length 125; 6; Indels

85.1%; 85.6%;

Matches 107; Conservative

ò 셤 8 8 8

Local Similarity

Query Match

1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGNTY QVQLQESGPGLVKPSETLSLTCTVSGGSIST -- YYWSWIRQPPGKGLEWIGYIYYTGNTY

New human G-protein Chemokine Receptor gene (HDGNR10) useful for treating, preventing, ameliorating or monitoring diseases or disorders associated with aberrant expression of HDGNR10 e.g. cancer.

Ruben SM;

Roschke V, Rosen CA, WPI; 2002-643455/69.

N-PSDB; ABS68607

(HUMA-) HUMAN GENOME SCI INC.

2001US-0328447P. 2001US-0341725P.

12-OCT-2001; 21-DEC-2001;

09-FEB-2001; 2001WO-US004153. 12-JUN-2001; 2001US-0297257P. 08-AUG-2001; 2001US-0310458P.

2001US-00779880

09-FEB-2001;

08-FEB-2002; 2002WO-US003634

Example 55; Fig 4; 562pp; English.

QVQLQESGBGLVKPSETLSLTCTVSGGSISSFYWSWIRQPAGKGLDWIGRIYTSGNTNYN 60 1 QVQLQESGPGLVKPSETLSLTCTVSGGSISTYYWSWIRQPPGKGLEWIGYIYYTGNTYYN Gaps g

Human immunoglobulin variable light domain #1.

(first entry)

19-NOV-2002

ABG92884;

ABG92884 standard; protein; 121 AA

117 VSVSS 121 VTVSS 125

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Search completed: November 9, 2005, 12:55:32 Job time: 75.6015 secs

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9, 2005, 11:29:55; Search time 18.802 Seconds (without alignments) 480.403 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20, Sequence 39, Sequence 65, Sequence 39, Sequence 65, Sequence 65, Sequence 65, Sequence 65, Sequence 65,
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651
1 QVQLQESGGPGLVKPSETLSL......WLVPDAFDIWGQGTMVSVSS
                                                                                                                                                                                                                                                                                                                                          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-025-769B-39
US-09-490-070A-39
US-09-490-070A-65
US-09-490-153-39
US-09-490-153-39
US-09-490-153-65
US-09-490-153-65
US-09-490-153-25
US-09-490-070A-25
US-09-490-070A-25
US-09-490-070A-25
US-09-490-070A-25
US-09-138-091A-77
                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                          513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length
                                                                       November
                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
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Maximum DB 8
                                               OM protein
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                                                                      Run on:
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Sequence 1 Sequence 1 Sequence 7

US-09-800-729-145 US-09-472-087-7 US-09-472-087-86

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140, App
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75, Appli
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Sequence 20, Application US/09424840B

Sequence 20, Application US/09424840B

GENERAL INFORMATION:

APPLICANT: Berchtcld, Peter

TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES

FILE REFERENCE: 100564-09049

CURRENT APPLICATION NUMBER: US/09/424,840B

PRIOR FILING DATE: 1999-12-03

PRIOR FILING DATE: 1998-05-08

PRIOR FILING DATE: 1998-05-06

PRIOR APPLICATION NUMBER: DE 19755227.7

PRIOR PILING DATE: 1999-12-12

PRIOR FILING DATE: 1999-06-06

NUMBER OF SEQ ID NOS: 128

SOFTWARE: Patentin version 3.1

SEQ ID NO 20

LENGTH: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.7%; Score 538.5; DB 4; Length : 85.4%; Pred. No. 1.9e-46; ive 6; Mismatches 7; Indels
         US-08-360-125-5
US-08-450-125-5
US-08-450-578-5
US-09-014-880-5
US-08-450-363-5
US-08-450-363-5
US-08-545-809A-140
US-08-793-450-8
US-08-793-450-8
US-08-476-349A-75
US-08-476-349A-75
US-08-471-276-888
US-08-652-816A-10
US-08-545-809A-142
US-08-545-809A-142
US-08-545-809A-142
US-08-545-809A-142
US-08-545-809A-142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 39, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: 1lag, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 82.7%;
Best Local Similarity 85.4%;
Matches 105; Conservative
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VSS 121
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US-09-424-840B-20
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APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 39, Application US/09490070A Patent No. 6696248 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 65:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-09-025-769B-65
                                                                                                                                      COMPUTER READABLE FORM:
                                                                       New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 S 121
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                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5,
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Moroney, Simon
APPLICANT: Plueckthut, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEB: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTE: New York
ZIP: 1003A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 65, Application US/09025769B
; Sequence 65, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
    APPLICANT: Knappik, Achim
    APPLICANT: Pack, Peter
    APPLICANT: Ilag, Vic
    APPLICANT: Moroney, Simon
    APPLICANT: Moroney, Simon
    APPLICANT: Pluckthun, Andreas
    TITLE OF INVENTION: Protein/(Poly)peptide libraries
    NUMBER OF SEQUENCES: 373
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.3%; Score 536; DB 3; Length 119;
85.1%; Pred. No. 3.4e-46;
iive 7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Halley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECHONE: (212)596-9090
TELEFAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 85.1
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                           ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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61 PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARWGGDGFY--AMDYWGQGTLVTVS 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
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COMPUTER: 1BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 82.3%; Score 536; DB 3; Length 119; Best Local Similarity 85.1%; Pred. No. 3.4e-46; Matches 103; Conservative 7; Mismatches 9; Indels
SOFTWARE: PACENTIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: AMPHO/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin R CURRENT APPLICATION DATA:
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61 PSLKSRVTVSVDTSKNOFSLKLNSVTAADTAVYYCARDPGQWLVPDAFDIWGQGTMVSVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
                                                                                                                                                                                                                                                                                                              Length 119;
                                                                                                                                                                                                                                                                                                        Query Match 82.3%; Score 536; DB 4; Length 11 Best Local Similarity 85.1%; Pred. No. 3.4e-46; Matches 103; Conservative 7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18 FFEB-1998
APPLICATION NUMBER: EP 95
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSE: James F. Haley, Jr., Esq. STREET: 1231 Avenue of the Americas CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794 REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 65:
                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 912-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 39, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
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                                                                                                            INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acida
TYPE: amino acid
                                                                                          (202) 912-2020
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COMPUTER READABLE FORM:
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                                                                                        TELEFAX:
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US-09-490-153-39
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STREET: 1666 K Street, N.W., Suite 300
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 65, Application US/09490070A

Patent No. 6698248

GENERAL INFORMATION:
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
ITILE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 536; DB 4;
Pred. No. 3.4e-46;
                                                             APPLICATION NUMBER: EP 95 11 3021.0 FILLING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
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FILING DATE: 18-AUG-1995
APPLICATION NUMBER: US/09/490,070A
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                                                                                                                                                                                                                                                                                                     LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
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NAME: Colin G. Sandercock, Esq.
                                                                                                                                                                                                                  TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                           FILING DATE: 24-Jan-2000 PRIOR APPLICATION DATA:
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ZIP: 20006
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US-09-490-070A-65
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TELECOMMUNICATION INFORMATION:
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Patent No. 6828422
GENERAL INFORMATION:
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                     85.1%;
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SEQUENCE CHARACTERISTICS
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COMPUTER READABLE FORM:
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               Query Match 82.3
Best Local Similarity 85.1
Matches 103; Conservative
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Best Local Similarity 85.1
Matches 103; Conservative
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STATE: New York
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
                                                                                                                                                 82.3%; Score 536; DB 4; Length 119;
85.1%; Pred. No. 3.4e-46;
ive 7; Mismatches 9; Indels
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Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5 TELECOMMUNICATION:
               TYPE: amino acid

STRANDEDNESS: «Unknown»

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-153-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 65: US-09-490-153-65
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Patent No. 6706484
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 119 amino acids
TYPE: amino acid
LENGTH: 119 amino acids
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Pack, Peter
Ilag, Vic
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COMPUTER READABLE FORM:
                                                                                                                                               Query Match
Best Local Similarity 85.1
Matches 103; Conservative
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                                                      Gaps
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE PATENTIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
Score 536; DB 4; Length 119;
Pred. No. 3.4e-46;
7; Mismatches 9; Indels
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Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
CORRESPONDENCES: 373
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85.1%; Pred. No. 3.4e-46;
tive 7; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: James F. Haley, Jr., Esg. STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FB8-1998
APPLICATION NUMBER: EF 95 11 3021.0
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/490,324 FILING DATE: 24-Jan-2000 PRIOR APPLICATION DATA:
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; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-324-39
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 84.3
Matches 102; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                         New York
       121 S 121
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                                                                              61 PSLKSRVIISVDTSKNQFSLKLSSVTAADTAVYYCARWGGDGFY--AMDYWGQGTLVTVS 118
                                                          PSLKSRVTVSVDTSKNQFSLKLNSVTAADTAVYYCARDPGQMLVPDAFDIWGQGTWVSVS 120
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1 QVQLQESGPGLVKPSETLSLTCTVSGGSISTYYWSWIRQPPGKGLEWIGYIYYTGNTYYN 60
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COMPUTER READABLE FORM:

MEDUW TYPE: Floppy disk

COMPUTER: BEADALD Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION DATA: US/09/490,324

FILING DATE: 18-4-1998

APPLICATION NUMBER: US/09/025,769

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EPS-1998

APPLICATION NUMBER: EPS-1998

APPLICATION NUMBER: B-55 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                Moroney, Simon
Plueckthur, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 82.3%; Score 536; DB 4; Length 119; Best Local Similarity 85.1%; Pred. No. 3.4e-46; Matches 103; Conservative 7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 TOPOLOGY: linear 7 MOLECULE TYPE: procein 7 SEQUENCE DESCRIPTION: SEQ ID NO: 65: US-09-490-324-65
                                                                                                                                                                                                                                                              Sequence 65, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
PAPLICANT: Knappik, Achim
Pack, Peter
1199, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (212) 596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
                                                                                                                                                                      S 119
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61 PSLKSRVTVSVDTSKNQFSLKLNSVTAADTAVYYCARDPGQMLVPDAFDIWGQGTMVSVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILLING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILLING DATE: 18-405-1995
ATTORNEY/AGENT INFORMATION:
NAME: Janes F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                          ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 525.5; DB 3; Length
Pred. No. 3.8e-45;
8; Mismatches 8; Indels
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: 11ag, Vic
APPLICANT: Ge, Liming
APPLICANT: Plucckthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Halev Tr
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61 PSLKSRVTVSVDTSKNQFSLKLNSVTAADTAVYYCARDPGQWLVPDAFDIWGQGTMVSVS 120
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                                                                                                                                                                                   COMPUTER READABLE FORM:

WEDUM TYPE: Floppy disk
COMPUTER: Ploppy disk
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
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                                                                     c/o Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 118;
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Pack, Peter
11ag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
IITLE OF INVENTION: Protein/(Poly)peptide libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
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                   NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq.
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., F
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: <Unknown>TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                     CITY: New York
STATE: New York
                                                                                                                                                                    COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGBIYHSGSTNYN 60
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                                                                                                                                                                                                                                        ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.7%; Score 525.5; DB 4; Length 118; 84.3%; Pred. No. 3.8e-45;
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                                                                                         Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUTCATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFRA: (202) 912-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-070A-25
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Moroney, Simon
Plueckthun, Andreas
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Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 118 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: <Unknown>
                        APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                              CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 84.3
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20006
GENERAL INFORMATION:
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61 PSLKSRVTVSVDTSKNQFSLKLNSVTAADTAVYYCARDPGQMLVPDAFDIWGQGTMVSVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQESGPGLVKPSETLSLTCTVSGGSISTYYWSWIRQPPGKGLEWIGYIYYTGNTYYN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 QVQLQQSGPGLVKPSETLSLTCTVSGDSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYN 62
                                                                        3 QVQLQQSGPGLVKPSETLSLTCTVSGDSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYN
                                             1 QVQLQESGPGLVKPSETLSLTCTVSGGSISTYYWSWIRQPPGKGLEWIGYIYYTGNTYYN
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    Gaps
  7;
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  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: single chain antibody (scFv) fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Adams, Camellia W.
APPLICANT: Carter, Paul J.
APPLICANT: Fendly, Brian M.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: 9491-013-27
CURRENT APPLICATION NUMBER: US/09/118,091A
CURRENT FILING DATE: 1996-08-21
PRIOR APPLICATION NUMBER: US 60/056,736
PRIOR PILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 77
SUGMER PALES FASTESEQ FOR Windows Version 4.0
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: November 9, 2005, 11:46:42
Job time : 19.802 secs
                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 77, Application US/09138091A
; Patent No. 6737249
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 82.6
Matches 100; Conservative
  Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGRGGGGV---FDYWGQGTLVTVS 117
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                                                                                                     COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 80.7%; Score 525.5; DB 4; Length 118; Best Local Similarity 84.3%; Pred. No. 3.8e-45; Matches 102; Conservative 8; Mismatches 3
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                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Adams, Camellia
APPLICANT: W.
APPLICANT: W.
APPLICANT: Carter, Paul J.
APPLICANT: Carter, Paul J.
TYPLE OF INVENTION: Agonist Antibodies
TILE REPRENCE: P0979
CURRENT FILING DATE: 1997-08-25
CURRENT FILING DATE: 1997-08-25
SEQ ID NO 79
                                                                                                                                                                                                                                                                                                                                                                                       NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-324-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 118 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
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82.6%;
                                                              COMPUTER READABLE FORM:
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us-10-660-357a-37.rapb

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PSLKSRVTVSVDTSKNQFSLKLNSVTAADTAVYYCARDPGQWLVPDAFDIWGQGTMVSVS 120
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; APPLICANT: Gudas, Jean; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN; FILER REFRENCE: ABGRNIX.022A; CURRENT FILING DATE: 2002-12-26; PRIOR APPLICATION NUMBER: 60/346299; PRIOR FILING DATE: 2001-12-18; NUMBER OF SEQ ID NOS: 40; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 651; DB 14;
100.0%; Pred. No. 2.4e-51;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 121; Conservative
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ORGANISM: Homo Sapiens
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Sequence 37, A
Sequence 37, A
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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12: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
21: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
22: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
                                                                                                                                                                                                                     QVQLQESGPGLVKPSETLSL......WLVPDAFDIWGQGTMVSVSS
GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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US-10-330-530-37
US-10-330-613-9
US-10-330-513-9
US-10-330-513-9
US-10-330-613-1
US-10-330-613-1
US-10-330-530-1
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Maximum Match 100%
Listing first 45 summaries
                                                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Perfect score:
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Maximum DB
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US-10-660-357-17
US-10-309-762-11
US-10-292-088-142
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US-10-292-088-142
US-10-371-942-102
US-10-371-942-102
US-10-309-762-8
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US-10-309-762-73
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61 PSLKSRVTVSVDTSKNQFSLKLNSVTAADTAVYYCARDPGQWLVPDAFDIWGQGTMVSVS 120
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; APPLICANT: GLAdas, Jean; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES; FILE REFERENCE: ABGRNIX. 031A; CURRENT PELING DATE: 2002-12-26; PRIOR APPLICATION NUMBER: US 60/346414; PRIOR APPLICATION NUMBER: US 60/346414; MUMBER OF SEQ ID NOS: 40; NUMBER: FREESE 2001-12-18; NUMBER: FREESE FREESE FOR WINDOWS VERSION 4.0
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                                                                                                                                                                                                                                                    APPLICANT: Gudas, Jean
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
FILE REPERRNCE: ADGENIX.022A
CURRENT APPLICATION NUMBER: US/10/330,613
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: 60/346299
PRIOR PILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
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90.9%; Pred. No. 1.5e-46;
tive 7; Mismatches 4;
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Pred. No. 1.5e-46;
7; Mismatches 4;
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, Publication No. US20030147809A1
; GENERAL INFORMATION:
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Best Local Similarity 90.9
Matches 110; Conservative
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Best Local Similarity 90.9
Matches 110; Conservative
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US-10-330-613-9
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ORGANISM: Homo Sapiens
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Publication No. US20030152514A1
GENERAL INFORMATION:
APPLICANT: Gudda, Jean
TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
FILE REPRENEUE: AGGENIX.031A
CURRENT PILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: US 60/346414
PRIOR RILING DATE: 2011-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FRASES for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 651; DB 14; Length 121; Best Local Similarity 100.0%; Pred. No. 2.4e-51; Matches 121; Conservative 0; Mismatches 0; Indels 0
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| Publication No. US20040115205A1
| GENERAL INFORMATION:
| APPLICANT: Bar-Eli, Menashe
| APPLICANT: Bar-Eli, Menashe
| TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
| TITLE OF INVENTION: WENGEN ANTIGEN
| FILE REFERENCE: ABGENIX.030C1
| CURRENT APPLICATION NUMBER: US/10/660,357
| CURRENT APLICATION NUMBER: 10/330,580
| PRIOR APPLICATION NUMBER: 10/330,580
| PRIOR FILING DATE: 2002-12-26
| NUMBER OF SEQ ID NOS: 40
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Similarity 100.0%; Pred. No. 2.4e-51;
21; Conservative 0; Mismatches 0;
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Best Local Similarity 100.
Matches 121; Conservative
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ORGANISM: Homo Sapiens
US-10-330-530-37
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LENGTH: 121
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ORGANISM:
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91.7%; Score 597; DB 14; Length 121;
Best Local Similarity 90.9%; Pred. No. 1.9e-46;
Matches 110; Conservative 7; Mismatches 4; Indels
                                                                                                                                                                                                                                                Sequence 17, Application US/10330613
Publication No. US2030147809A1
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: ABGRIX.022A
CURRENT APPLICATION NUMBER: US/10/330,613
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION WHERE: 60/346299
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 40
SEQ ID NOS: 40
SEQ ID NO 17
LENGTH: 121
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Publication No. US20030152514A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
FILE REFERENCE: ABGENIX.031A
CURRENT APPLICATION UNMBER: US/10/330,530
CURRENT FILING DATE: 2002-12-26
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90.9%; Pred. No. 1.9e-46;
tive 7; Mismatches 4;
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PRIOR FILING DAFE: 2001-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PastSEQ for Windows Version 4.0
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Best Local Similarity 90.9
Matches 110; Conservative
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LENGTH: 121
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; Sequence 1, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
    APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                             Sequence 9, Application US/10660357;
Publication No. US20040115205A1
GENERAL INFORMATION:
APPLICANT: Bar-Eli, Menashe
APPLICANT: Green, Larry L.
TITLE OF INVENTION: ANTIEND
FILE REFERENCE: ABGENIX. 030C1
CURRENT TAILNG DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 10/330,580
PRIOR FILING DATE: 2002-12-26
NUMBER OF SEQ ID NOS: 40
SUGNARER FEEL NOS: 40
SPRIOR FILING DATE: 2002-12-26
SUMMER OF SEQ ID NOS: 40
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Pred. No. 1.5e-46;
7; Mismatches 4;
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Pred. No. 1.9e-46;
7; Mismatches 4;
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90.9%;
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ilarity 90.9%;
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Best Local Similarity 90.9
Matches 110; Conservative
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US-10-660-357-9
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Best Local Similarity
Matches 110; Conserv
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LENGTH: 121
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61 PSLKSRVTISVDTSKNQFSLRSSVTAADTAVYYCARDQQQWLLPDAFDIWGQGTMVTVS 120
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                                            1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN 60
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; Sequence 11, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Goltz, Jen
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
; TITLE OF INVENTION: AUTHORITY (20.17)
; FILE REFERENCE: ABGENIX: 02.074
; CURRENT FILING DATE: 2002-12-02
; PRIOR PILLING DATE: 2001-12-03
; NUMBER OF SEC 1D NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                   US-10-660-357-17

Sequence 17, Application US/10660357

Publication No. US20040115205A1

GENERAL INFORMATION:
APPLICANT: Bar-Eli, Menashe
TITLE OF INVENTION: USE OF NATIBODIES AGAINST THE MUC18

TITLE OF INVENTION: ANTIGEN
FILE REFERENCE: ABGENIX.030C1
CURRENT APPLICATION NUMBER: US/10/660,357

CURRENT FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-12-26

PRIOR FILING DATE: 2002-12-26
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Pred. No. 1.9e-46;
7; Mismatches 4;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ 1D NO 17
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Best Local Similarity 90.9%;
Matches 110; Conservative
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TYPE: PRT
ORGANISM: Homo Sapiens
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LENGTH: 125
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                                                                    61 PSLKSRVIISVDISKNQFSLRLSSVTAADTAVYYCARDQGQMLLDDAFDIWGQGTMVTVS 120
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                                            PSLKSRVTVSVDTSKNQFSLKLNSVTAADTAVYYCARDPGOWLVPDAFDIWGQGTMVSVS 120
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1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYN 60
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                                                                                                                                                                                                                                                                                    Sequence 17, Application US/10330530

Publication No. US20030152514A1

GENERAL INFORMATION:

APPLICANT GLODES, Joan

TITLE OF INVENTION:

FILE REFERENCE: ABGENTX.031A

CURRENT FILING DATE: 2002-12-26

PRIOR FILING DATE: 2001-12-16

PRIOR FILING DATE: 2001-12-18

NUMBER OF SEQ ID NOS: 40

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.7%; Score 597; DB 16; Length 121; 90.9%; Pred. No. 1.9e-46; tive 7; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.7%; Score 597; DB 14; Length 121; 90.9%; Pred. No. 1.9e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/10660357

Publication No. US20040115205A1

GENERAL INFORMATION:
APPLICANT: Green, Lary L.
TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
TITLE OF INVENTION: ANTIGEN
FILE REFERENCE: ABGENIX. 030C1
CURRENT APPLICATION NUMBER: US/10/660,357
CURRENT APPLICATION NUMBER: 10/330,580
PRIOR PILING DATE: 2002-12-26
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: 121

LENGTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
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Best Local Similarity 90.9
Matches 110; Conservative
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Best Local Similarity 90.9
Matches 110; Conservative
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Fublication No. US20050118643A1
GENERAL INFORMATION:
APPLICANT: BUGGESS, TERESA L.
APPLICANT: COXON, ANGELA
APPLICANT: COXON, ANGELA
TITLE OF INVENTION SPECIFIC BINDING AGENTS TO HEPATOCYTE GROWTH FACTOR
FILE REFERENCE: 06643.0051-00000
CURRENT PILING DATE: 2004-07-16
FRIOR APPLICATION NUMBER: US/10/893,576
CURRENT FILING DATE: 2003-07-18
FRIOR PILING DATE: 2003-07-18
SOFTWARE: PATENTIN VUMBER: US 60/488,681
SOFTWARE: PATENTIN VUMBER: US 60/488,681
SOFTWARE: PATENTIN VOIS: 194
SOFTWARE: PATENTIN VOIS: 3.2
LENGTH: 142
                                                                                                                                                                                                                                                                59 YNPSLKSRVTVSVDTSKNQFSLKLNSVTAADTAVYYCARDPGOWLV--PDAFDIWGOGTM 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic HGF 2.4.4; OTHER INFORMATION: Heavy chain V region (Vh, VG 4-31)-hulgG2 C region US-10-893-576-37
                                                                                                                                                                                                                                                                                          59 YNPSLKSRVTVSVDTSKNQFSLKLNSVTAADTAVYYCARDPGQWLVPDAFDIWGQGTWVS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGNTY 60
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                                                                                                                                                                            1 QVQLQESGPGLVKPSETLSLTCTVSGGSIST--YYWSWIRQPPGKGLEWIGYIYYTGNTY
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                                                                                                                                     Gaps
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                                                                                 Query Match 85.1%; Score 554; DB 15; Length 125; Best Local Similarity 85.6%; Pred. No. 1.5e-42; Matches 107; Conservative 8; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

84.8%; Score 552; DB 17; Length 142;
Best Local Similarity 85.4%; Pred. No. 2.7e-42;
Matches 105; Conservative 9; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 142, Application US/10292089
Publication No. US20030211100A1
GENERAL INFORMATION:
APPLICANT: BEDIAN, VAHE
APPLICANT: GLADUE, RONALD P.
APPLICANT: CORVALAN, JOSE
APPLICANT: UA, XIAO-CHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                  ; ORGANISM: Homo sapiens
US-10-309-762-11
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121 VTVSS 125
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US-10-292-088-142
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TYPE: PRT
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61 PSLKSRVTVSVDTSKNQFSLKLNSVTAADTAVYYCARDPGQWLVPDAFDIWGQGTMVSVS 120
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                                                                                                                                                                                                                                                                                                        Length 118;
                                                                                                                                                                                                                                                                                                                                                   5; Indels
                                                                                                                                                                                                                                                                                                        DB 15;
                                                                                                                                                                                                                                                                                                      84.1%; Score 547.5; DB 1986.0%; Pred. No. 5.6e-42; Live 9; Mismatches 5
TITLE OF INVENTION: ANTIBODIES TO CD40
FILE REFERENCE: ABX-PF/3 US
CURRENT APPLICATION NUMBER: US/10/292,088
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 60/348,980
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 147
SEQ ID NO 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: November 9, 2005, 12:43:03 Job time : 67.2222 secs
                                                                                                                                                                                                                                                                                                                          Best Local Similarity 86.09
Matches 104; Conservative
                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                      Query Match
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Correct years and the second

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein

9, 2005, 12:25:58 ; Search time 13.0401 Seconds (without alignments) 892.802 Million cell updates/sec November Run on:

US-10-660-357A-37 651 Title: Perfect score:

1 QVQLQESGPGLVKPSETLSL.......WLVPDAFDIWGQGTMVSVSS 121 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB 8 Maximum DB 8

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | Description | variable region | | | heavy chain V r | heavy chain V r | neavy chain V r | neavy chain pre | _ | heavy chain V r | | chain V | lambda chain V | chain | | heavy chain pre | chain | chain V | chain V | heavy chain V r | chain V | heavy chain V-D | heavy chain V r | | heavy chain V r | chain pr | chain | heavy chain V r | | heavy chain V4. |
|-----------|----------------|-----------------|--------|--------|-----------------|-----------------|-----------------|-----------------|--------|-----------------|--------|---------|----------------|--------|--------|-----------------|--------|---------|---------|-----------------|---------|-----------------|-----------------|--------|-----------------|----------|--------|-----------------|------|-----------------|
| | Desc | | | | | Ig P | | _ | _ | | | | | _ | | | | | _ | | | _ | | | | | | | | _ |
| SUMMARIES | ID | I37782 | S31512 | S31511 | S31690 | S13519 | S31586 | S78051 | S20780 | S30534 | S31676 | S44113 | S44125 | S78052 | 826906 | B26340 | 830530 | S12416 | 809711 | S26802 | S26803 | S44110 | S31696 | A49045 | S44114 | A26340 | 826801 | 809710 | н. | S47010 |
| | DB | 8 | ~ | 7 | • | ~ | • | ~ | ~ | ~ | ~ | 7 | N | ~ | ~ | ~ | ~ | ~ | ~ | ~ | ~ | ••• | • | | | ~ | • | 7 | • | 7 |
| | Length | 140 | 155 | 155 | 130 | 147 | 139 | 135 | 118 | 130 | 137 | 121 | 105 | 140 | 97 | 116 | | 97 | 146 | 66 | 66 | 110 | 139 | 140 | | _ | | 146 | 66 | 126 |
| ٠ | Query
Match | 82.5 | 82.3 | 81.6 | • | 80.5 | 80.3 | 79.4 | 79.2 | 78.7 | 78.0 | 76.5 | 76.3 | 75.7 | 75.1 | 75.0 | 75.0 | 74.7 | 74.5 | 74.3 | 74.3 | 74.3 | 74.2 | 74.2 | 73.3 | 73.3 | 73.0 | 73.0 | 72.4 | 72.3 |
| | Score | 537 | 536 | 531 | 527 | 524 | 522.5 | 517 | 515.5 | 512.5 | 507.5 | 498 | 497 | 492.5 | 489 | 488 | 488 | 486 | 485 | 484 | 484 | 483.5 | 483 | œ | 477.5 | 477 | 475 | 475 | 471 | 470.5 |
| | sult
No. | 1 | 7 | m | 4 | Ŋ | 9 | 7 | 8 | 6 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 56 | 27 | 28 | 59 |

| Ig heavy chain V r | Ig heavy chain V r | | Ig heavy chain pre | heavy | | Ig gamma-1 heavy c | Ig heavy chain v r | heavy chain | Ig heavy chain V r | heavy. chain | ٠. | Ig heavy chain V r | Ig heavy chain V r | | |
|--------------------|--------------------|--------|--------------------|----------|--------|--------------------|--------------------|-------------|--------------------|--------------|------------|----------------------|--------------------|--------|----------|
| S24443 | S31604 | A24770 | S78055 | PH0876 | B49028 | A49444 | S12412 | S26800 | S31684 | D2HUWA | 831585 | S26804 | S18557 | S12421 | S37456 |
| ~ | ~ | N | 7 | ~ | ~ | | N | N | ~ | - | ~ | 7 | ~ | ~ | 7 |
| 118 | 135 | 140 | 145 | 97 | 143 | 220 | 66 | 66 | 124 | 129 | 137 | 97 | 116 | 86 | 116 |
| | | | | | | | | | | | | | | | |
| 72.1 | 72.0 | 72.0 | 72.0 | 71.9 | 71.9 | 71.6 | 71.4 | 71.0 | 71.0 | 71.0 | 70.9 | 70.8 | 70.8 | 70.7 | 70.7 |
| 469.5 72.1 | _ | Φ. | 468.5 72.0 | 468 71.9 | _ | | | 462 71.0 | ~ | ۵, | 461.5 70.9 | _ | | | 460 70.7 |

ALIGNMENTS

RESULT 1

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Ig variable region (VDJ) (clone T23-9) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: 137782; 825476
R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
R;Demaison, C.; Chastagner, P.; Theze, J.; Souali, M.
R;Deference number: A36876; MUID:94119917; PMID:8290556
A;Cccssion: 137782
A;Cccssion: 137782
A;Residues: 1-140 <RES.
A;Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;46-128/Domain: immunoglobulin homology <IMM>
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Length 140;

ö 9 1 QVQLQESGPGLVKPSETLSLTCTVSGGSISTYYWSWIRQPPGKGLEWIGYIYYTGNTYYN Gaps ; 0 Query Match 82.5%; Score 537; DB 2; Length 14 Best Local Similarity 84.3%; Pred. No. 1.1e-40; Matches 102; Conservative 7; Mismatches 12; Indels 8

20 QVQLQESGPGLVKPSETLSLICTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYN 79 셤 ઠે

61 PSLKSRVTVSVDTSKNQFSLKLNSVTAADTAVYYCARDPGQWLVPDAFDIWGQGTMVSVS 120 80 PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARHNSSSWYGRYFDYWGQGTLVTVS 139 g

ઠ 유 831512

Ig heavy chain - human

C; Species: Homo sapiens (man)

C; Species: Homo sapiens (man)

C; Species: Homo sapiens (man)

C; Accession: 31112

R; Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.

R; Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.

R; Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.

R; Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.

R; Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.

R; Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.

R; Reference number: 831509

A; Reference number: 831512

A; Reference number: 831512

A; Reference number: 831512

A; Residues: Dreliminary

A; Residues: 1-155

C; Residues: 1-155

C; Reywords: heterotetramer; immunoglobulin homology

Length 130;

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Score 527; DB 2; L
Pred. No. 7.8e-40;
8; Mismatches 8;
                      Query Match
Best Local Similarity 81.1%;
Matches 103; Conservative
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Local Similarity 82.9%;
les 102; Conservative
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124 TLVTVSS 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C; Accession: 831511
R; Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A; Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autc
A; Reference number: 83150
A; Reference number: 83151
A; Residues: Preliminary
A; Residues: Preliminary
A; Residues: 1-155 < CHA>
A; Residues: EMBL: X69866; NID: 933094; PIDN: CAA49500.1; PID: 933095
C; Superfemily: immunoglobulin immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 47-129/ Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: S31690 R.Y. Boubli, L.; Fougereau, M.; Tonnelle, C. Submitted to the EMBL Data Library, June 1992 A;Bescription: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: S31585
                                                                                 1;
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                                                                                                                                                                                                                      93 PPIKSRVIISVDISKNQFSLKVSSVTAADTAVYYCARGGGISSWYYYGMDVWGQGTTVT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PSLKSRVTVSVDTSKNQFSLKLNSVTAADTAVYYCARDPG--QWLVPDAFDIWGQGTMVS 118
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                                                                                                                                          QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYMSMIRQPPGKGLEWIGYIYYTGSATYN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
                                                                                                                    QVQLQESGPGLVKPSETLSLTCTVSGGSISTYYWSWIRQPPGKGLEWIGYIYYTGNTYYN
                                                                                                                                                                                               PSLKSRVTVSVDTSKNOFSLKLNSVTAADTAVYYCARDPG--QWLVPDAFDIWGQGTMVS
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A; Residues: 1-130 <CUI>
A; Croser-references: BML:214199; NID:g30984; PIDN:CAA78568.1; PID:g30985
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;20-102/Domain: immunoglobulin homology <IMM>
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                                          Length 155;
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                                                                             12; Indels
                                      Score 536; DB 2;
Pred. No. 1.5e-40;
8; Mismatches 12
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F;47-129/Domain: immunoglobulin homology <IMM>
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82.1%;
                                    Query Match
Best Local Similarity 82.1%;
Matches 101; Conservative
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Matches 101; Conservative
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Ig heavy chain V region precursor - human C,Species: Homo sapiens (man) C,Species: Homo sapiens (man) C,Species: Homo sapiens (man) C,Species: 25-Reb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999 C,Accession: S13519 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999 R,Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W. Nucleic Acids Res. 19, 673, 1991 A,Title: Immunospollobulin variable heavy chain CDNA sequence from a patient with X-linked A,Recession: S13519 MUD:91187691; PMID:2011536 A,Accession: S13519 A,Accession: S13519 A,Accession: Lype: mRNA A,Retsidues: 1-147 <MOR>
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19 heavy chain V region - human (fragment)

19 heavy chain V region - human (fragment)

2, Species: Homo sapiens (man)

2, Species: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C, Accession: 831586

E, Cuishiner, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.

Bubmitted to the EMBL Data Library, June 1992

A, Description: Mechanisms that generate human immunoglobulin diversity operate in A, Reference number: 831585
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                                                                                                                                                                                                                                                                  66 PSLKSRVTISVDTSKNOPSLKLSSVTAADTAVYYCARGSSVLLWFGELLY--YFDYWGQG 123
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                                                                         QVQLQESGPGLVKPSETLSLTCTVSGGSISTXYWSWIRQPPGKGLEWIGYIYYTGNTYYN
                                                                                                                                              OVOLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWSRQPPGKGLEWIGYIYYSGSTNYN
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Gaps
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-139 <CUI>A;CUI>A;CUI>A;CUI>A;CUI>A;CUI>A;CUI>A;CUI>A;COSS-references: EMBL:Z14196; NID:g30978; PIDN:CAA78565.1; PID:g30979
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>
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Pred. No. 1.6e-39;
9; Mismatches 8; Indels
   Indels
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Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: 831676
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
B;Cuisinier, A.M.; Gauthier, Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate fa;Reference number: 831585
A;Accession: 831676
A;Status: preliminary
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                     61 PSLKSRVTVSVDTSKNOFSLKLNSVTAADTAVYYCARDPGQWLVPDAFDIWGQGTMVSVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
C;Accession: S30534
A;Reference number: S30520
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-130 <MAR>
                                                                                                                                                                                                                                                                                          1 QVQLQESGPGLVKPSETLSLTCTVSGGSISTYYWSWIRQPPGKGLEWIGYIYYTGNTYYN
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                           A,Molecule type: DNA
A;Residues: 1-118 <MOR>
A;Residues: 1-118 <MOR>
A;Cross-references: EMBL:211958; NID:g33893; PIDN:CAA78015.1; P:C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM'>
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Pred. No. 7.3e-39;
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Best Local Similarity 80.0%; Pred. No. 1.5e-38;
Matches 104; Conservative 7; Mismatches 10
                                                                                                                                                                                          79.2%;
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Ig heavy chain V region - human
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A; Molecule type: mRNA
A; Residues: 1-135 <HARN
A; Cross-references: EMBL:XS4437; NID:g37814; PIDN:CAA38306.1; PID:g930117
B; Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins Int. Immunol. 3, 865-875, 1991
A; Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and H
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C_Spaces: Homo sapiens (man)
C_Spaces: O-reb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C_SAccession: S20780
R;Mortari, F.; Wang, J.; Schroeder, H.W.
submitted to the RMEL Data Library, April 1992
A;Description: Analysis of human cord blood Ig heavy chain IgA and IgG repertoire.
A;Reference number: S20764
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                                                                                          1 QVQLQESGPGLVKPSETLSLTCTVSGGSISTYYWSWIRQPPGKGLEWIGYIYYTGNTYYN 60
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                                                      Gaps
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                                                   1;
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F;1-13/Domain: signal sequence (fragment) #status predicted <SIG>
F;14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>
F;27-111/Domain: immunoglobulin homology <IMM>
  Length 139;
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A,Residues: 13-111 <HAM>
A,Residues: 13-111 <HAM>
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Superfamily: immunoglobulin V region; immunoglobulin begion; immunoglobulin begion; immunoglobulin begion; immunoglobulin begion: signal sequence (fragment) #status predicted <SI(
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80.6%; Pred. No. 6.2e-39; Lindels
                                                 Indels
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A;Accession: S23716
  Score 522.5; DB 2;
Pred. No. 2.1e-39;
7; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, August 1990
80.3%;
ilarity 85.1%;
Conservative
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                        Similarity
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TVSS 135
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                      Best Local Simi
Matches 103;
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Best Local Similarity
Matches 92; Conserv
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44113
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idlotypic vaccination against human B-cell lymphoma: rescue of variable shacesion: S44113
A;Accession: S44113
A;Accession: S44113
A;Accession: preliminary
A;Molecule type: DNA
A;Residues: 1-121 <HAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig lambda chain V region - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan.1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: 544125
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
B;Ubmitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable A;Reference number: 544105
A;Accession: 544125
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                                                                                                                                                                                                                                                                                              61 YNPSLKSRVTLSVDTSKNQFSLKLSSVTAADTGVYYCSRLSGGYY--SDFDYWSQGTLVT 118
                                                                                                                                                                                                                                                                       61 PSLKSRVTVSVDTSKNOFSLKLNSVTAADTAVYYCARD-PGQWLVPDAFDIWGQGTMVSV 119
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                                                                                                                                                 Gaps
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A,Cross-references: EMBL:214182; NID:931031; PIDN:CAA78551.1; PID:931032 (S.Quperfemally: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;34-116/Domain: immunoglobulin homology <IPM>
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                                                                                                        Length 137;
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Pred. No. 2.6e-37;
9; Mismatches 13; Indels
                                                                                                                                             Indels
                                                                                                                                             6
                                                                                                    DB 2;
                                                                                                                         Pred. No. 4.4e-38;
8; Mismatches 9
                                                                                                      78.0%; Score 507.5; 82.0%; Pred. No. 4.4
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Best Local Similarity 78.99
                                                                                                                         Local Similarity 82.0 tes 100; Conservative
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A;Molecule type: DNA
A;Residues: 1-105 <HAW>
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                                                                                                        Query Match
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A;Molecule type: mRNA
A;Residues: 1-140 cHAR>
A;Cross-references: EMBL:X54441; NID:g37815; PIDN:CAA38308.1; PID:g930118
A;Cross-references: EMBL:X54441; NID:g37815, PIDN:CAA38308.1; PID:g930118
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkin
Int. Immunol. 3, 865-875, 1991
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Ig heavy chain V region (DP-71 / VH 4.11 / 4.15) - human (fragment)
Ig heavy chain V region (DP-71 / VH 4.11 / 4.15) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26906; S09421; $12415
C;Accession: N., Walter, G., Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups A;Reference number: S26885; MUID:93021117; PMID:1404388
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                                                                                                                                                                                                                                                                                                                                                    1 OVOLOESGPGLVKPSETLSLTCTVSGGSISTYYWSWIRQPPGKGLEWIGYIYYTGNTYYN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig heavy chain precursor V-D-J region (clone mAB 63VH) - human (fragment) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Decies: 10.00v-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999 C;Accession: S78052; S23717 R;Harindranath, N.
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A;Cross-references: EMBL:Z31383; NID:g472978; PIDN:CAA83258.1; PID:g940535 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P:15-97/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                        Length 105;
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A;Residues: 15-111 <HAW>
A;Crose-references: EMBL:X5441
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
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                                                                                                                                                                                            Score 497; DB 2;
Pred. No. 2.8e-37;
                                                                                                                                                                                                                                                                        6; Mismatches
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Search completed: November 9, 2005, 13:08:05 Job time: 13.0401 secs

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C,Accession: B26340
R;Kodaira, M.; Kinashi, T.; Umemura, I.; Matsuda, F.; Noma, T.; Ono, Y.; Honjo, T.
Nol. Biol. 190, 529-541, 1986
A;Title: Organization and evolution of variable region genes of the human immunoglobulin A;Reference number: A26340; MUID:87061007; PMID:3097326
A;Cross-references: EMBL:Z12371; NID:g32962; PIDN:CAA78241.1; PID:g32963
A;Note: designated DP-71
R;Sanz, I; Kelly, P; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A;Title: The smaller human V(H) gene families display remarkably little polymorphism.
A;Reference number: S09421; MUID:90059975; PMID:2511001
A;Accession: S09421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig heavy chain precursor V-II region (71-4) - human
C;Species: Homo sapiens (man)
C;Date: 05-Jun-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
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A;Cross-references: GB:X05711; NID:g33602; PIDN:CAA29183.1; PID:g296660
A;Note: the authors translated the codon GAG for residue 25 as Gln
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;1-19/Domain: signal sequence #status predicted <SIG>F;20-116/Product: IG heavy chain V region 71-4 #status predicted <MAT>F;34-116/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                        A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-97 <8A2>
A;Cross-references: EMBL:X56359
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <!MM>
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Pred. No. 1.3e-36;
5; Mismatches 1; Indels
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                                                                                                                                                                                                 A;Status: preliminary; translation not shown A;Molecule type: DNA
A;Residues: 1-97 <SAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 93.8%;
Matches 91; Conservative
                                                                                                                                                                                                                                                                                     A)Cross-references: EMBL:X56355
A;Note: designated 4.11
A;Accession: S12415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Introns: 16/1
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Class Carried Control of the Control

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November 9, 2005, 11:46:52 ; Search time 62.4712 Seconds (without alignments) 991.843 Million cell updates/sec
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                                                                                                                                                                                                                    US-10-660-357A-37
651
1 QVQLQESGFGLVKPSETLSL......WLVPDAFDIWGQGTMVSVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                  1612378
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                  1612378 segs, 512079187 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                Scoring table:
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                                                                                                                               Run on:
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| IES | Description | O6qmx1 homo sapien | рошо | Q7z379 homo sapien | Q6gmx6 homo sapien | homo | рошо | рошо | рошо | homo | | homo | P01824 homo | Q6nyh3 homo sapien | P06331 homo | рошо | Q6gmx5 homo sapien | рошо | ношо | homo | Q8izd7 homo | P01825 homo | рошо | homo | Q99m22 mus musculu | Q6mzx7 homo sapien | homo | m snm 55q190 | P01822 mus | Q65zil mus | | E P18532 mus musculu |
|-----------|-------------|--------------------|--------|--------------------|--------------------|-------|--------|--------|--------|--------|--------|--------|-------------|--------------------|-------------|--------|--------------------|--------|--------|--------|-------------|-------------|--------|--------|--------------------|--------------------|--------|--------------|------------|-----------------|------------|----------------------|
| SUMMARIES | ΩI | Q6GMX1 | Q9UL73 | Q7Z379 | Q6GMX6 | OSEX0 | Q6GMX7 | Q86SX2 | Q7Z374 | 095973 | Q96KX8 | Q6P4I8 | HV2F HUMAN | Q6NYH3 | HV2I HUMAN | Q8WUX4 | Q6GMX5 | Q9BU10 | Q96AA6 | Q9BQB8 | Q8IZD7 | HV2G_HUMAN | Q7Z3Y6 | QBTC63 | Q99M22 | Q6MZX7 | Q9UL75 | OGTBOS | HV46 MOUSE | 0652 <u>1</u> 1 | HV47 MOUSE | HV61_MOUSE |
| | DB | 7 | ~ | ~ | ~ | 7 | ~ | ~ | 7 | ~ | ~ | ~ | - | ~ | Н | ~ | ~ | ~ | ~ | ~ | ~ | - | N | 7 | ~ | ~ | 7 | ~ | Н | ~ | H | - |
| | Lengt | 476 | 119 | 478 | 465 | 620 | 477 | 139 | 492 | 150 | 496 | 576 | 129 | 478 | 146 | 595 | 597 | 597 | 625 | 597 | 130 | 117 | 116 | 473 | 479 | 476 | 122 | 136 | 137 | 262 | 113 | 116 |
| d | 양선 | 82.6 | 78.8 | 77.6 | 77.5 | 77.3 | 77.2 | 76.0 | 74.8 | 74.6 | 72.9 | 71.5 | 71.0 | 69.4 | 69.0 | 68.8 | 68.8 | 68.8 | 68.8 | 68.2 | 67.8 | 9 | 64.6 | 64.3 | 62.4 | 61.8 | 61.7 | Ч | 8.09 | 60.2 | 60.1 | 56.9 |
| | Score | 538 | 513 | 505.5 | 504.5 | 503.5 | 502.5 | 495 | 487 | 485.5 | 474.5 | 465.5 | 462 | 452 | 449.5 | 448 | 448 | 448 | 448 | 4 | 441.5 | 431 | 420.5 | 418.5 | 406 | 402 | 401.5 | σ | 396 | 392 | 391 | 370.5 |
| | | | 7 | e | 4 | ស | 9 | 7 | 8 | σ | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 |

| BUM | | | | | | | | | | | | | homo sapien |
|------------|-----------------|------------|--------|------------|------------|------------------------|--------|--------|--------|--------|--------|--------|-------------|
| P18531 | Q91x92 | P18533 | Q99ng4 | P01819 | P20957 | Q811u5 | O8wuk1 | Q6pja4 | Q9u174 | Q6in78 | Q652C9 | Q9u191 | 09u196 |
| HV60 MOUSE | Q91X <u>9</u> 2 | HV62 MOUSE | Q99NG4 | HV43 MOUSE | HV02 XENLA | <u>0811</u> <u>0</u> 5 | QBWUK1 | Q6PJA4 | Q9UL74 | Q61N78 | Q652C9 | Q9UL91 | Q9UL96 |
| - | N | Н | ~ | ч | ч | N | N | ~ | ~ | ~ | N | ~ | ~ |
| 116 | 182 | 117 | 121 | 144 | 135 | 118 | 613 | 470 | 118 | 466 | 240 | 118 | 121 |
| | * | | | | | | | | | | | | |
| | 56.8 | 56.2 | 55.4 | 54.2 | 53.8 | 52.8 | 52.8 | 52.5 | 52.1 | 52.1 | 51.2 | 50.9 | 50.8 |
| 56.8 | | | | | | | | | | | | | |

ALIGNMENTS

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01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp686K04218 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                            478 AA; 51620 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 VSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                       59 YNPSLKSRVTVSVDTSKNQFSLKLNSVTAADTAVYYCARDPGQW-----LVPDAFDIWGQ 113
                                                                                                                                                                           80 YNPSLKSRVTISLDTSKNQFSLKOMSVTAADTAVYFCAR-AGVWGSFRSWAIDGFNIWGQ 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PSLKSRVTISVDRSKNQFSLKIJSLIAADJAVYFCAR-LSNW-GPYYFDYWGQGTLVTVS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PSLKSRVTVSVDTSKNOFSLKLNSVTAADTAVYYCARDPGOWLVPDAFDIWGOGTMVSVS 120
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                                                                                                                20 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGDYYWSWIRQPPGKGLEWIGYIYYSGSTY
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                                                                                                  1 QVQLQESGPGLVKPSETLSLTCTVSGGSIST -- YYWSWIRQPPGKGLEWIGYIYYTGNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                       8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.8%; Score 513; DB 2; Length 119; 81.8%; Pred. No. 5e-43; ive 8; Mismatches 12; Indels
                                        Length 476;
                                                                                                                                                                                                                                                                                                                                 Q9UL73;
Q9UL73;
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last amocation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                     6; Indels
Hypothetical protein.
SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;
                                        82.6%; Score 538; DB 2;
81.2%; Pred. No. 7.5e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clin. Immunol. Immunopathol. 87;184-192(1998).
EMBL; ARD036041; AAD56277.1; -.
FIR; PH0876; PH0876.
PIR; S12416; S12416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          478 AA.
                                                                                                                                                                                                                                                                                                                        119 AA
                                                                    10; Mismatches
                                                                                                                                                                                                                                                                                                                        PRT;
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InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
SWART; SW00406; IGv. 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                    Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                    GTMVSVSS 121
                                                                                                                                                                                                                                     ||||:|||
GTMVTVSS 146
                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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ID Q72379
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Matches
                                                                                                                                                                                                                                                                                          RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 YNPSLKSRVTVSVDTSKNQFSLKLNSVTAADTAVYYCARDPGQWLVPDAFDIWGQGTMVS 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Primary B-Cells;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Straubsberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Rlausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brossk S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQESGPGLVKPSETLSLTCTVSGGSIST--YYWSWIRQPPGKGLEWIGYIYYTGNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapa
                                                                                                                                                                                                         TISSUE=Human rectum tumor; Bloecker H., Boecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A., Bloecker H., Boecher M., Wiemann S.; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BX538066; CAD97996.1; -. HSSP; P01820; 1G7J.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 th 77.6%; Score 505.5; DB 2; Length 478; Similarity 76.4%; Pred. No. 1.2e-41; 94; Conservative 18; Mismatches 6; Indels 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4AFCB541F3217CA1 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     465 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR00110; Ig-like.
InterPro; IPR003597; Ig c1.
InterPro; IPR003596; Ig WHC.
InterPro; IPR003596; Ig V.
Pfam; PF07654; C1-set; Z.
SMART; SM0406; IGV, I.
PROSITE; PS00290; IG LIKE; 4.
PROSITE; PS00290; IG WHC; UNKNOWN_Z.
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Os-JUL-2004 (TrEMBLrel. 27, La 05-JUL-2004 (TrEMBLrel. 27, La Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77.38;
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                                                                                                                                                                                                                                                                                         IISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q6GMX7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q6GMX7
           요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PSLKSRVTVSVDTSKNOFSLKLNSVTAADTAVYYCARDPGQWLVPDAFDIWGQGTMVSVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 PSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCAR - GRFTY - - - FDYWGQGTLVTVS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPAGKGLEWIGRIYTSGSTNYN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLQESGPGLVKPSETLSLTCTVSGGSISTYYWSWIRQPPGKGLEWIGYIYYTGNTYYN 60
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FACINGLY B. Cells, MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Parange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NOBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 465;
                                                                                                                                                                                                                                                                                              Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

R EMBL; BC073766; AAH73766.1; -.

R InterPro; IPR00110; 19.

R InterPro; IPR00110; 19.

R InterPro; IPR00110; 19.

R InterPro; IPR0013597; 19.c1.

R InterPro; IPR0013596; 19.w.

R Pfam; PF07654; C1.set; 3.

R Pfam; PF07067; 19; 4.

R SMART; SM00409; IG; 2.

R SMART; SM00409; IG; 1.

R PR051TE; PS50835; IG_LIKE; 4.

R PROSITE; PS50835; IG_LIKE; 4.

R PROSITE; PS00290; IG_MIC, IUNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           il protein.
465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 504.5; DB 2;
Pred. No. 1.5e-41;
8; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.5%;
82.6%;
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                            cDNA sequences.
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Matches 100, Conservative
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                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IGHM protein.
Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                  Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical
                                                                                                                                                                            and mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
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      8
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61 PSLKSRVTVSVDTSKNQFSLKLNSVTAADTAVYYCARDPGQWLVPD-AFDIWGQGTMVSV 119
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glbbs R.A., Fahey J., Helton E., Ketreman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bourfard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buttow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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ب
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | InterPro; IRR001559; IG. | InterPro; IRR001559; IG. | InterPro; IRR001559; IG. | InterPro; IRR001509; IG. | InterPro; IRR0013006; IG. | InterPro; IRR0013006; IG. | InterPro; IRR001306; IG. | InterPro; IRR00165; IG. | InterPro; IRR00165; IG. | Id. | I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011857; AAH11857.2; -.
PIR; S15590; S15590.
HSSP; P01820; 167J.
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Last annotation update)
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Pred. No. 2.6e-41;
8; Mismatches 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                477 AA.
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92

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59 YNPSLKSRVTVSVDTSKNQFSLKLNSVTAADTAVYYCAR---DPGGWLVPDAFDIWGQGT 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLQESGPGLVKPSETLSLTCTVSGGSISTYYWSWIRQPPGKGLEWIGYIYYTGNTYYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Human rectum tumor;
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A., Pobo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX538077; CAD98001.1;
HSSP; P01820; 1G7J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
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                                                                                                                                                                                                                                                                                                                                            76.0%; Score 495; DB 2; Length 139; 93.9%; Pred. No. 3.6e-41; ive 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;
                                                                                                                                                                                                                                                                                7D1E2302410E4F8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARD 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q72374 PRELIMINARY; PRT; 492 AA. Q72374; 01-CCT-2003 (TrEMBLrel. 25, Created) 01-CCT-2004 (TrEMBLrel. 25, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Hypothetical protein DKFZp686C02218 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PSLKSRVTVSVDTSKNQFSLKLNSVTAADTAVYYCARD 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR00110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF07654; C1-set; Z.
SMART; SM0406; IGv.
PROSITE; PS09355; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                        NON TER 1 _1
SEQUENCE 139 AA; 15573 MW;
                                HISSP, PRO1820, 167J.
INTERPRO, IPR00710; IG-like.
INTERPRO, IPR00356; IG-V.
SWART, SW00406; IGV; I-PROSITE; PS50835; IG_LIKE; I-PROSITE;         EMBL; BX248300; CAD62627.1;
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 93.99
Matches 92, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein
NON TER 1
SEQUENCE 492 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|:|||
147 LVTVSS 152
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
Q7Z374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQTAGKGLEWIGYISHSGSTTYN 79
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hulyk S.W., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQESGPGLVKPSETLSLTCTVSGGSISTYYWSWIRQPPGKGLEWIGYIYYTGNTYYN
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUNA-2004 (TrEMBLrel. 26, Last annotation update)
Full-length cDNA clone CSODLO04M19 of B cells (Ramos cell line) of Homo sapiens (human) (Fragment).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC03765; AAH73765.1;
InterPro; IPR00110; Ig-11ke.
InterPro; IPR001599; Ig c1.
InterPro; IPR003596; Ig MHC.
InterPro; IPR003596; Ig WHC.
InterPro; IPR003596; Ig WHC.
InterPro; IPR003596; Ig W.
Pfam; PF07654; C1-set; Z.
Pfam; PF07654; C1-set; Z.
Pfam; PR00409; IG; 4.
SMART; SM00409; IG; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 77.2%; Score 502.5; DB 2; Length Local Similarity 81.0%; Pred. No. 2.5e-41; les 98; Conservative 9; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUB=B cells;
Li W.B., Gruber C., Jessee J., Polayes D.;
Submitted (FBE-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genoscope;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00230; IG_MHC; UNKNOWN_2.
Hypotherical protein.
SEQUENCE 417 AA; 51631 MW; 9FES9C09CSOCFF85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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74.8%;
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                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 74.89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=IGHD;
Homo sapiens (Human).
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TLVTVSS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 TMVSVSS 121
                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IGHD protein.
                                                                                                                                          TISSUE=Lung;
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Q6P4I8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 YNPSLKSRVTVSVDTSKNOFSLKLNSVTAADTAVYYCARDPGOWLVPDAFDIWGGGTMVS 118
                                                                                                                                                                                                                                                                                                                                                                                                                     20 QLQLQESGPGLVKPSETLSLSCTVSGGSISSTNYYWGWIRQPPEKGLEWIGSLHNSGSDY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Klausen R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.K., Stapleton M. Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz B. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Braak S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                       OVQLQESGPGLVKPSETLSLTCTVSGGSIST - - YYWSWIRQPPGKGLEWIGYIYYTGNTY
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleogtomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                       74.6%; Score 485.5; DB 2; Length 150; larity 77.2%; Pred. No. 3.4e-40; Conservative 11; Mismatches 10; Indels 7
                                                                                                                                                                                                                                                                                              Potential.
VH4 heavy chain variable region.
                                                                                                                                                        Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.,
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF103795, AAC79084.1;
PIR, 331673, S31673.
PIR, S78056, S78056.
                                                                                                                                                                                                                                                                                                                                 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;
                                        01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) WH4 heavy chain variable region precursor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
         150 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      496 AA.
                                (TrEMBLrel. 10, Created)
         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                 InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
        PRELIMINARY;
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                                                                                                                                                                                                                                                                                             19
>150
                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                        HSSP; P01820; 1G7J
                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                          NCBI_TaxID=9606;
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                                01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                               98;
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Best Local S
Matches 95
                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                            Name=IGM
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                   095973;
                                                                                                                                                                                                                                                                                   Signal.
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MEDLINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
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Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
"Generation and initial analysis of more than 15,000 full-length human
and mouse CDNA sequences.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 OLOLOESGPGLVKSSETLSLTCTVSGGSISSSSYYWGWIROPPGKGLEWIANTYYSGITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 YNPSLKSRVTVSVDTSKNQFSLKLNSVTAADTAVYYCARD----PGQWLVPDAFDIWGQG
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Pred. No. 1.5e-38;
9; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: BCO16.59; AAH16169.1; --
HSSP; PO1876; 10W0.
HRSP; P01876; 10W0.
InterPro; IPR001710; 1g-1ike.
InterPro; IPR001597; 1g-c1.
InterPro; IPR001597; 1g-q.
InterPro; IPR001596; 1g-WHC.
Pfam; PP07644; C1-8et; 2.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWARTE; SMUNAUG; 18.4.
PROSITE; PSS0835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
CERNIENCE 496 AA; 53391 MW; D346929849040D69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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TISSUE=Blood;
                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                         Query Match
                                                                                                                                                                NON TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q6NYH3
                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
      ST TY BRANT TO S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 NPSLKSRVTVSVDTSKNOFSLKLNSVTAADTAVYYCARDPGQWLVPDAF----DIWGQGT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 QVQLQESGPGLVKPSGTLSLTCAVSGGSISSSNWWSWVRQPPGKGLEWIGEIYHSGSTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLQESGPGLVKPSETLSLTCTVSGGSI-STYYWSWIRQPPGKGLEWIGYIYYTGNTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.; "Complete amino acid sequence of the delta heavy chain of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunoglobulin D.";
Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
-!- MISCELLANEOUS: This chain was isolated from an IgD myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 576;
                                                                                                                                                                                                                 A Straubberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC063384; AAH63384.1; -.
HSSP; PO1820; LA7N.
R InterPro; IPR001359; Ig.
R InterPro; IPR001359; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003596; Ig.
R Pfam; PF00647; Ig.
R Pfam; PF00647; Ig. 1.
R SMART; SM00409; IG.1.
R SMART; CM00409; IG.1.
R SMART; SM00409; IG.1.
R PROSITE; PS000290; IG.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Contains 1 immunoglobulin-like domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.5%; Score 465.5; DB 2;
73.8%; Pred. No. 1.4e-37;
ive 12; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
19 heavy chain V-II region WAH.
Homo sapiens (Human).
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HSSP; P01820; 1G7J.
GlycosuiteDB; P01824; --
GO; GO:0005876; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=8222235; PubMed=6806818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 73.8%
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 TVTVSS 146
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ID HV2F HUMAN
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altachul S.F., Jeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altachul S.F., Jeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altachul S.F., Jeberg B., Berow K.H., Schaefer C.F., Bhat N.K.,
Antachul S.F., Jeberg B., Berow K.H., Schaefer C.F., Bhat N.K.,
Antachul S.F., Jermer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A. Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A. Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A. Marta M.J., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A. Jones S.J., Marra M.A.,
B. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 YNPSLRGRVTISVDTSRNQFSLNLRSMSAADTAMYYCARGNPPPYYDIGTGSDDGIDVWG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 YNPSLKSRVTVSVDTSKNOFSLKLNSVTAADTAVYYCAR-DPGOWL-----VPDAFDIWG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLQESGPGLVKPSETLSLTCTVSGGSI - - STYYWSWIRQPPGKGLEWIGYIYYTGNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                               71.0%; Score 462; DB 1; Length 129; 69.0%; Pred. No. 6.2e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                        129 AA; 14117 MW; D5D53D47ABE51319 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
           InterPro; IPR001110; Ig-like.
InterPro; IPR001110; Ig-like.
InterPro; IPR001396; Ig-v.
Pfam; PF00047; ig; 1.
SNART; SN00406; IGv; 1.
PROSITE; PSS0935; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin V region.
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Mismatches
GO; GO:0006955; P:immune response; NAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (FEB-2004) to the
EMBL; BC066594; AAH66594.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 QGTTVHVSS 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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MEDLINE-22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Felngold E.A., Grouse L.H., Derge J.G.,

Alusener R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S. I., Wang J., Hsieh F.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Girmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

Jones S.J., Marra M.A.;

Jones S.J., Marra M.A.;

Jones S.J., Marra M.A.;

Jones J. J. Holton E. J. More than 15,000 full-length human
                                                                                    21 QVQLQQWGAGLVKPSETLSLTCAVFGGSFSGYYWSWIRQPPGRGLEWIGEINHSGSTNYK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLQESGPGLVKPSETLSLTCTVSGGSISTYYWSWIRQPPGKGLEWIGYIYYTGNTYYN
                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
Hypothetical protein.
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     al protein.
595 AA; 65290 MW; 0D4B50776545714E CRC64;
                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00406; LCC, LIKE; 5. PROSITE; PS00290; IC_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                              PRT;
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Submitted (DEC-2001) to the EN EMBL; BC019235; AAH19235.2; -.
PIR; G34964; G34664.
HSSP; P01861; 1ADQ.
Pfam; PR07664; C1-set; 4.
SMART; SM00409; IG; 2.
SMART; SM00406; IGc1; 4.
                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
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                                                                                                                                                                              141 TVTVSS 146
                                                                                                                                          116 MVSVSS 121
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                                                                                                                                                                                                                                                                                                                                    20 QVDLQESGPGLVKPSETLSLTCSVSGDSIASYYWSWIRKSPQGGMEWIGYIFHSGTTLYN
                                                                                                                                                                                                                                                                                                                  QVQLQESGPGLVKPSETLSLTCTVSGGSISTYYWSWIRQPPGKGLEWIGYIYYTGNTYYN
                                                                                                                                                                                                                                                                            Gaps
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PIN; A02101, GiHUH2.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
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Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig heavy chain V-II region ARH-77. V segment.
J segment.
J segment.
By similarity.
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                                                                                                                                                                                                                                    69.4%; Score 452; DB 2; Length 478; 71.1%; Pred. No. 2.5e-36; ive 16; Mismatches 17; Indels
                                                                                                                                                                                                478 AA; 51856 MW; 5F8B98F60F077256 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16228 MW; 8D7FD52BB218171F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V-II region ARH-77 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 AA.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF07654; C1-set; Z.
SWART; SW00409; IG; 4;
SWART; SW00406; IG; 1;
SWART; SW00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
HYDOTHEL; PS099; IG_MHC; UNKNOWN_Z.
HYDOTHELIAI protein.
SEQUENCE 478 AA; 51856 MW; SF8B98F6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
FROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                      1 Similarity 71.1%
86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 71.4%
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 S 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HV2I HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138
                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQÜENCE
                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HV2I_HUMAN
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1 QVQLQESGPGLVKPSETLSLTCTVSGGSISTYYWSWIRQPPGKGLEWIGYIYYTGNTYYN 60

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Gaps

Length 595; 17; Indels 9

86

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        Qy
        61 PSLKSRVTVSVDTSKNQFSLKLANSVTAADTAVYXCAR-----DPGQMLVPD---AFDIWG 112

        Db
        87 PSLKSRVTISVDTSKKQLSLKLSSVNAADTAVYYCARVITRASPG----TDGRYGMDVWG 142

        Qy
        113 QGTWVSVSS 121

        Pb
        143 QGTTVTVSS 151

        Db
        143 QGTTVTVSS 151

        Search completed: November 9, 2005, 13:05:52

        Job time: 63.4712 secs
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